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Developing ethical and transparent artificial intelligence algorithms to support decision making in healthcare based on brain research and personal care events of patients

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Abstract:

We propose a new research methodology that develops ethical and transparent artificial intelligence algorithms to support decision making in healthcare. This development relies on a diverse statistical and data analysis methodology based on real-life data gathered in brain research and care events of different patient groups. The proposed new research methodology is created, developed and carried out in a broad international multidisciplinary research collaboration with various patient and disabled people's groups, healthcare professionals, educational institutions, and laboratory measurements of experimental brain research conducted at a biomedical research institute. The proposed new research methodology is motivated by the previous research that has given successful classification results with various bio-inspired artificial intelligence algorithms, based on unsupervised learning (such as various clustering algorithms) and supervised learning (such as artificial neural network algorithms) that are implemented following the structural and functional principles of real-life living biological tissues.

Keywords: artificial intelligence; care decision making; brain research; neuroscience; learning; algorithm; personalized care; care event; patient; disabled; the patient's rights; microbiological measurement; human-computer interaction measurement

1. Background

Our proposed new research methodology develops ethical and transparent artificial intelligence algorithms to support decision making in healthcare based on brain research and personal care events of different patients. Our proposed new research methodology relies on various iteratively evolving experimental programming and testing procedures that employ diverse multidisciplinary knowledge resources and multidisciplinary research collaboration with people representing different backgrounds and complementing expertise.

We consider that a specific novelty and contribution of our proposed new research methodology is how our research proposal gets inspiration and is motivated by various previous research results of multidisciplinary domains (among others psychology, cognitive science, neuroscience, biology, perception and affectivity studies, health surveys, human-computer interaction

research, usability, machine learning and artificial intelligence) and how we link them with our current research proposal.

Since our expected new research results offer new practical artificial intelligence algorithm formulations it is natural that our development work exploits various fundamental advanced programming techniques, among others including also machine learning. Machine learning is a methodology that aims at learning to recognize statistical patterns in data, typically relying on either an unsupervised or supervised approach. Various alternative machine learning models have been developed for both general and specific purposes, and among these models artificial neural networks have achieved a high accuracy in classification tasks (Gehrmann et al., 2018).

Our proposed new research methodology develops the new artificial intelligence algorithms by taking influence from the broad spectrum of the previously developed clustering algorithms, artificial neural network models, other deep learning architectures and their various hybrids, emphasizing adaptation of such solutions that can address the specific circumstances of the phenomena currently under investigation (Karim et al., 2021) .

Among various artificial neural network models convolutional neural network models have been successfully applied in classification of medical literature, patient records, clinical narratives and patient phenotypes (Zhao et al., 2017; Gehrmann et al., 2018; Rojas-Barahona et al., 2018; Shickel et al. 2020; Hughes et al., 2017; Yao et al. 2019; Qing et al., 2019), and it achieves good results with both image and textual input data (Bhandare et al., 2016).

Our proposed new research methodology is motivated and takes inspiration from the broad review and comparative analysis of Karim et al. (2021) about unsupervised deep learning-based clustering analysis techniques for bioinformatics research. The review and comparative analysis of Karim et al. (2021) especially focuses on parallel experimental setups carrying out a comparison of clustering performance of several deep learning-based clustering approaches in the three subdomains of bioinformatics use cases that are bioimaging, cancer genomics and biomedical text clustering.

The review and comparative analysis of Karim et al. (2021) mentions that despite of the great amount of biological data that is currently generated from diverse medical devices, the applications of clustering are still limited concerning genomic medicine and microarray analysis focusing on gene clustering with a limited amount of data (Jaskowiak et al., 2013; De Souto et al., 2008). In addition, according to Karim et al. (2021), in the domains of bioimaging, human-genetics, plant and animal ecology, biomedical texts and genomic data the potential of cluster analysis is not fully explored and is still in an early development stage when compared to investigations carried out so far for for example microarrays (for example using RNA-Seq technology for gene expression-level measurements) (Jaskowiak et al., 2018). A need for further developing and application of clustering analysis is motivated, according to Karim et al. (2021), also by the currently emerging bioinformatics research domain concerning single-cell experiments in which clustering is a crucial part of the analysis (Eraslan et al., 2019).

Our proposed new research methodology is also motivated by the alternative approaches developed for comparisons between biological data clustering algorithms that can be often done based on the quality of produced clusters that can be measured in respect to either a known classification scheme or in respect to some theoretical standards (Lu et al., 2019).

Furthermore, our proposed new research methodology is motivated and takes inspiration from the previous research that has proposed various ways to explain how the brain learns and uses models (among others, Behrens et al. (2018), Gläscher et al. (2010), Kolling et al. (2016), O'Reilly & Frank (2006)), and it has been estimated (Botvinick et al., 2019) that a suitably holistic and promising model is a computational Meta-Reinforced Learning model (Meta-RL model, Wang et al. (2016), Wang et al. (2018) and a resembling proposal of Duan et al. (2016) at around the same time).

The previous neural research has identified that the episodic memory circuits can return for a reuse the activation patterns of the cerebral cortex (Ritter et al., 2018b), including the regions supporting the working memory, and also identified a connection between the episodic and model-based learning (Vikbladh et al., 2017). Motivated by this it has been proposed an episodic Meta-Reinforced Learning model (episodic Meta-RL model, Ritter et al. (2018a), Ritter et al. (2018b),

Santoro et al. (2016), Wayne et al. (2018), Graves et al. (2016), Vikbladh et al. (2017)) which can be implemented with a reinforcement learning method so that the model can return for reuse the previous information about the task (Santoro et al. 2016; Wayne et al., 2018; Graves et al., 2016). This episodic Meta-RL model can be considered to produce inductive bias especially based on the architectural and algorithmic formalisms (Botvinick et al., 2019) which can be biologically motivated as a slow learning process generated by the evolution (Botvinick et al., 2019). On the other hand, the ordinary Meta-RL model can be considered to produce inductive bias especially based on learning formalisms (Botvinick et al., 2019).

An important motivator for our proposed new research methodology is also that the patient's rights have gained increasing protection by legislation in the European region, Finland being among the pioneers (Lahti, 2012; Townend et al., 2016), and European Commission has proposed artificial intelligence regulation (European Commission, 2021a). The European Commission's Coordinated Plan on Artificial Intelligence 2021 Review (European Commission, 2021b) recognizes the importance of developing application of artificial intelligence (AI) in various domains of health and healthcare, including also supporting humans in clinical decisions and treatment choices as well as improving analysis of health images, laboratory and histological data, diagnostic accuracy, and access to healthcare.

The proposed new research project methodology is actively created, developed and carried out by Lauri Lahti and it benefits from a broad international multidisciplinary research collaboration with various patient and disabled people's groups, healthcare professionals, educational institutions, and laboratory measurements of experimental brain research conducted at a biomedical research institute.

Lauri Lahti's research contributions in the learning-oriented research domains include, among others, developing a system supporting the interpretation of texts for the visually impaired persons (Lahti & Kurhila, 2007), developing a method for computer-assisted learning with an adaptive guidance in knowledge networks (Lahti, 2009; Lahti, 2011; Lahti, 2013; Lahti, 2015), developing a method to support diagnostics and decision making in healthcare by modular methods of computational linguistics (Lahti, 2016), developing a method to identify distinctive topic patterns in health-related online discussions (Lahti et al., 2018), developing a method to support care by interpretation of expressions about the patient experience with machine learning (Lahti, 2017; Lahti, 2018; Lahti, 2020), developing a method to link statistical patterns of human interpretations to machine learning results to enable better human-understandable machine learning models (Lahti, 2021a; Lahti, 2021b; Lahti, 2022a), and developing patient-driven artificial intelligence based on personal rankings of care decision making steps (Lahti, 2022b).

So far, in the previous and ongoing research collaboration concerning experimental brain research Lauri Lahti has carried out diversely different data analyses by using statistical and algorithmic methods developed by himself. Lauri Lahti has, among others, analyzed the size of brain ventricles (Minkeviciene et al., 2019) and the co-localization of two different molecules in images recorded with a superresolution technique (Abouelezz et al., 2020; Lahti 2021c; Micinski et al., 2022), and Lauri Lahti is a co-author in these just mentioned three published peer-reviewed research articles.

2. Method

2.1 General description and main research questions

Since developing artificial intelligence that can address complex dependencies in real-life circumstances requires handling large entities of high-dimensional data, a traditional challenge is how to enable sufficient transparency for the human evaluators so that the generated artificial intelligence solutions and their motivation can be sufficiently clearly represented, explained, interpreted and evaluated in a well human-understandable way (European Commission, 2021a; European Commission, 2021b).

Addressing this traditional challenge (i.e., how to enable transparent, human-understandable, explainable artificial intelligence) is one of the major contributions in our proposed new research methodology. We address this traditional challenge by exploiting an extensive combination of complementing knowledge sources, data analysis techniques, iterative programming and testing, and experimental setups, motivated by the previous research (Karim et al., 2021; Lu et al., 2019; Botvinick et al., 2019; Wang et al., 2016; Wang et al., 2018; Duan et al., 2016; Ritter et al. 2018a; Abd-Alrazaq et al., 2020; Laranjo et al., 2018; Sinclair et al., 2020a; Lahti, 2022a; Lahti, 2022b).

To address this traditional challenge, an important new methodological approach that we have designed specifically for our proposed new research methodology, based on the previous research (Karim et al., 2021; Lu et al., 2019; Botvinick et al., 2019; Wang et al., 2016; Wang et al., 2018; Duan et al., 2016; Ritter et al. 2018a; Abd-Alrazaq et al., 2020; Laranjo et al., 2018; Sinclair et al., 2020a; Lahti, 2022a; Lahti, 2022b), is that we carry out extensive series of alternative microbiological and human-computer interaction measurements, data pattern modeling and experimental clustering and deep learning-based computational analysis concerning the fundamental processes of biologically naturally emerging classifications and decision making steps of the human mind in our carefully designed new experimental setups.

Our proposed research methodology relies on four complementing *major research goals* that have interconnecting influences. Firstly, we use classification mechanisms identified in the data of microbiological experiments of brain research to develop, test and validate new artificial intelligence algorithms (*biology-based algorithms*) to be used for analyzing and classification of microbiological measurements of brain research. Secondly, we use these new artificial intelligence algorithms developed based on the data of microbiological experiments of brain research to carry out testing and validation of their usability for analyzing and classification of data of personal care event measurements concerning care decision making steps. Thirdly, we use classification mechanisms identified in the data of personal care events of different patients concerning care decision making steps to develop, test and validate new artificial intelligence algorithms (*care path-based algorithms*) to be used for analyzing and classification of personal care event measurements concerning care decision making steps. Fourthly, we use these new artificial intelligence algorithms developed based on the data of personal care events of different patients concerning care decision making steps to carry out testing and validation of their usability for analyzing and classification of data of microbiological measurements.

In the proposed new research methodology, we focus on developing, testing and validation of various alternative artificial intelligence algorithm formulations concerning general principles of our proposed new methodology and describe an illustrative empirical application of the methodology with our gathered experimental data. The above-mentioned previous research and current challenges motivate us now to address the following two *main research questions* (RQ):

> **RQ1:** What kinds of new artificial intelligence algorithms (*biology-based algorithms*) can be developed, tested and validated based on the classification mechanisms identified in the data of microbiological experiments of brain research so that they can be successfully used for analyzing and classification of microbiological measurements of brain research and data of personal care event measurements concerning care decision making steps.
>
> **RQ2:** What kinds of new artificial intelligence algorithms (*care path-based algorithms*) can be developed, tested and validated based on the classification mechanisms identified in the data of personal care event measurements concerning care decision making steps so that they can be successfully used for analyzing and classification of personal care event measurements concerning care decision making steps and microbiological measurements of brain research.

2.2 Development and evaluation of new artificial intelligence algorithms

The proposed new research methodology is motivated by the previous research that has identified various classification mechanisms and algorithms that are inherently present and measurable in diverse structures and functions of biological processes (Karim et al., 2021; Lu et al., 2019; Botvinick

et al., 2019; Wang et al., 2016; Wang et al., 2018; Duan et al., 2016; Ritter et al. 2018a; Abd-Alrazaq et al., 2020; Laranjo et al., 2018; Sinclair et al., 2020a; Lahti, 2022a; Lahti, 2022b). Various computational architectures and measurable parameter values recommended by the previous research (Karim et al., 2021; Lu et al., 2019; Botvinick et al., 2019; Wang et al., 2016; Wang et al., 2018; Duan et al., 2016; Ritter et al. 2018a; Abd-Alrazaq et al., 2020; Laranjo et al., 2018; Sinclair et al., 2020a; Lahti, 2022a; Lahti, 2022b) are used in the proposed new research methodology as building blocks of the new artificial intelligence algorithms and to carry out cross-evaluations about the applicability of the algorithms in various use contexts.

Our proposed new research methodology is motivated and takes inspiration from the broad review and comparative analysis of Karim et al. (2021) about unsupervised deep learning-based clustering analysis techniques for bioinformatics research. The review and comparative analysis of Karim et al. (2021) especially focuses on parallel experimental setups carrying out a comparison of clustering performance of several deep learning-based clustering approaches in the three subdomains of bioinformatics use cases that are bioimaging, cancer genomics and biomedical text clustering.

The previous research (Karim et al., 2021; Oyelade et al., 2016; Masood & Khan, 2015; Thalamuthu et al., 2006; Estivill-Castro, 2002) has proposed various clustering analysis approaches including hierarchical clustering (Søorlie et al., 2001), centroid-based clustering (such as K-means (MacQueen, 1967), partitioning around medoids (K-medoids) (Kaufman & Rousseeuw, 1990)), distribution-based clustering (DC) (MacQueen, 1967), density-based clustering (DC1) and self organizing maps (SOMs) (Kohonen, 1998). In addtion, the previous research (Gan et al., 2007) has proposed for example probabilistic clustering, grid-based clustering, spectral clustering and non-negative matrix factorization.

The previous research, according to Karim et al. (2021), has proposed various deep learning-based clustering analysis approaches that can be grouped into two major types: The first type consists of pipeline methods for learning a representation using deep neural network architectures and clustering using a machine learning-based clustering algorithm. The second type consists of single-model methods for end-to-end clustering. The pipeline methods for learning a representation using deep neural network architectures can be formulated with for example multilayer perceptrons (MLPs), convolutional neural networks (CNNs), deep belief networks (DBNs), generative adversarial networks (GANs) (Goodfellow, 2016), variational autoencoders (VAEs), denoising autoencoders (DAEs) and adversarial autoencoders (AAEs) (Makhzani et al., 2015).

Our proposed new research methodology is also motivated by the alternative approaches developed for comparisons between biological data clustering algorithms that can be often done based on the quality of produced clusters that can be measured in respect to either a known classification scheme or in respect to some theoretical standards (Lu et al., 2019; Jay et al., 2012; Chen et al. 2002; Datta & Datta, 2006).

In respect to the known classification scheme the comparison can use domain-specific knowledge (such as ontological enrichment (Subramanian et al., 2005; Huang et al., 2007), geographical alignment (De Vries et al., 2010) or legacy delineation (Liu & Samal, 2002)).

In respect to some theoretical standards the comparison can use statistical quality metrics and a typical choice is to use the cluster density. Furthermore, various other metrics include for example the modularity (Newman, 2006) (i.e., measuring the density of connections within clusters in contrast with the density of connections between clusters), the clustering coefficient (Luce & Perry, 1949; Wasserman & Faust, 1994), (i.e. the proportion of triplets for which transitivity holds), and the silhouette coefficient (Rousseeuw, 1987) (i.e., how similar a node is to its own cluster in comparison with other clusters), and the adjusted rand index (Rand, 1971), the homogeneity (Hansen & Jaumard 1997), the completeness (Hubert, 1973), the V-measure (Rosenberg & Hirschberg, 2007), and the adjusted mutual information (Vinh et al., 2010).

The proposed new research methodology is motivated by our previous research (Lahti, 2022a) in which we proposed and experimentally motivated a new methodology that enabled us to identify in interpretation tasks done by humans how statistically significant rating differences were linked to machine learning results thus helping to develop better human-understandable machine

learning models. Furthermore that previous research (Lahti, 2022a) provided empirical evidence about the applicability of machine learning to support interpretation of the need for help in the patient's expressions. Explaining in more detail, the machine learning experiments of that previous research (Lahti, 2022a) showed the applicability of a baseline convolutional neural network model to support detecting the need for help in the patient's expressions in respect to groupings relying on the answer values of each background question.

Extending on the foundation and promising results of our previous research (Lahti, 2022a), our subsequent research (Lahti, 2022b) gathered (reported in Lahti (2022b)) from diverse population groups (n=1075) self-ratings for 437 expression statements about healthcare situations in respect to the interpretation dimension of "the need for help", "the advancement of health", "the hopefulness", "the indication of compassion" and "the health condition", and 45 answers about the person's demographics, health and wellbeing, also the duration of giving answers. These self-rated expression statements enable analyzing representations of decision making steps in healthcare situations in respect to various interpretation task entities, interpretation dimensions and respondent groupings.

Thus in our previous research (Lahti, 2022b) we proposed a new methodology, questionnaire data and its statistical patterns which enabled analyzing with self-rated expression statements the representations of decision making steps in healthcare situations and their chaining, agglomeration and branching in the large knowledge entities of personalized care paths, such as patient records, patient diaries, care plans and care guidelines. Identified differences and dependencies in personal interpretation ratings and their durations in respect to the person's background (reported in Lahti (2022b)) enable building new artificial intelligence solutions that can manage to interpret increasingly complex linguistic structures of decision making steps when helping to address the patient's needs and preferences concerning his/her care.

Our proposed new research methodology develops new algorithmic solutions that are tailored to help people using these solutions to carry out ethical decision making, thus taking carefully into account the interests and rights (among others, the human rights and patient's rights) of the people concerned and affected by the current decision making. Therefore the development of the new algorithmic solutions is aimed to address the diversity of personal needs and preferences in varied life situations and also to support equality and empowerment of challenged people.

Emphasizing the above-mentioned issues about addressing the patient's rights, European Union (EU) data privacy regulation and European Commission's proposal for artificial intelligence regulation, ethical guidelines, key requirements and the self-assessment list to enable trustworthy artificial intelligence (Lahti, 2012; Townend et al., 2016; European Commission, 2019, 2020, 2021a, 2021b), our current research is actively advancing multidisciplinary research collaboration efforts to develop trustworthy artificial intelligence solutions that can support especially personalized healthcare decision making. To enable the development of these solutions, in our previous research (reported in Lahti (2022b)) we have already gathered with our online questionnaire from diverse population groups self-rated interpretations about health-related expression statements in respect to various interpretation dimensions. Thus we have gathered a large variety of personal interpretations about real-life and imagined healthcare situations and these interpretations collectively represent modular conceptualization components that enable to formulate decision making steps. We have then analyzed (reported in Lahti (2022b)) these interpretations to identify statistically significant differences of ratings and their durations in respect to respondent groupings based on background information about the person. Therefore our just recently gathered collection of human interpretations (reported in Lahti (2022b)) offers new possibilities for understanding better the variety of alternative conceptualizations, perspectives, reactions and preferences emerging in decision-making processes of the human mind. Relying on that our just recently gathered data (reported in Lahti (2022b)) our new proposed research methodology starts now building new advanced increasingly trustworthy, safe and open measures and methods of artificial intelligence so that the patient's appropriate involvement can be ensured in the implementation of all the decision making steps concerning his/her care.

When aiming to measure and predict multiple dimensions of the person's health it has been found out that a self-rated health condition answered to a single question has shown a strong validity

and reliability (Gallagher et al., 2016; Wu et al., 2013). Anyway, the phrasing, scales and ordering used in questions and answer options can affect the evaluation of the self-rated health (Cullati et al., 2020; Garbarski et al., 2016; Joffer et al., 2016; Borraccino et al., 2019). There is a need for further systematic development of reliable evaluation metrics that can be applied for practical solutions in healthcare and wellbeing services, such as healthcare chatbots (Abd-Alrazaq et al., 2020) and their algorithms to address successful semantic understanding (Laranjo et al., 2018). It is important to advance now analytical and computational solutions that enable understandable and accurate communication between the patient and healthcare personnel so that the patient can be appropriately and sufficiently involved in decision making that addresses his/her needs (Sinclair et al., 2020a; Sinclair et al., 2020b). In our proposed new research methodology we develop new algorithmic solutions to address the needs of the patient.

Relying on the successful results of our previous research (reported in Lahti (2022b)) our proposed new research methodology exploits in various experimental setups a measuring methodology that is an adaptation from the dimensional affective models of the previous research which suggests that in human experience and response systems the dimensions of pleasure, arousal, dominance and approach-avoidance have a fundamental role (Bradley & Lang, 1999; Warriner et al., 2013; Mauss & Robinson, 2009). Our approach gets motivation also from the previous research that has experimentally gathered a collection of self-identified most significant mental imagery describing the patient's pain in combination with the associated triggers, affects, meanings and avoidance patterns (Berna et al., 2011).

The successful results of our previous research (reported in Lahti (2022b)) motivate the overall design in our proposed new research methodology concerning the measuring methodology and the data analysis of the gathered measurements and their exploitation in subsequent steps of developing the new ethical and transparent artificial intelligence algorithms. The results of our previous research (reported in Lahti (2022b)) offer diverse complementing observations relying on both the interpretation tasks and background questions that highlight various new possibilities to identify hidden dependencies between interpretational measurements of real-life and corresponding imaginary situations. These analytical possibilities offered by the results of our previous research (reported in Lahti (2022b)) get valuable support from the previous findings which have indicated that patterns of neural activation during imagery and actual perception have a strong overlap (Ganis et al., 2004; McNorgan, 2012; Pearson et al., 2013). Furthermore, neuroimaging experiments have shown that self-report ratings of vividness of mental imagery can correlate with activation emerging in the same sensory-specific cortices that are activated in perception (Cui et al., 2007; Herholz et al., 2012; Belardinelli et al., 2009).

We suggest that in the broad context of circumstances, the development of artificial intelligence solutions can be considered as an effort to develop computational solutions to understand increasingly better the processes of life and to support solving emerging challenges in life. Thus encouraged by the results of the previous research ((Karim et al., 2021; Lu et al., 2019; Botvinick et al., 2019; Wang et al., 2016; Wang et al., 2018; Duan et al., 2016; Ritter et al. 2018a; Abd-Alrazaq et al., 2020; Laranjo et al., 2018; Sinclair et al., 2020a; Lahti, 2022a; Lahti, 2022b)), we suggest that our proposed new research methodology develops new kinds of methodologies and algorithmic solutions that can be referred as *life computation*. As we now refer to our proposed new methodologies and algorithmic solutions as life computation we aim to highlight the fundamental underlying biological computational processes of living organisms, their evolution, life cycles and interaction, and how analyzing them can reveal for us all essential increased understanding about new advanced ways to protect and support life and its diverse purposes.

Our proposed new research methodology is motivated and takes inspiration from the previous research that has proposed various ways to explain how the brain learns and uses models (among others, Behrens et al. (2018), Gläscher et al. (2010), Kolling et al. (2016), O'Reilly & Frank (2006)), and it has been estimated (Botvinick et al., 2019) that a suitably holistic and promising model is a computational Meta-Reinforced Learning model (Meta-RL model, Wang et al. (2016), Wang et al. (2018)) and a resembling proposal of Duan et al. (2016) at around the same time). According to this

model in the prefrontal cortex (PFC) recurrent neural networks perform a fast learning mechanism. This is motivated by, among others, the biological results that PFC has been recognized as essential in fast learning (Behrens et al., 2018; Rushworth et al., 2011) and that the neural cells of PFC are coding parameter values that enable such learning (Tsutsui et al., 2016). Those parameter values are related to such items as the current option, previous action, previous gained reward and interaction between the previous action and previous gained reward. When research data (Tsutsui et al., 2016) was used as an input to train a Meta-RL model (Wang et al., 2018), the model produced a resembling learning mechanism in which additionally the coding was expressed similarly as in the dlPFC neural cell of the primates.

According to a certain kind of standard model (Botvinick et al. 2019) the dopamine neurons in the midbrain are assumed to convey the signal of the reward prediction error (RPE) concerning the learning of the temporal change (Montague et al., 1996; Glimcher, 2011; Watabe-Uchida et al., 2017). This is carried out so that the dopamine can gradually adjust the synapse in the corpus striatum leading to reinforcement learning which is assumed to happen in a model-free formulation (Botvinick et al., 2019). On the other hand, recent results show that the dopamine can convey model-based information (Daw et al., 2011; Sadacca et al., 2016; Sharpe et al., 2017), and this can be explained with the Meta-RL model.

When the research data (Miller et al., 2017) was used as an input to train a Meta-RL model (Wang et al., 2018), the recurrent neural networks of the model expressed in their activation dynamics a model-based learning mechanism (among others, a significant degree of model-based information was identified in the RPE values) although the training was implemented in a model-free formulation. Thus it has been interpreted (Botvinick et al., 2019) that the Meta-RL model offers an interesting proposal (Schweighofer & Doya, 2003; Ishii et al., 2002; Khamassi et al., 2013) as a functional principle of the brain in which the dopamine-based model-free gradual learning processes adjust the recurrent neural networks of the PFC to serve as algorithms that exploit the logical structures of the input to learn efficiently.

In the Meta-RL model (Wang et al., 2018) the prefrontal cortex (and the basal ganglion and the thalamus directly connected to it) has been modeled with recurrent neural networks in which the synaptic values are adjusted by the reinforcement learning algorithm based on the dopamine transmission. In these networks the current observation and the input units coding the previous action and reward are all connected to each other with hidden units that are fully connected units of the Long Short-Term Memory model (Hochreiter & Schmidhuber, 1997).

The previous neural research has identified that the episodic memory circuits can return for a reuse the activation patterns of the cerebral cortex (Ritter et al., 2018b), including the regions supporting the working memory, and also identified a connection between the episodic and model-based learning (Vikbladh et al., 2017). Motivated by this it has been proposed an episodic Meta-Reinforced Learning model (episodic Meta-RL model, Ritter et al. 2018a; Ritter et al. 2018b; Santoro et al. 2016; Wayne et al. 2018; Graves et al. 2016; Vikbladh et al. 2017) which can be implemented with a reinforcement learning method so that the model can return for reuse the previous information about the task (Santoro et al. 2016; Wayne et al., 2018; Graves et al., 2016). This episodic Meta-RL model can be considered to produce inductive bias especially based on the architectural and algorithmic formalisms (Botvinick et al., 2019) which can be biologically motivated as a slow learning process generated by the evolution (Botvinick et al., 2019). On the other hand, the ordinary Meta-RL model can be considered to produce inductive bias especially based on learning formalisms (Botvinick et al., 2019).

In respect to the Meta-RL model and the episodic Meta-RL model, some of the research topics that have been considered (Botvinick et al., 2019) currently important for further research are, among others, to develop methods of inductive bias that can support efficient learning (Battaglia et al., 2018; Kulkarni et al., 2016; Vinyals et al., 2016; Spelke & Kinzler, 2007; Botvinick, 2007; Rougier et al., 2005; Plaut, 2002; Sporns et al., 2004; Bullmore & Sporns, 2012; Modha & Singh, 2010), and these have been proposed in respect to, among others, limiting the connections in the network's initial phase (Finn et al., 2017), adjusting the synaptic learning rules (Andrychowicz et al., 2016; Bengio et al.,

1991; Jaderberg et al., 2016), creating clarifying and modular representations (Battaglia et al., 2018; Higgins et al., 2016; Higgins et al., 2017) and internal prediction models (Wayne G. et al., 2018).

2.3 Knowledge, data and algorithmic resources used in the development of new artificial intelligence algorithms

In our proposed new research methodology when developing new artificial intelligence algorithms, based on the previous research (Karim et al., 2021; Lu et al., 2019; Botvinick et al., 2019; Wang et al., 2016; Wang et al., 2018; Duan et al., 2016; Ritter et al. 2018a; Abd-Alrazaq et al., 2020; Laranjo et al., 2018; Sinclair et al., 2020a; Lahti, 2022a; Lahti, 2022b), we carry out extensive series of alternative microbiological and human-computer interaction measurements, data pattern modeling and experimental clustering and deep learning-based computational analysis concerning the fundamental processes of biologically naturally emerging classifications and decision making steps of the human mind in our carefully designed new experimental setups.

These our experimental setups are designed to address the four above-mentioned complementing major research goals and the two above-mentioned main research questions RQ1 and RQ2.

Firstly, we use classification mechanisms identified in the data of microbiological experiments of brain research to develop, test and validate new artificial intelligence algorithms (*biology-based algorithms*) to be used for analyzing and classification of microbiological measurements of brain research. Secondly, we use these new artificial intelligence algorithms developed based on the data of microbiological experiments of brain research to carry out testing and validation of their usability for analyzing and classification of data of personal care event measurements concerning care decision making steps. These just discussed two approaches address the main research question RQ1.

Thirdly, we use classification mechanisms identified in the data of personal care events of different patients concerning care decision making steps to develop, test and validate new artificial intelligence algorithms (*care path-based algorithms*) to be used for analyzing and classification of personal care event measurements concerning care decision making steps. Fourthly, we use these new artificial intelligence algorithms developed based on the data of personal care events of different patients concerning care decision making steps to carry out testing and validation of their usability for analyzing and classification of data of microbiological measurements. These just discussed two approaches address the main research question RQ2.

On a practical level, in our proposed new research methodology our new experimental setups are designed based on a diverse collection of complementing knowledge, data and algorithmic resources.

2.3.1 The microbiological measurement data resources for the development of new artificial intelligence algorithms

The microbiological measurement data can be gained from a broad collection of open access data sets provided by the previous research and thus also enabling our new results to be beneficially comparable with the results of the previous research, and we provide here some examples of these microbiological measurement resources.

1) The review and comparative analysis of Karim et al. (2021) refers to the following three open access resources:

> 1a) The breast microscopy image data set of "Grand Challenge on the BreAst Cancer Histology (BACH)" (Aresta et al., 2019) that is composed of 400 labeled microscopy high-resolution (2040 x 1536 pixels), uncompressed and annotated haematoxylin and eosin stain (H & E) stain images.

1b) The biomedical text data set relying on 215 063 reviews from the web site https://www.drugs.com/ (Drug-information service Drugs.com, 2022) concerning specific drugs, conditions and a 10-star rating which reflects overall user satisfaction so that the reviews include information about the effectiveness of the drugs and possible side-effects.

1c) The gene expression data set relying on a random subset of "The Pan-Cancer Analysis Project" (Weinstein et al., 2013) that is based on data from thousands of patients with primary tumors occurring in different locations of the body covering 12 tumor types.

2) The research article of Lu et al. (2019) refers to the entity of open access resources describing the transcriptomic gene co-expression data set publicly available from the "Gene Expression Omnibus" (Barrett et al. 2013)

In addition, a special resource of microbiological measurement data, based on Lauri Lahti's previous and currently on-going research collaboration, has been kindly offered by research colleagues who carry out laboratory measurements of experimental brain research conducted at a biomedical research institute. These research colleagues investigate molecular mechanisms related to the development and learning of the brain and different psychiatric diseases.

2.3.2 The human-computer interaction measurement data resources for the development of new artificial intelligence algorithms

The human-computer interaction measurement data can be gained from the already gathered broad open access data set of interpretation tasks collected by Lauri Lahti (reported in the publications Lahti (2022a) and Lahti (2022b)) and new data sets that will be gathered with experimental measurement setups resembling the previous data acquisition (reported in the publications Lahti (2022a) and Lahti (2022b)) with the research collaborators that are recruited based on Lauri Lahti's already previously established research contacts and already done shared planning. We provide here some examples of these data resources published so far:

1) The open access data set of interpretation tasks reported in the publication of Lahti (2022a) is available at specific journal web pages:

1a) https://bmcmedresmethodol.biomedcentral.com/articles/10.1186/s12874-021-01502-8

1b) https://static-content.springer.com/esm/art%3A10.1186%2Fs12874-021-01502-8/MediaObjects/12874_2021_1502_MOESM1_ESM.pdf

1c) https://static-content.springer.com/esm/art%3A10.1186%2Fs12874-021-01502-8/MediaObjects/12874_2021_1502_MOESM2_ESM.xlsx

2) The open access data set of interpretation tasks reported in the manuscript of Lahti (2022b) is available at the the Arxiv repository web pages:

2a) https://arxiv.org/abs/2205.07881

2b) https://arxiv.org/pdf/2205.07881

The human-computer interaction measurements can take diverse alternative formulations depending on the context. A common type of a human-computer interaction measurement (an interpretation task) is carried out so that in an online questionnaire the person is asked to interpret expression statements or data patterns, presented in the form of texts, images and videos, on rating scales in respect to certain given interpretation dimensions, such as the semantic affectivity of "the need for help" in the shown textual care event description or the degree of clustering in the shown plotted data pattern. Thus the human-computer interaction measurements (interpretation tasks) gather human answers about the person's interpretations about various kinds of stimuli (expression statements or data patterns), and the variety of alternative conceptualizations, perspectives, reactions and preferences related to them emerging in decision-making processes of the human mind.

Example 1: An example about a human-computer interaction measurement about the shown textual care event description:

> *Step 1 of 2:* The person is provided with a text that describes a dialogue segment (an expression statement) spoken in a decision making task when a patient and a healthcare professional discuss together to carry out diagnosis and care planning: "I have a difficulty breathing." -> "Do you have pain in lungs?" -> "Yes, and it is gradually worsening."
> *Step 2 of 2:* The person is asked to interpret this textual care event description (expression statement) on a rating scale 0-10 in respect to the interpretation dimension of the semantic affectivity of "the need for help" in the shown textual care event description. The rating scale ranges from the smallest possible need for help (value 0) to the greatest possible need for help (value 10).

Example 2: An example about a human-computer interaction measurement about the shown plotted data pattern:

> *Step 1 of 2:* The person is provided with a visualization of a microbiological neural image (a data pattern) that illustrates how from an original grayscale microbiological neural image a certain automated clustering algorithm (for example k means clustering) has identified and highlighted with a red curve certain regions that the algorithm has decided to belong to separate cluster entities based on the brightness value distributions.
> *Step 2 of 2:* The person is asked to interpret this plotted data pattern on a rating scale in respect to the degree of personal agreement that he/she has with the clustering that the algorithm has identified and highlighted in the image (i.e., how well the clustering identified automatically by the algorithm matches with the clustering that the person individually intuitively identifies when looking at the original image). The rating scale ranges from the smallest possible agreement (value 0) to the greatest possible agreement (value 10).

Lauri Lahti's already previously established and planned research collaborators consist of the representatives of diverse population groups both in Finland and other international locations, including people belonging to various patient and disabled people's population groups and people who are healthcare professionals or studying for a profession in the health sector, people in various educational institutions (learners and educators), as well as people representing various demographics.

2.3.3 The algorithmic resources for the development of new artificial intelligence algorithms

In our proposed new research methodology when developing new artificial intelligence algorithms a large variety of the algorithmic resources motivated by the previous research can be used as building blocks for experiments and evaluations, and we provide here some examples of these algorithmic resources.

1) The review and comparative analysis of Karim et al. (2021) refers to the open access resources available at a specific GitHub web page (https://github.com/rezacsedu/Deep-learning-for-clustering-in-bioinformatics) describing the deep learning-based clustering approaches reviewed and compared in that publication, including links to the original papers and their algorithmic implementations.
2) The research article of Lu et al. (2019) refers to the open access resources available at a specific journal web page (https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-019-3089-6/tables/1) describing the algorithm implementations available for the clustering methods evaluated in that publication.
3) The research article of Wang et al. (2018) provides supplementary material (https://www.nature.com/articles/s41593-018-0147-8) that refers to, among others, the following open access resources describing the algorithmic implementations motivated and evaluated in that publication:

> 3a) Supplementary Figure 1: Pseudo-code for advantage actor-critic algorithm

(https://www.nature.com/articles/s41593-018-0147-8/figures/8).

3b) Supplementary Figure 3: Cortico–basal ganglia–thalamic loops (https://www.nature.com/articles/s41593-018-0147-8/figures/10).

3c) Supplementary Figure 7: New simulation to directly test model-based reasoning in meta-RL(https://www.nature.com/articles/s41593-018-0147-8/figures/14).

4) "Neural image brightness cluster analysis script" developed, created and programmed by Lauri Lahti that is openly available in the Data analysis supplement 1 of this current research article: *Lahti, Lauri (2022). Data analysis supplement 1 to the research article "Lahti, Lauri (2022). Developing ethical and transparent artificial intelligence algorithms to support decision making in healthcare based on brain research and personal care events of patients". 15 July 2022 at aaltodoc.aalto.fi.*

References:

Abd-Alrazaq, A., Safi, Z., Alajlani, M., Warren, J., Househ, M., & Denecke, K. (2020). Technical metrics used to evaluate health care chatbots: scoping review. Journal of Medical Internet Research. 2020;22(6):e18301. https://doi.org/10.2196/18301

Abouelezz, Amr, Stefen, Holly, Segerstråle, Mikael, Micinski, David, Minkeviciene, Rimante, Lahti, Lauri, Hardeman, Edna C., Gunning, Peter W., Hoogenraad, Casper C., Taira, Tomi, Fath, Thomas, & Hotulainen, Pirta (2020). Tropomyosin Tpm3.1 is required to maintain the structure and function of the axon initial segment. iScience. 2020 Apr 12;23(5):101053. doi: 10.1016/j.isci.2020.101053. https://www.sciencedirect.com/science/article/pii/S2589004220302388 (Open access: https://doi.org/10.1016/j.isci.2020.101053)

Andrychowicz M. et al. (2016). Learning to learn by gradient descent by gradient descent. Adv. Neural Inf. Process. Syst. 2016; : 3981-3989

Aresta G , Araújo T , Kwok S , et al. (2019). BACH: grand challenge on breast cancer histology images . Med Image Anal 2019 ; 56 : 122 –139.

Barrett T, Wilhite SE, Ledoux P, Evangelista C, Kim IF, Tomashevsky M, Marshall KA, Phillippy KH, Sherman PM, Holko M, Yefanov A, Lee H, Zhang N, Robertson CL, Serova N, Davis S, Soboleva A. (2013). NCBI GEO: archive for functional genomics data sets--update. Nucleic Acids Res. 2013 Jan;41(Database issue):D991-5. https://doi.org/10.1093/nar/gks1193 and https://www.ncbi.nlm.nih.gov/geo/

Battaglia P.W. et al. (2018). Relational inductive biases, deep learning, and graph networks. arXiv. 2018; : 1806.01261

Behrens T.E.J. et al. What is a cognitive map? organizing knowledge for flexible behavior. Neuron. 2018; 100: 76-82

Belardinelli, M., Palmiero, M., Sestieri, C., Nardo, D., Di Matteo, R., Londei, A., D'Ausilio, A., Ferretti, A., Del Gratta, C., & Romani, G. (2009). An fMRI investigation on image generation in different sensory modalities: the influence of vividness. Acta Psychologica, 2009;132:190-200. https://doi.org/10.1016/j.actpsy.2009.06.009

Bengio Y. et al. (1991). Learning a synaptic learning rule. in: Proceedings from IJCNN-91 Seattle International Conference on Neural Networks, IEEE 21991: 696 (1991)

Berna, C., Vincent, K., Moore, J., Tracey, I., Goodwin, G., & Holmes, E. (2011). Presence of mental imagery associated with chronic pelvic pain: a pilot study. Pain Medicine, 2011;12:issue 7, pages 1086-1093. https://doi.org/10.1111/j.1526-4637.2011.01152.x

Bhandare A, Bhide M, Gokhale P, Chandavarkar R. (2016). Applications of convolutional neural networks. International Journal of Computer Science and Information Technologies (IJCSIT), vol. 7(5) (2016), 2206-2215. https://ijcsit.com /docs/Volume%207/vol7issue5 /ijcsit20160705014.pdf.

Borraccino, A., Pera, R., & Lemma, P. (2019). "What being healthy means to me": a qualitative analysis uncovering the core categories of adolescents' perception of health. PLOS One. 2019;14(6):e0218727. https://doi.org/10.1371/journal.pone.0218727

Botvinick M.M. (2007). Multilevel structure in behaviour and in the brain: a model of Fuster's hierarchy. Philos. Trans. R. Soc. Lond. B: Biol. Sci. 2007; 362: 1615-1626

Botvinick, Matthew, Ritter, Sam, Wang, Jane X., Kurth-Nelson, Zeb, Blundell, Charles, Hassabis. Demis. (2019). Reinforcement Learning, Fast and Slow. Trends in Cognitive Sciences, Volume 23, Issue 5, 2019, Pages 408-422, ISSN 1364-6613, https://doi.org/10.1016/j.tics.2019.02.006.

Bradley, M., & Lang P. (1999). Affective norms for English words (ANEW): Instruction manual and affective ratings. Technical Report C-1, The Center for Research in Psychophysiology, University of Florida, USA. http://www.uvm.edu/pdodds/teaching/courses/2009-08UVM-300/docs/others/everything/bradley1999a.pdf

Bullmore, E., & Sporns, O. (2012). The economy of brain network organization. Nat. Rev. Neurosci. 2012; 13: 336

Chen G, Jaradat SA, Banerjee N, Tanaka TS, Ko MS, Zhang MQ. (2002). Evaluation and comparison of clustering algorithms in analyzing es cell gene expression data. Stat Sin. 2002; 12(1):241–62.

Cui, X., Jeter, C., Yang, D., Montague, P., & Eagleman D. (2007). Vividness of mental imagery: individual variability can be measured objectively. Vision Research, 2007;47(4):474-478. https://doi.org/10.1016/j.visres.2006.11.013

Cullati, S., Bochatay, N., Rossier, C., Guessous, I., Burton-Jeangros, C., & Courvoisier, D. (2020). Does the single-item self-rated health measure the same thing across different wordings? Construct validity study. Quality of Life Research: An International Journal of Quality of Life Aspects of Treatment, Care and Rehabilitation. 2020;29(9):2593-2604. https://doi.org/10.1007/s11136-020-02533-2

Datta, S., & Datta, S. (2006). Evaluation of clustering algorithms for gene expression data. BMC Bioinformatics 7, S17 (2006). https://doi.org/10.1186/1471-2105-7-S4-S17

Daw N.D. et al. (2011). Model-based influences on humans' choices and striatal prediction errors. Neuron. 2011; 69: 1204-1215

De Souto MCP , Costa IG , de Araujo DSA, et al. (2008). Clustering cancer gene expression data: a comparative study . BMC Bioinform 2008 ; 9 (1): 497.

De Vries GK, Van Hage WR, Van Someren M. (2010). Comparing vessel trajectories using geographical domain knowledge and alignments. In: Data Mining Workshops (ICDMW), 2010 IEEE International Conference On. IEEE: 2010. p. 209–16.

Drug-information service Drugs.com (2022). A free online drug-information service available and described at the web addresses https://www.drugs.com and https://www.drugs.com/support/about.html

Duan Y. et al. (2016). Rl2: fast reinforcement learning via slow reinforcement learning. arXiv. 2016; : 1611.02779

Eraslan G , Simon LM , Maria, et al. (2019). Single-cell RNA-seq denoising using a deep count autoencoder . Nat Commun 2019 ; 10 (1): 390 .

Estivill-Castro V . (2002). Why so many clustering algorithms: a position paper . SIGKDD Explorations 2002 ; 4 (1): 65 –75 .

European Commission (2019). Ethics Guidelines for Trustworthy AI. High-Level Expert Group on Artificial Intelligence, European Commission, Directorate-General for Communications Networks, Content and Technology, 2019. Publications Office. ISBN 978-92-76-12796-3 (print), ISBN 978-92-76-11998-2 (online). https://doi.org/10.2759/346720 and https://data.europa.eu/doi/10.2759/346720 and https://op.europa.eu/s/snXz

European Commission (2020). The Assessment List for Trustworthy Artificial Intelligence (ALTAI) for self assessment. High-Level Expert Group on Artificial Intelligence, European Commission, Directorate-General for Communications Networks, Content and Technology, 2020. Publications Office. ISBN 978-92-76-20009-3 (print), ISBN 978-92-76-20008-6 (online). https://doi.org/10.2759/002360 and https://data.europa.eu/doi/10.2759/002360 and https://op.europa.eu/s/ssOB

European Commission (2021a). Proposal for a Regulation of the European Parliament and of the Council. Laying Down Harmonised Rules on Artificial Intelligence (Artificial Intelligence Act) and Amending Certain Union Legislative Acts. COM(2021) 206 final, 2021/0106(COD). European Commission, Directorate-General for Communications Networks,

Content and Technology, 21 April 2021, Brussels, Belgium. https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX:52021PC0206

European Commission (2021b). Annexes to the Communication from the Commission to the European Parliament, the European Council, the Council, the European Economic and Social Committee and the Committee of the Regions. Fostering a European approach to Artificial Intelligence. Coordinated Plan on Artificial Intelligence 2021 Review. COM(2021) 205 final, ANNEX. 21 April 2021, Brussels, Belgium. https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX:52021DC0205 and https://ec.europa.eu/newsroom/dae/redirection/document/75787

Finn C. et al. (2017). Model-agnostic meta-learning for fast adaptation of deep networks. arXiv. 2017; : 1703.03400

Gallagher, J., Wilkie, A., Cordner, A., Hudgens, E., Ghio, A., Birch, R., & Wade, T. (2016). Factors associated with self-reported health: implications for screening level community-based health and environmental studies. BMC Public Health, 16, 640 (2016). https://doi.org/10.1186/s12889-016-3321-5

Gan G , Ma C , Wu J . (2007). Data clustering: theory, algorithms, and applications , Vol. 20 . SIAM , 2007 .

Ganis, G., Thompson, W., & Kosslyn, S. (2004). Brain areas underlying visual mental imagery and visual perception: an fMRI study. Cognitive Brain Research, 2004;20(2):226-241. https://doi.org/10.1016/j.cogbrainres.2004.02.012

Garbarski, D., Schaeffer, N., & Dykema, J. (2016). The effect of response option order on self-rated health: a replication study. Quality of Life Research: An International Journal of Quality of Life Aspects of Treatment, Care and Rehabilitation. 2016;25(8):2117–2121. https://doi.org/10.1007/s11136-016-1249-y

Gehrmann S, Dernoncourt F, Li Y, Carlson E, Wu J, Welt J, Foote J Jr, Moseley E, Grant D, Tyler P, Celi L. (2018). Comparing deep learning and concept extraction based methods for patient phenotyping from clinical narratives. PLOS One. 2018;13(2):e0192360. https://doi.org/10.1371/journal.pone.0192360.

Glimcher P.W. (2011). Understanding dopamine and reinforcement learning: the dopamine reward prediction error hypothesis. Proc. Natl. Acad. Sci. U. S. A. 2011; 108: 15647-15654

Gläscher J. et al. (2010). States versus rewards: dissociable neural prediction error signals underlying model-based and model-free reinforcement learning. Neuron. 2010; 66: 585-595

Goodfellow, I . (2016). Nips 2016 tutorial: generative adversarial networks. arXiv preprint, arXiv:1701.00160 , 2016 .

Graves A. et al. (2016). Hybrid computing using a neural network with dynamic external memory. Nature. 2016; 538: 471

Hagler, D. J., Jr, Saygin, A. P., & Sereno, M. I. (2006). Smoothing and cluster thresholding for cortical surface-based group analysis of fMRI data. NeuroImage, 33(4), 1093–1103. https://doi.org/10.1016/j.neuroimage.2006.07.036

Hansen P, Jaumard B. (1997). Cluster analysis and mathematical programming. Math Program. 1997; 79(1-3):191–215.

Herholz, S., Halpern, A., & Zatorre, R. (2012). Neuronal correlates of perception, imagery, and memory for familiar tunes. Journal of Cognitive Neuroscience, 2012;24(6):1382-1397. https://doi.org/10.1162/jocn_a_00216

Higgins I. et al. (2016). Beta-vae: learning basic visual concepts with a constrained variational framework. 5th International Conference on Learning Representations. 2016;

Higgins I. et al. (2017). Darla: improving zero-shot transfer in reinforcement learning. arXiv. 2017; : 1707.08475

Hochreiter, S., & Schmidhuber, J. (1997). Long short-term memory. Neural Comput. 1997; 9: 1735-1780

Holmes, S., & Huber, W. (2020). Modern Statistics for Modern Biology. Lab 9: Image Data, 7th May 2020. https://www.huber.embl.de/msmb/course_spring_2020/Lab09_image_data.html

Huang DW, Sherman BT, Tan Q, Kir J, Liu D, Bryant D, Guo Y, Stephens R, Baseler MW, Lane HC, et al. (2007). Nucleic Acids Res. 2007; 35(suppl_2):169–75.

Hubert L. (1973). Min and max hierarchical clustering using asymmetric similarity measures. Psychometrika. 1973; 38(1):63–72.

Hughes M, Li I, Kotoulas S, Suzumura T. (2017). Medical text classification using convolutional neural networks. Studies in Health Technology and Informatics, volume 235, pages 246-250. PMID: 28423791.

Ishii S. et al. (2002). Control of exploitation-exploration meta-parameter in reinforcement learning. Neural Netw. 2002; 15: 665-687

Jaderberg M. et al. (2016). Decoupled neural interfaces using synthetic gradients. arXiv. 2016; : 1608.05343

Jaskowiak PA , Campello RJGB , Filho IGC . (2013) Proximity measures for clustering gene expression microarray data: a validation methodology and a comparative analysis . IEEE/ACM Trans Comput Biol Bioinform 2013 ; 10 (4): 845 –57 .

Jaskowiak PA , Costa IG , Campello RJGB . (2018). Clustering of rna-seq samples: comparison study on cancer data . Methods 2018 ; 132 :42 –9 .

Jay JJ, Eblen JD, Zhang Y, Benson M, Perkins AD, Saxton AM, Voy BH, Chesler EJ, Langston MA. (2012). A systematic comparison of genome-scale clustering algorithms. BMC Bioinformatics. 2012; 13:7.

Joffer, J., Jerdén, L., Öhman, A., & Flacking, R. (2016). Exploring self-rated health among adolescents: a think-aloud study. BMC Public Health, 16, 156 (2016). https://doi.org/10.1186/s12889-016-2837-z

Karim, Md Rezaul, Beyan, Oya, Zappa, Achille, Costa, Ivan G., Rebholz-Schuhmann, Dietrich, Cochez, Michael, Decker, Stefan (2021). Deep learning-based clustering approaches for bioinformatics, Briefings in Bioinformatics, Volume 22, Issue 1, January 2021, Pages 393–415, https://doi.org/10.1093/bib/bbz170

Kaufman, L., Rousseeuw, PJ. . (1990). Partitioning around medoids (program pam) . In Finding Groups in Data: An Introduction to Cluster Analysis. John Wiley & Sons , 1990 ;68 –125 .

Khamassi M. et al. (2013). Medial prefrontal cortex and the adaptive regulation of reinforcement learning parameters. Progress in Brain Research. Vol. 202. Elsevier, 2013: 441-464

Kohonen T . (1998). The self-organizing map . Neurocomputing 1998 ; 21 (1–3): 1 –6 .

Kolling N. et al. (2016). Value, search, persistence and model updating in anterior cingulate cortex. Nat. Neurosci. 2016; 19: 1280

Kulkarni T.D. et al. (2016). Hierarchical deep reinforcement learning: integrating temporal abstraction and intrinsic motivation. Adv. Neural Inf. Process. Syst. 2016; : 3675-3683

Lahti, Lauri, & Kurhila, Jaakko (2007). Low-cost portable text recognition and speech synthesis with generic software, laptop computer and digital camera. Proc. 12th Human Computer Interaction International 2007, Part II (Universal Access in Human-Computer Interaction - Ambient Interaction), 22–27 July 2007, Beijing, China (ed. Stephanidis, C.). LNCS 4555, Springer, 918–927. Print ISBN 978-3-540-73280-8 and Online ISBN 978-3-540-73281-5. http://link.springer.com/chapter/10.1007%2F978-3-540-73281-5_100 (Open access: http://urn.fi/URN:NBN:fi:aalto-201503182050)

Lahti, Lauri (2009). Guided generation of pedagogical concept maps from the Wikipedia. Proc. World Conference on E-Learning in Corporate, Government, Healthcare and Higher Education 2009 (E-Learn 2009). 26–30 October 2009, Vancouver, B.C., Canada (eds. Bastiaens, T. et al.). Association for the Advancement of Computing in Education (AACE), Chesapeake, Virginia, USA, 1741–1750. ISBN 1-880094-76-2. http://www.editlib.org/p/32712/ (Open access: http://urn.fi/URN:NBN:fi:aalto-201503182039)

Lahti, Lauri (2011). Educational concept mapping method based on high-frequency words and Wikipedia linkage. Proc. 4th International Conference on Internet Technologies and Applications (ITA11), 6–9 September 2011, Wrexham, North Wales, UK (eds. Grout, V. et al.). Glyndwr University, Wrexham, Wales, UK. ISBN 978-0-946881-68-0. http://www.ita11.org/papers.html and http://www.ita11.org/detailedProgramme.html and http://www.lulu.com/shop/vic-grout-and-stuart-cunningham-and-denise-oram-and-rich-picking/proceedings-of-the-fourth-international-conference-on-internet-technologies-and-applications-ita-11/ebook/product-17431522.html (Open access: http://urn.fi/URN:NBN:fi:aalto-201503182041)

Lahti, Lauri (2013). Educational framework based on cumulative vocabularies, conceptual networks and Wikipedia linkage. Proc. London International Conference on Education 2013 (LICE 2013). 4–6 November 2013, London, UK (eds. Shoniregun, C., & Akmayeva, G.), 470–478. ISBN 978-1-908320-16-2. (Open access: http://urn.fi/URN:ISBN:978-1-908320-16-2)

Lahti, Lauri (2015). Computer-assisted learning based on cumulative vocabularies, conceptual networks and Wikipedia linkage. Doctoral dissertation. Department of Computer Science, Aalto University School of Science, Finland. Unigrafia Oy, Helsinki, Finland. ISBN 978-952-60-6163-4 (printed), ISBN 978-952-60-6164-1 (pdf). (Open access: http://urn.fi/URN:ISBN:978-952-60-6164-1)

Lahti, Lauri (2016). Supporting diagnostics and decision making in healthcare by modular methods of computational linguistics. Proc. E-Learn 2016 - World Conference on E-Learning, 14–16 November 2016, Washington, D.C., USA (eds. Ho, C., & Lin, G.), 1513-1519. Association for the Advancement of Computing in Education (AACE), Chesapeake, VA, USA. ISBN 978-1-939797-25-4. https://www.learntechlib.org/p/174196 (Open access: http://urn.fi/URN:ISBN:978-1-939797-25-4)

Lahti, Lauri (2017). Interpretation of health-related expressions and dialogues: enabling personalized care with contextual measuring and machine learning. International Journal of New Technology and Research (IJNTR), volume 3, issue 11, November 2017, pages 171-179, ISSN 2454-4116. Open access: https://www.ijntr.org/download_data/IJNTR03110081.pdf and http://urn.fi/URN:NBN:fi:aalto-201712298340

Lahti, Lauri. (2018). Supporting care by interpretation of expressions about patient experience with machine learning. International Journal of New Technology and Research (IJNTR), volume 4, issue 12, December 2018, pages 27-34, ISSN 2454-4116. Open access: https://doi.org/10.31871/IJNTR.4.12.16 and https://www.ijntr.org/download_data/IJNTR04120016.pdf and http://urn.fi/URN:NBN:fi:aalto-201812015463

Lahti, Lauri; Tenhunen Henni; & Nieminen, Marko (2018). How patients talk about care? Identifying patient experience expressions from online discussions. Proc. Medical Informatics Europe Conference (MIE 2018), 24-26 April 2018, Gothenburg, Sweden (eds. Ugon, A., Karlsson, D., Klein, G., & Moen, A.). Building Continents of Knowledge in Oceans of Data: The Future of Co-Created eHealth. Studies in Health Technology and Informatics, volume 247. European Federation for Medical Informatics (EFMI) and IOS Press, Amsterdam, the Netherlands. Pages 116-120. ISBN 978-1-61499-851-8 (print), ISBN 978-1-61499-852-5 (online). ISSN 0926-9630 (print) and ISSN 1879-8365 (online). PMID: 29677934. Open access: http://ebooks.iospress.nl/volumearticle/48765 and http://urn.fi/URN:NBN:fi:aalto-201812106386 (also https://doi.org/10.3233/978-1-61499-852-5-116). A supplementing document for this research article is: Data supplement to the research article Lahti, Lauri, Tenhunen, Henni, & Nieminen, Marko, "How patients talk about care? Identifying patient experience expressions from online discussions", 2018 (http://urn.fi/URN:NBN:fi:aalto-201802021206).

Lahti, Lauri (2020). Interpretation of the patient's need for help can be supported with machine learning. In Mansnérus, Juli, Lahti, Raimo, & Blick, Amanda (eds.), Personalized medicine: legal and ethical challenges. Faculty of Law, University of Helsinki, Finland, Forum Iuris Series, Helsinki, 2020. ISBN 978-951-51-6940-2 (printed), ISBN 978-951-51-5021-9 (online), ISSN 2670-1219. Open access: https://helda.helsinki.fi/handle/10138/326164 and https://doi.org/10.31885/9789515169419

Lahti, Lauri (2021a). Development of care decision-making model. A manuscript completed and self-archived on 14 July 2021 in the open-access Aaltodoc publication archive at https://aaltodoc.aalto.fi/handle/123456789/108753 and http://urn.fi/URN:NBN:fi:aalto-202107148007

Lahti, Lauri (2021b). Trustworthy artificial intelligence for personalized healthcare decision making: development of open and safe measures, models and methods. Proc. 7th International Symposium ICF Education, 23-24 October 2021. Poster number 13. Poster booklet for the online symposium organized by Brazilian representatives of ICF Education (icfeducation.org). Celebrating 20 years of ICF: Quo vadis. ICF Education Editorial Team, October 2021. Open access: https://icfmobile.org/wp-content/uploads/2022/01/7th-INTERNATIONAL-SYMPOSIUM-ICF-EDUCATION-Poster-Booklet.pdf and http://urn.fi/URN:NBN:fi:aalto-202110259779

Lahti, Lauri (2021c). Data analysis supplement to the research article Abouelezz, Stefen, Segerstråle, Micinski, Minkeviciene, Lahti, Hardeman, Gunning, Hoogenraad, Taira, Fath, & Hotulainen (2020), "Tropomyosin Tpm3.1 Is Required to Maintain the Structure and Function of the Axon Initial Segment". Open access: http://urn.fi/URN:NBN:fi:aalto-202109109107

Lahti, Lauri (2022a). Detecting the patient's need for help with machine learning based on expressions. BMC Medical Research Methodology, volume 22, article number 60 (2022), ISSN 1471-2288. PMCID: PMC8898191. PMID: 35249538. This research article is supplemented with two supplementing documents : Additional file 1 and Additional

file 2. Open access: https://bmcmedresmethodol.biomedcentral.com/articles/10.1186/s12874-021-01502-8 and https://doi.org/10.1186/s12874-021-01502-8

Lahti, Lauri (2022b). Developing patient-driven artificial intelligence based on personal rankings of care decision making steps. A research article manuscript completed and self-archived on 11 May 2022 on the open-access Arxiv repository (https://arxiv.org/abs/2205.07881). This manuscript (104 pages) is supplemented with seven supplementing documents (2781 pages). Open access: https://arxiv.org/pdf/2205.07881 and https://doi.org/10.48550/arXiv.2205.07881

Lahti, Raimo (2012). Medical law and biolaw. In Nuotio, K., Melander, S., & Huomo-Kettunen, M. (eds.), Introduction to Finnish Law and Legal Culture. Faculty of Law, University of Helsinki, Helsinki, Finland. Forum Iuris Series, Helsinki. Pages 249-260. ISBN 978-952-10-7817-0. Reprinted in the compilation publication: Lahti, Raimo (2021). Towards an Efficient, Just and Humane Criminal Justice: Nordic Essays on Criminal Law, Criminology and Criminal Policy 1972-2020. Publications of the Finnish Lawyers' Association, Series D (Ius Finlandiae), No. 8. The Finnish Lawyers' Association, Helsinki, Finland. Pages 528-541. ISBN 978-951-855-386-4 (printed), ISBN 978-951-855-387-1 (online), ISSN 0456-7206. Open access: https://edition.fi/lakimiesyhdistys/catalog/book/121 and https://edition.fi/lakimiesyhdistys/catalog/download/121/68/223-3

Laranjo, L., Dunn, A., Tong, H., Kocaballi, A., Chen, J., Bashir, R., Surian, D., Gallego, B., Magrabi, F., Lau, A., & Coiera, E. (2018). Conversational agents in healthcare: a systematic review. Journal of the American Medical Informatics Association, 2018;25(9):1248-1258. https://doi.org/10.1093/jamia/ocy072

Liu M, Samal A. (2002). Cluster validation using legacy delineations. Image Vis Comput. 2002; 20(7):459–67.

Lu, Y., Phillips, C.A. & Langston, M.A. (2019). A robustness metric for biological data clustering algorithms. BMC Bioinformatics 20, 503 (2019). https://doi.org/10.1186/s12859-019-3089-6

Luce RD, & Perry AD. (1949). A method of matrix analysis of group structure. Psychometrika. 1949; 14(2):95–116.

MacQueen J. (1967). Some methods for classification and analysis of multivariate observations . In: Proceedings of the 5th Berkeley Symposium on Mathematical Statistics & Probability , Vol. 1 . Oakland, USA : University of California Press , 1967 , 281 –97 .

Makhzani A, Shlens , J, Jaitly, N, et al. .(2015). Adversarial autoencoders . arXiv preprint, arXiv:1511.05644 , 2015 .

Masood MA, & Khan MNA . (2015). Clustering techniques in bioinformatics . Int J Modern Educ Comput Sci 2015 ; 1 :38 –46 .

Mauss, I., & Robinson, M. (2009). Measures of emotion: a review. Cognition and Emotion, 2009;23(2):209-237. https://doi.org/10.1080/02699930802204677

McNorgan C. (2012). A meta-analytic review of multisensory imagery identifies the neural correlates of modality-specific and modality-general imagery. Frontiers in Human Neuroscience, 6, article 285. https://doi.org/10.3389/fnhum.2012.00285

Micinski, David, Lahti, Lauri, & Abouelezz, Amr (2022). Measuring Properties of the Membrane Periodic Skeleton of the Axon Initial Segment using 3D-Structured Illumination Microscopy (3D-SIM). Journal of visualized experiments : JoVE, (180), 10.3791/63327. https://doi.org/10.3791/63327

Miller K.J. et al. (2017). Dorsal hippocampus contributes to model-based planning. Nat. Neurosci. 2017; 20: 1269

Min E, Guo X, Qiang, et al. (2018). A survey of clustering with deep learning: from the perspective of network architecture. IEEE Access 2018; 6:39501–14.

Minkeviciene, Rimante, Hlushchenko, Iryna, Virenque, Anaïs, Lahti, Lauri, Khanal, Pushpa, Rauramaa, Tuomas, Koistinen, Arto, Leinonen, Ville, Noe, Francesco M., & Hotulainen, Pirta (2019). MIM-deficient mice exhibit anatomical changes in dendritic spines, cortex volume and brain ventricles, and functional changes in motor coordination and learning. Frontiers in Molecular Neuroscience, 12:276. DOI: 10.3389/fnmol.2019.00276. https://www.frontiersin.org/articles/10.3389/fnmol.2019.00276/full (Open access: https://doi.org/10.3389/fnmol.2019.00276)

Modha D.S. & Singh R. (2010). Network architecture of the long-distance pathways in the macaque brain. Proc. Natl. Acad. Sci. U. S. A. 2010; 107: 13485-13490

Montague P.R. et al. (1996). A framework for mesencephalic dopamine systems based on predictive Hebbian learning. J. Neurosci. 1996; 16: 1936-1947

Newman ME. (2006). Modularity and community structure in networks. Proc Natl Acad Sci. 2006; 103(23):8577–82.

O'Reilly R.C. & Frank Michael J. (2006). Making working memory work: a computational model of learning in the prefrontal cortex and basal ganglia. Neural Comput. 2006; 18: 283-328

Oyelade J , Isewon I , Funke, et al. (2016). Clustering algorithms: their application to gene expression data . Bioinform Biol Insights 2016 ; 10: BBI–S38316 .

Pearson, D., Deeprose, C., Wallace-Hadrill, S., Heyes, S., & Holmes, E. (2013). Assessing mental imagery in clinical psychology: a review of imagery measures and a guiding framework. Clinical Psychology Review, 2013;33(1):1-23. https://doi.org/10.1016/j.cpr.2012.09.001

Plaut D.C. (2002). Graded modality-specific specialisation in semantics: a computational account of optic aphasia. Cogn. Neuropsychol. 2002; 19: 603-639

Qing L, Linhong W, Xuehai D. (2019). A novel neural network-based method for medical text classification. Future Internet. 2019;11(12):255. DOI: https://doi.org/10.3390/fi11120255

Rand WM. (1971). Objective criteria for the evaluation of clustering methods. J Am Stat Assoc. 1971; 66(336):846–50.

Ritter S. et al. (2018a). Been there, done that: meta-learning with episodic recall. International Conference on Machine Learning. 2018; : 4351-4360

Ritter S. et al. (2018b). Episodic control as meta-reinforcement learning. bioRxiv. 2018; : 360537

Rojas-Barahona L, Tseng B, Dai Y, Mansfield C, Ramadan O, Ultes S, Crawford M, Gašić M. (2018). Deep learning for language understanding of mental health concepts derived from cognitive behavioural therapy. Proceedings of the Ninth International Workshop on Health Text Mining and Information Analysis, 2018. DOI: https://doi.org /10.18653/v1/w18-5606

Rosenberg A, & Hirschberg J. (2007). V-measure: A conditional entropy-based external cluster evaluation measure. EMNLP-CoNLL 2007. 2007:410.

Rougier N.P. et al. (2005). Prefrontal cortex and flexible cognitive control: rules without symbols. Proc. Natl. Acad. Sci. U. S. A. 2005; 102: 7338-7343

Rousseeuw PJ. (1987). Silhouettes: a graphical aid to the interpretation and validation of cluster analysis. J Comput Appl Math. 1987; 20:53–65.

Rushworth M.F.S. et al. (2011). Frontal cortex and reward-guided learning and decision-making. Neuron. 2011; 70: 1054-1069

Sadacca B.F. et al. (2016). Midbrain dopamine neurons compute inferred and cached value prediction errors in a common framework. eLife. 2016; 5: e13665

Santoro A. et al. (2016). Meta-learning with memory-augmented neural networks. International Conference on Machine Learning. 2016; : 1842-1850

Schweighofer N. & Doya K. (2003). Meta-learning in reinforcement learning. Neural Netw. 2003; 16: 5-9

Sharpe M.J. et al. (2017). Dopamine transients are sufficient and necessary for acquisition of model-based associations. Nat. Neurosci. 2017; 20: 735

Shickel, B., Siegel, S., Heesacker, M., Benton, S., & Rashidi, P. (2020). Automatic detection and classification of cognitive distortions in mental health text. Proc. 2020 IEEE 20th International Conference on Bioinformatics and Bioengineering (BIBE), 26-28 October 2020, Cincinnati, Ohio, USA, pages 275-280. Added to IEEE Xplore on 16 December 2020. https://ieeexplore.ieee.org/document/9288097 and https://doi.org/10.1109/BIBE50027.2020.00052 (Open access research article manuscript published on 23 September 2019 at https://arxiv.org/abs/1909.07502)

Sinclair, S., Jaggi, P., Hack, T., Russell, L., McClement, S., Cuthbertson, L., Selman, L., & Leget, C. (2020). Initial validation of a patient-reported measure of compassion: determining the content validity and clinical sensibility among patients living with a life-limiting and incurable illness. The Patient - Patient-Centered Outcomes Research, 2020, volume 13, pages 327-337, https://doi.org/10.1007/s40271-020-00409-8

Sinclair, S., Jaggi, P., Hack, T., McClement, S., & Cuthbertson, L. (2020). A practical guide for item generation in measure development: insights from the development of a patient-reported experience measure of compassion. Journal of Nursing Measurement, 2020, 28(1), https://doi.org/10.1891/JNM-D-19-00020

Søorlie T , Perou CM , Robert, et al. (2001). Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications . Proc Natl Acad Sci 2001 ; 98 (19): 10869 –74 .

Spelke E.S. & Kinzler K.D. (2007). Core knowledge. Dev. Sci. 2007; 10: 89-96

Sporns O. et al. (2004). Organization, development and function of complex brain networks. Trends Cogn. Sci. 2004; 8: 418-425

Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, Paulovich A, Pomeroy SL, Golub TR, Lander ES, et al. (2005). Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proc Natl Acad Sci. 2005; 102(43):15545–50.

Thalamuthu A , Mukhopadhyay I , Xiaojing, et al. (2006). Evaluation and comparison of gene clustering methods in microarray analysis . Bioinformatics 2006 ; 22 (19): 2405 –12 .

Townend, D., Clemens, C., Shaw, D., Brand, H., Nys, H., & Palm, W. (2016). Patients' rights in the European Union: mapping exercise: final report. Written by PRE-MAX Consortium, March 2016. European Commission, Directorate-General for Health and Food Safety, 2018. Publications Office. Published 25 January 2018. ISBN 978-92-79-66960-6. https://doi.org/10.2875/751285 and https://data.europa.eu/doi/10.2875/751285 and https://op.europa.eu/s/snVa

Tsutsui K.-I. et al. (2016). A dynamic code for economic object valuation in prefrontal cortex neurons. Nat. Commun. 2016; 7: 12554

Vikbladh O. et al. (2017). Episodic contributions to model-based reinforcement learning. Annual Conference on Cognitive Computational Neuroscience CCN. 2017;

Vinh NX, Epps J, Bailey J. J. (2010). Information Theoretic Measures for Clusterings Comparison: Variants, Properties, Normalization and Correction for Chance. Mach Learn Res. 2010; 11(Oct):2837–2854.

Vinyals O. et al. (2016). Matching networks for one shot learning. Adv. Neural Inf. Process. Syst. 2016; : 3630-3638

Wang J.X. et al. (2016). Learning to reinforcement learn. arXiv. 2016; : 1611.05763

Wang J.X. et al. (2018). Prefrontal cortex as a meta-reinforcement learning system. Nat. Neurosci. 2018; 21: 860

Warriner, A., Kuperman, V., & Brysbaert, M. (2013). Norms of valence, arousal, and dominance for 13,915 English lemmas. Behavior Research Methods, 2013; 45(4), 1191-1207. https://doi.org/10.3758/s13428-012-0314-x and http://link.springer.com/article/10.3758/s13428-012-0314-x

Wasserman S, Faust K. (1994). Social Network Analysis: Methods and Applications. vol. 8. Cambridge: Cambridge university press; 1994.

Watabe-Uchida M. et al. (2017). Neural circuitry of reward prediction error. Annu. Rev. Neurosci. 2017; 40: 373-394

Wayne G. et al. (2018). Unsupervised predictive memory in a goal-directed agent. arXiv. 2018; : 1803.10760

Weinstein JN , Collisson EA, Mills GB, et al. (2013). The cancer genome atlas pan-cancer analysis project . Nat Genet 2013 ; 45 (10): 1113 .

Wu, S., Wang, R., Zhao, Y., Ma, X., Wu, M., Yan, X., & He, J. (2013). The relationship between self-rated health and objective health status: a population-based study. BMC Public Health. 13, 320 (2013). https://doi.org/10.1186/1471-2458-13-320

Yao L, Mao C, Luo Y. (2019). Clinical text classification with rule-based features and knowledge-guided convolutional neural networks. BMC Med Informatics Decision Making. 2019;19:71. https://doi.org/10.1186/s12911-019-0781-4.

Zhao X, Miao C, Xing Z. (2017). Identifying cognitive distortion by convolutional neural network based text classification. Int J Information Technol. 2017;23(No. 1): pp. 1-12 (2017), Singapore Computer Society, LILY Research Centre, Nanyang Technological University, Singapore. http://www.intjit.org/cms/journal /volume/23/1/231_4.pdf.

Lahti, Lauri (2022). Data analysis supplement 1 to the research article "Lahti, Lauri (2022). Developing ethical and transparent artificial intelligence algorithms to support decision making in healthcare based on brain research and personal care events of patients". 15 July 2022 at aaltodoc.aalto.fi.

This data analysis supplement 1 is developed and created by Lauri Lahti, Department of Computer Science, Aalto University School of Science, Finland (email: lauri.lahti@aalto.fi), first published on 15 July 2022 at aaltodoc.aalto.fi.

"Neural image brightness cluster analysis script" developed, created and programmed by Lauri Lahti, Department of Computer Science, Aalto University School of Science, Finland (email: lauri.lahti@aalto.fi), first published on 15 July 2022 at aaltodoc.aalto.fi.

Description:

Motivated by the previous research and open source algorithm components (Holmes & Huber 2020; Hagler et al. 2006) Lauri Lahti developed and created a new cluster analysis method and programmed a new R language script to identify and analyze the emergence of brightness clusters in the given neural images (input images). This new script (referred to as "Neural image brightness cluster analysis script") and its related protocol is openly available in the research article manuscript (Lahti, 2022). The script relies on, among others, R language libraries magrittr, tidyverse, imager, magick, spatstat, EBImage and ggplot2. The script takes as inputs the maximum intensity projection tiff images and their corresponding manually defined mask images. The script computes and outputs visualizations and exact numeric result files describing pixel regions that the script has identified in the input image file matching the conditions defined by the script's adjustable parameter values about the minimum brightness threshold value (for example 0.4). These numeric result files describe the number of identified brightness regions per image and the area of each of these brightness regions. To support identification of brightness clusters based on agglomerating separate but relatively closely positioned bright pixels, the script enables using supplementary smoothed versions of input image files to identify brightness regions. These supplementary smoothed versions of input image files can be generated with the scripts functionality that implements Gaussian blurring with desired adjustable parameter values of the size of "the brush" of the Gaussian kernel and the value of the sigma for "the brush" of the Gaussian kernel.

Part 1/2 of the script: Generating smoothed versions of input image files by implementing Gaussian blurring:

```
#   20220129: GENEROIDAAN PEHMENNETTYJÄ KUVAVERSIOITA POHJATUEN KAHTEEN FOR-SILMUKAAAN:
#   A) TIEDOSTONIMILUETTELON (HUOM. KIRJATTU ILMAN .tif-LOPPUPÄÄTETTÄ) LÄPIKÄYMISEN MYÖTÄ
#   B) sigma_value_for_brush-ARVOJEN LÄPIKÄYMISEN MYÖTÄ



# huom. tärkeitä kirjastoja:

library("EBImage")
library("magrittr")
library("tibble")
library("ggplot2")




#  luettelo tiedostonimistä:

#  huom. seuraavassa tiedostonimet ilman .tif-päätettä
#  huom. tässä luettelossa lueteltavien elementtien viimeisen elementin jälkeen ei ole pilkkua

filepath_of_image_for_input_initial_withoutending_list = c(
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im003" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im004" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im005" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im006" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im007" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im008" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im009" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im010" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im011" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im012" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im013" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im014" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im015" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im016" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im017" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im018" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im019" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im020" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im021" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im022" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im023" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im024" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im025" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im026" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im027" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im028" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im029" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im030" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im031" ,
"C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\ni20220615b_exp1a_im032"
)


#  luettelo sigma_value_for_brush-arvoista:

sigma_value_for_brush_list = c( 0.7, 0.8, 0.9 )


#  for-silmukka tiedostonimien läpikäymiseen:

for( filepath_of_image_for_input_initial_withoutending_list_counter in 1:(   length( filepath_of_image_for_input_initial_withoutending_list )  ) )  {

print(    filepath_of_image_for_input_initial_withoutending_list[filepath_of_image_for_input_initial_withoutending_list_counter] )


#  for-silmukka sigma_value_for_brush-arvojen läpikäymiseen:

for( sigma_value_for_brush_list_counter in 1:(   length( sigma_value_for_brush_list )  ) )  {
```

```
print(    sigma_value_for_brush_list[sigma_value_for_brush_list_counter] )



#   POIS KÄYTÖSTÄ: sigma_value_for_brush = 1

sigma_value_for_brush = sigma_value_for_brush_list[sigma_value_for_brush_list_counter]


#   filepath_of_image_for_input_combined =
"D:\\bio_data_20210816\\experiments20211017\\MAX_080621_15DIV_Gas7_GFP_10min_100_uM_LY294002_C01_Z2_ns_imagej_zprojf1t17maxint_expim.tif"



#  huom. seuraavassa tiedostonimi ilman .tif-päätettä

#  POIS KÄYTÖSTÄ:  filepath_of_image_for_input_initial_withoutending =
"D:\\bio_data_20220128\\experiments20220128\\inputimages20220129a\\MAX_080621_15DIV_Gas7_GFP_10min_100_uM_LY294002_C01_Z2_ns_imagej_zprojf1t17maxint_expim"


filepath_of_image_for_input_initial_withoutending =
filepath_of_image_for_input_initial_withoutending_list[filepath_of_image_for_input_initial_withoutending_list_counter]


filepath_of_image_for_input_combined = paste( filepath_of_image_for_input_initial_withoutending  , ".tif", sep="")

#    filepath_of_image_for_output_combined = paste(
"D:\\bio_data_20210816\\experiments20211017\\MAX_080621_15DIV_Gas7_GFP_10min_100_uM_LY294002_C01_Z2_ns_imagej_zprojf1t17maxint_expim", "_sm",  sigma_value_for_brush , ".tif", sep="")


filepath_of_image_for_output_combined = paste( filepath_of_image_for_input_initial_withoutending , "_sm",  gsub("\\.", "dot",
sigma_value_for_brush) , ".tif", sep="")


image_test_in_ebimageformat_exp <- readImage( filepath_of_image_for_input_combined )

plot(image_test_in_ebimageformat_exp)


image_test_in_ebimageformat_exp



w_brush = makeBrush(size = 51, shape = "gaussian", sigma = sigma_value_for_brush)

tibble(w_brush = w_brush[(nrow(w_brush)+1)/2, ]) %>% ggplot(aes(y = w_brush, x = seq(along = w_brush))) + geom_point()


#  oli aiemmin:  nucSmooth = filter2(getFrame(cells, 1), w)

nucSmooth = filter2(getFrame( image_test_in_ebimageformat_exp , 1), w_brush)


EBImage::display(nucSmooth, method = "raster")


# vaikutteita: https://rdrr.io/bioc/EBImage/man/io.html


writeImage(nucSmooth, filepath_of_image_for_output_combined )



}  #  loppusulku ehdolle:   for( sigma_value_for_brush_list_counter in 1:(   length( sigma_value_for_brush_list )  ) )  {


}  #  loppusulku ehdolle: for( filepath_of_image_for_input_initial_withoutending_list_counter in 1:(   length(
filepath_of_image_for_input_initial_withoutending_list )  ) )  {


#    qqqqqqqqqqqqqqqqqq
```

Part 2/2 of the script: Identifying and analyzing the emergence of brightness clusters in the given neural images (input images):

```
# TULEE ANTAA ALUKSI R-KIELENKOMENTOKEHOTEIKKUNASSA KIRJASTOJEN LATAUSKOMENTOJA JA MUITA ALUSTUSKOMENTOJA  (KS. EDELLÄ OLEVAA KUVAILUA)



image_x_axis_length = 1024
image_y_axis_length = 1024
x_func_axis_length = image_x_axis_length
y_func_axis_length = image_y_axis_length

library(magrittr)
library(tidyverse)
library(imager)
# huom. tärkeä kirjasto:
library(magick)

# huom. komento library(spatstat) on jo sijoitettu vaiheeseen 1/3 alustuskomentona, jotta nykyisessä funktiossa function_laurin_step007 komennot toimisivat, mutta huom. on todella olennaista, että ensin annetaan komento library(spatstat) ja sitten vasta komento komento library(EBImage) jotta pällekkäisen distmap-funktion osalta jäisi voimaan nimenoaan EBImage-kirjaston versio distmap-funktiosta, koska muuten (eli jos ensin annetaan komento library(EBImage) ja sitten vasta komento komento library(spatstat)  ) tulisi virheilmoituksia

library(spatstat)
# huom. tärkeä kirjasto:
library(EBImage)
library(ggplot2)
```

```
analysis_list_of_filenames_initial <- c(
"ni20220615b_exp1a_im003" ,
"ni20220615b_exp1a_im003_sm0dot7" ,
"ni20220615b_exp1a_im003_sm0dot8" ,
"ni20220615b_exp1a_im003_sm0dot9" ,
"ni20220615b_exp1a_im004" ,
"ni20220615b_exp1a_im004_sm0dot7" ,
"ni20220615b_exp1a_im004_sm0dot8" ,
"ni20220615b_exp1a_im004_sm0dot9" ,
"ni20220615b_exp1a_im005" ,
"ni20220615b_exp1a_im005_sm0dot7" ,
"ni20220615b_exp1a_im005_sm0dot8" ,
"ni20220615b_exp1a_im005_sm0dot9" ,
"ni20220615b_exp1a_im006" ,
"ni20220615b_exp1a_im006_sm0dot7" ,
"ni20220615b_exp1a_im006_sm0dot8" ,
"ni20220615b_exp1a_im006_sm0dot9" ,
"ni20220615b_exp1a_im007" ,
"ni20220615b_exp1a_im007_sm0dot7" ,
"ni20220615b_exp1a_im007_sm0dot8" ,
"ni20220615b_exp1a_im007_sm0dot9" ,
"ni20220615b_exp1a_im008" ,
"ni20220615b_exp1a_im008_sm0dot7" ,
"ni20220615b_exp1a_im008_sm0dot8" ,
"ni20220615b_exp1a_im008_sm0dot9" ,
"ni20220615b_exp1a_im009" ,
"ni20220615b_exp1a_im009_sm0dot7" ,
"ni20220615b_exp1a_im009_sm0dot8" ,
"ni20220615b_exp1a_im009_sm0dot9" ,
```

"ni20220615b_exp1a_im010" ,
"ni20220615b_exp1a_im010_sm0dot7" ,
"ni20220615b_exp1a_im010_sm0dot8" ,
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"ni20220615b_exp1a_im032_sm0dot8" ,
"ni20220615b_exp1a_im032_sm0dot9"
)


# lisäys 20211026, osio 1: tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä

analysis_list_of_filenames_initial_original_nonblurred_images <- c(
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)



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"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set109\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set110\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set111\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set112\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set113\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set114\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set115\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set116\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set117\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set118\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set119\\" ,
"C:\\tarkastelu_20220215alk_a\\experiments20220615b\\test20220615b_set120\\"
)


# tämä muuttuja max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed auttaa poistamaan segementoinnin myötä syntyneestä elementtijoukosta sellaiset elementit, joiden koko (eli pikseleiden määrä) on sen verran vähäinen, että ne halutaan sivuttaa tarkastelussa

# poistettu käytöstä tämä määrittely, koska tämä muuttujanarvo poimitaan nykyään mieluummin for-silmukassa luettelosta:
max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed <- 100


analysis_list_of_max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed <- c( -1, 25 )

analysis_list_of_brightness_thresholdvalue <- c( 0.04, 0.06, 0.08, 0.10, 0.12 )



# 20220507_muokkauksia:
# huom. jotta tulostuvissa tiedostonimissä saataisiin näkyviin myös brightness_thresholdvalue-lukuarvon lopussa mahdollisesti oleva/olevia nolla/nollia (trailing zeros) tukemaan johdonmukaisesti etenevää tiedostonimien muotoilua (jotta niiden selailu ja lajittelu aakkosjärjestyksiin olisi intuitiivista), niin pakotetaan näkyviin aina tietty määrä desimaaleja desimaalipisteen jälkeen, esim. kaksi numeroa desimaalipisteen jälkeen; seuraavassa kuvaillaan, miten tätä toteutetaan:
# lisättiin aivan seuraavassa olevaan kohtaan määrittely
# brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot = 2
# ja vähän myöhemmin tässä tiedostossa yhdeksässä kohdassa
# korvattiin ilmaisu
# gsub("\\.", "dot", brightness_thresholdvalue)
# ilmaisulla
# gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f',
digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  )
# huom. tuon em. Ilmaisujen korvaamisen yhteydessä lauri joutui käsityönä täsmentämään, kun copy-pasten myötä lainausmerkit ja heittomerkit muuntuivat word-ohjelman automaattisesti sähläämänä kaareviksi lainausmerkeiksi ja kaareviksi heittomerkeiksi, ja lauri siis joutui käsityönä korjaamaan nuo muuntuneet kaarevat lainausmerkit suoriksi lainausmerkeiksi ja kaarevat heittömerkit suoriksi heittomerkeiksi, jotta tämä ohjelmalistaus toimisi ilman virheitä r-kielen komentoikkunaan copy-paste-menetelmällä ajettavaksi vietynä

# 20220507_muokkauksia:

brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot = 2



# käydään for-silmukassa lävitse kaikki list-luettelossa analysis_list_of_filenames_initial olevat tiedostonimet ja toteutetaan kullekin niistä analyysi, joka generoi tuloksia omaan erilliseen kohdekansioon

for( counter_index_for_analysis in 1:length(analysis_list_of_filenames_initial) ) {
```

```
                # käydään for-silmukassa lävitse kaikki list-luettelossa
analysis_list_of_max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed olevat
max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed-arvot ja toteutetaan kullekin niistä analyysi, joka generoi
tuloksia samaan kohdekansioon

                for( counter_index_for_max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed in 1:length(
analysis_list_of_max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed ) ) {



              # käydään for-silmukassa lävitse kaikki list-luettelossa analysis_list_of_brightness_thresholdvalue olevat brightness_thresholdvalue-arvot
ja toteutetaan kullekin niistä analyysi, joka generoi tuloksia samaan kohdekansioon

                for( counter_index_for_brightness_thresholdvalue in 1:length(analysis_list_of_brightness_thresholdvalue) ) {


  print( paste( "counter_index_for_analysis on nyt arvoltaan ", counter_index_for_analysis, sep="" )  )



filepath_of_image_for_input_folder_initial <- "C:\\tarkastelu_20220215alk_a\\inputimages20220615b\\"

# 20220322: tässä määritellään mask-kuvatiedostojen kansiopolku, ja noiden tiedostojen osalta viitataan nyt 20220322 alkaen nimenomaan
tiedostonimiin, joissa on lisuke nb eli laajemmassa muodossaan _mask01nb
# siis tämän komennon, joka määrittelee mask-kuvatiedostojen kansiopolun, jälkeen on vähän edempänä erillinen toinen komento, jossa määritellään
poimittavaksi mask-kuvatiedostoja joissa 20220322_päivitettyfilenamenytmuotoon _mask01nb
filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_folder_initial <-
"C:\\tarkastelu_20220215alk_a\\maskimages20220615b\\"


# HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .tif
# poistettu käytöstä: filepath_of_image_for_input_filename_initial <-"ni20220601b_exp1a_im001"

# HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .tif
filepath_of_image_for_input_filename_initial <- analysis_list_of_filenames_initial[ counter_index_for_analysis ]


# lisäys 20211026, osio 2: tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä

# HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .tif
filepath_of_image_for_input_filename_initial_original_nonblurred_images <- analysis_list_of_filenames_initial_original_nonblurred_images[
counter_index_for_analysis ]




# HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .png
# poistettu käytöstä: filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_filename_initial <-
"ni20220601b_exp1a_im001_mask01_whiteoverblack"
# poistettu käytöstä: filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_filename_initial <- paste(
analysis_list_of_filenames_initial[ counter_index_for_analysis ] , "_mask01_whiteoverblack", sep="" )

# POISTETTU KÄYTÖSTÄ:   # HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .png
# POISTETTU KÄYTÖSTÄ:   filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_filename_initial <- paste(
analysis_list_of_filenames_initial[ counter_index_for_analysis ] , "_mask01", sep="" )

# 20220129_päivitetty # 20220322_päivitettyfilenamenytmuotoon _mask01nb
# HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .png
filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_filename_initial <- paste(
analysis_list_of_filenames_initial_original_nonblurred_images[ counter_index_for_analysis ] , "_mask01nb", sep="" )




# poistettu käytöstä: filepath_of_image_for_output_folder_initial <- "C:\\tarkastelu_20220215alk_a\\experiments20220601\\test20220601a_set1\\"

filepath_of_image_for_output_folder_initial <- analysis_list_of_folders_initial[ counter_index_for_analysis ]


# HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .tif
# poistettu käytöstä: filepath_of_image_for_output_filename_initial <- "ni20220601b_exp1a_im001"

# HUOM. tässä tarkoituksella tiedostonimi ilman lopussa olevaa päätettä .tif
filepath_of_image_for_output_filename_initial <- analysis_list_of_filenames_initial[ counter_index_for_analysis ]
```

```
# 20211215 POIS KÄYTÖSTÄ: brightness_thresholdvalue <- 0.3

brightness_thresholdvalue <- analysis_list_of_brightness_thresholdvalue[ counter_index_for_brightness_thresholdvalue ]



filepath_of_image_for_input_combined <- paste( filepath_of_image_for_input_folder_initial, filepath_of_image_for_input_filename_initial, ".tif", sep="" )


# lisäys 20211026, osio 3: tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä

filepath_of_image_for_input_original_nonblurred_images_combined <- paste( filepath_of_image_for_input_folder_initial, filepath_of_image_for_input_filename_initial_original_nonblurred_images, ".tif", sep="" )




# lisays20210927:

filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined <- paste( filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_folder_initial, filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_filename_initial, ".png", sep="" )



c2 <- readImage( filepath_of_image_for_input_combined )


plot(c2)


c2_gray = channel(c2, 'gray')

plot(c2_gray)




# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_originalaspngfile",  ".png", sep="" )



# HUOM. ERITTÄIN OLENNAISTA KÄYTTÄÄ ALLA OLEVAA MÄÄRETTÄ type="cairo" JOLLOIN KUVAT TALLENTUVAT PARHAALLA TERÄVYYDELLÄ ILMAN HARMAASÄVY-ANTIALIASINGIA, SILTÄ VAIKUTTAA

png(filename = filepath_of_image_for_output_temp, dim(c2_gray)[1] , dim(c2_gray)[2] , type="cairo" )

par(mar = c(0, 0, 0, 0))

plot(c2_gray)


dev.off()




# lisays20210927a_alk


# vaihe B4: filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined



#  kunnolla toimiva (eli ei enää virheellisesti valkoisia rajaviivoja alueiden ympärillä):

image_test_in_magickimageformat_observ <- image_read( filepath_of_image_for_input_combined )

plot(image_test_in_magickimageformat_observ)
```

```
# tarvittaessa pitää varmistaa, että on varmasstai pelkästää mustaa ja valkoita (eikä yhtään harmaasävyjä rajaviivalla tiedostsossa test_exp_20210730_temp.png )

# HUOM. ERITTÄIN OLENNAISTA KÄYTTÄÄ R-skripteissä YLLÄ ylempänä png-tallennuksen yhteydessä OLEVAA MÄÄRETTÄ type="cairo" JOLLOIN KUVAT TALLENTUVAT PARHAALLA TERÄVYYDELLÄ ILMAN HARMAASÄVY-ANTIALIASINGIA, SILTÄ VAIKUTTAA

image_test_in_magickimageformat_observ2 <- image_read( filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined )

plot(image_test_in_magickimageformat_observ2)



# lisays20210927:
# tulostetaan pelkkä mask-kuva (eli valkoinen maskialue mustalla taustalla)


# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_mask", ".png", sep="" )


# HUOM. NYT TÄRKEÄÄ KÄYTTÄÄ ALLA OLEVAA TALLENNUSKOMENTOA JOTTA LAYERED-MAGICIMAGEFORMAT-KUVA TALLENTUISI PARHAALLA TERÄVYYDELLÄ JA NIIN ETTÄ ALKUPERÄISEN KUVAN PORTAITTAISIET SÄVYT (SIIS NE SÄVYT JOTKA OLI OTETTU MASKIN RAJAUKSESSA MUKAAN TIETYN THRESHOLDIN YLITTÄVINÄ SÄVYARVOINA) TULEVAT NÄKYVIIN JA LISÄKSI PIKSELIN TARKASTI OVAT MASKIIN KUULUVAT PIKSELIJOUKOT JA YKSITTÄISETKIN PIKSELIIT NÄKYVISSÄ ILMAN ANTIALIASINGIA TAI MUUTA BLURRAUTUMISTA

image_write(image_test_in_magickimageformat_observ2, path = filepath_of_image_for_output_temp, format = "png")




#  uusi mask_transparent_overlay_over_original_image-osio 20220129 alkaa tästä

# lisays20210927:
# tulostetaan pelkkä mask_transparent_overlay_over_original_image-kuva (eli punaisella värillä määrätään läpikuultavasti maskialue niin, että sen läpi kuultaa alkuperäinen kuva taustalla)

# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt

# uusi20210728, päivitetty 20220129:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_masktr", ".png", sep="" )


# HUOM. NYT TÄRKEÄÄ KÄYTTÄÄ ALLA OLEVAA TALLENNUSKOMENTOA JOTTA LAYERED-MAGICIMAGEFORMAT-KUVA TALLENTUISI PARHAALLA TERÄVYYDELLÄ JA NIIN ETTÄ ALKUPERÄISEN KUVAN PORTAITTAISIET SÄVYT (SIIS NE SÄVYT JOTKA OLI OTETTU MASKIN RAJAUKSESSA MUKAAN TIETYN THRESHOLDIN YLITTÄVINÄ SÄVYARVOINA) TULEVAT NÄKYVIIN JA LISÄKSI PIKSELIN TARKASTI OVAT MASKIIN KUULUVAT PIKSELIJOUKOT JA YKSITTÄISETKIN PIKSELIIT NÄKYVISSÄ ILMAN ANTIALIASINGIA TAI MUUTA BLURRAUTUMISTA

# EI KÄYTÖSSÄ: image_write(image_test_in_magickimageformat_observ2, path = filepath_of_image_for_output_temp, format = "png")

# HUOM. KÄYTETTÄVÄ NIMENOMAAN EBImage-kirjaston mukaisia tiedostojen lukemis- ja kirjoittamis- yms. komentoja (ks. https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf)


#  EI KÄYTÖSSÄ:   maskimage_in_ebimageformat = readImage( filepath_of_image_for_output_temp )

maskimage_in_ebimageformat = readImage( filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined )

maskimage_in_ebimageformat_gray = channel(maskimage_in_ebimageformat, 'gray')

maskimage_thresholded = thresh(maskimage_in_ebimageformat_gray, 10, 10, 0.05)



# lisäys 20220129 (tavallaan lisäys 20211026, osio 5extra20220129): tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä
```

```
c2_gray_original_nonblurred_image <- readImage( filepath_of_image_for_input_original_nonblurred_images_combined )


plot(c2_gray_original_nonblurred_image)


c2_gray_original_nonblurred_image_gray = channel(c2_gray_original_nonblurred_image, 'gray')

plot(c2_gray_original_nonblurred_image_gray)



#  huom. muuttujassa c2_gray_original_nonblurred_image_gray on jo aiemmin nimenomaanomaan EBImage-muodossa ladattu alkuperäinen harmaasävykuva, jota EI OLE BLURRATTU (SITÄ EI SIIS OLE PEHMENNETTY)


# transp_overl_kokeilu_1/2: yritetään ensimmäisenä kokeiluna harmaasävykuvien avulla, mutta tällöin ei saada värillisiä transparent_overlay-merkintöjä näkyviin:

#  EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded_gray , c2_gray_original_nonblurred_image_gray  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))

#  EI KÄYTÖSSÄ:     display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title=' output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')



# transp_overl_kokeilu_2/2: yritetään toisena kokeiluna värikuvien (eli ei vain harmaasävykuvien) avulla, yritetään saada värillisiä transparent_overlay-merkintöjä näkyviin:

# ilmeisesti tärkeää erikseen antaa komento c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image ) JOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN (ks. https://stackoverflow.com/questions/45660935/add-color-elements-to-single-frame-greyscale-image), JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT
#  MUTTA SEN SIJAAN TUOTTAISI ONGELMIA (eli harmaasävyt näytettäisiin vain punaisen kanavan muodossa esitettyinä punasävyinä) KÄYTTÄÄ KOMENTOA: c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')
# SIIS KOMENTO c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )
#  AUTTAA SIINÄ, ETTÄ saadaan ebimage-muodossa oleva kuva käsitellyksi värikuvamuodossa, jotta saadaan harmaasävyisen alkuperäiskuvan päälle värillisiä transp_overl_merkintöjä; alun perin ebimagen lukemiskomento tuntuu (ehkä muistin säästämiseksi) lataavan kuvan harmaasävymuodossa, ks. esim. tuloste:
#  EI KÄYTÖSSÄ:  > c2_gray_original_nonblurred_image
#  EI KÄYTÖSSÄ:  Image
#  EI KÄYTÖSSÄ:    colorMode    : Grayscale
#  EI KÄYTÖSSÄ:   storage.mode : double
#  EI KÄYTÖSSÄ:    dim          : 1024 1024
#  EI KÄYTÖSSÄ:    frames.total : 1
#  EI KÄYTÖSSÄ:    frames.render: 1
#  EI KÄYTÖSSÄ:
#  EI KÄYTÖSSÄ:  imageData(object)[1:5,1:6]
# joten lienee käytettävä komentoa  z = Image(m, colormode='Color')  (ks. https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf )


# EI KÄYTÖSSÄ:   c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')

# EI KÄYTÖSSÄ:   plot(c2_gray_original_nonblurred_image_incolormode)

# TÄLLÄ KOMENNOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN, JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT:

c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )

plot(c2_gray_original_nonblurred_image_incolormode_keepinggrayshades)


# HUOM. MUUTTUJALLA maskimage_thresholded ON storage.mode : integer JA MUUTTUJALLA maskimage_in_ebimageformat_gray ON storage.mode : double
# KUITENKIN TUNTUISI SILTÄ, ETTÄ TÄSTÄ EROSTA HUOLIMATTA VOIDAAN MOLEMPIA KÄYTTÄÄ PaintObject-komennossa parametreina MUTTA KUITENKIN LAURI HUOMASI, ETTÄ EDELLÄ TAPAHTUNEESSA MUUTTUJAN maskimage_thresholded MÄÄRITTELELYSSÄ EI SAATU KOROSTUNEEKSTI TULEVAAN ÄÄRISIVIIVOJEN RAJAAMAA ALUETTA VALITUKSI SITEN KUIN LAURIN KOKEILUSSA
# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt
```

```
#
#  > nuc = readImage(system.file('images', 'nuclei.tif', package='EBImage'))
#  >
#  > nmask = thresh(nuc, 10, 10, 0.05)
#  >
#  > plot( nuc )
#  >
#  > plot( nmask )
# JOKA POHJAUTUU ESIMERKKIIN  (https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf JA ) JA TÄTEN LAURI PÄÄTYI KÄYTTÄMÄÄN MUUTTUJAAN EDELLÄ TEHTYÄ MÄÄRITTELYÄ, JOTTA LAURI SAA TRANSPARENT_LAYERIN-GENEROIDUKSI NIMENOMAAN ALUEEN (JA MYÖS ÄÄRIVIIVAN) MAALATEN, EIKÄ VAIN ÄÄRILAITOJEN JA ÄÄRILAITAVIIVAN SISÄOSION (SIIS EI ÄÄRIVIIVOEN RAJAAMANA ALUEEN, VAAN ÄÄRIVIVAN SISÄOSION) VÄRITYKSEEN TYYTYEN, KUTEN NÄYTTÄISI KÄYVÄN MUUTTUJALLA PaintObject-komentoa SUORITETTAESSA, SIIS YHTEENVETONA: LAURI PÄÄTYI KÄYTTÄMÄÄN KOMENTOA: maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))
#
# TAUSTATARKASTELUA:
#   > maskimage_thresholded
#   Image
#     colorMode    : Grayscale
#     storage.mode : integer
#     dim          : 1024 1024
#     frames.total : 1
#     frames.render: 1
#
#   imageData(object)[1:5,1:6]
#        [,1] [,2] [,3] [,4] [,5] [,6]
#   [1,]    0    0    0    0    0    0
#   [2,]    0    0    0    0    0    0
#   [3,]    0    0    0    0    0    0
#   [4,]    0    0    0    0    0    0
#   [5,]    0    0    0    0    0    0
#   >
#   > maskimage_in_ebimageformat_gray
#   Image
#     colorMode    : Grayscale
#     storage.mode : double
#     dim          : 1024 1024
#     frames.total : 1
#     frames.render: 1
#
#   imageData(object)[1:5,1:6]
#        [,1] [,2] [,3] [,4] [,5] [,6]
#   [1,]    0    0    0    0    0    0
#   [2,]    0    0    0    0    0    0
#   [3,]    0    0    0    0    0    0
#   [4,]    0    0    0    0    0    0
#   [5,]    0    0    0    0    0    0
#   >

# EI KÄYTÖSSÄ, KOSKA EI SAADA ÄÄRIVIIVOJEN RAJAAMAA ALUETTA KUNNOLLA MAALATUKSI, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))


#  KÄYTÖSSÄ, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# huom. määritellään väri ja läpikuultavuus sekä ääriviivalle että sen raajamalle alueelle käyttäen vektorimuodossa olevia kahden elementin c(arvo1, arvo2)-luetteloita:
# aiemmin käytössä OUTLINEpurple_INSIDEyellow: col=c('#ff00ff', '#ffff00'), opac=c(0.1, 0.1)

maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.1, 0.1) )


plot( maskimage_transparentlyoverlayed_over_orginalnonblurredimage )

#  EI KÄYTÖSSÄ:  display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title='
output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')


#  seuraavalla komennolla toteutetaan mask_transparent_overlay_over_original_image-kuvatiedoston tallentaminen tiedostoon:

writeImage(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, filepath_of_image_for_output_temp, quality=100);
```

```
#  uusi mask_transparent_overlay_over_original_image-osio 20220129 loppuu tähän

# lisayksen 20210927 jälkeistä:


# 20210729: lauri vaihtoi muuttujan nimen johdonmukaisemmaksi:
# oli ennen: image_test_in_magickimageformat2_blackcolorchangedtobetransparent
# on nyt: image_test_in_magickimageformat2_whitecolorchangedtobetransparent

image_test_in_magickimageformat_observ2_whitecolorchangedtobetransparent <- image_transparent(image_test_in_magickimageformat_observ2,
'white')

plot(image_test_in_magickimageformat_observ2_whitecolorchangedtobetransparent)

image_layer_list_observ <- c(image_test_in_magickimageformat_observ,
image_test_in_magickimageformat_observ2_whitecolorchangedtobetransparent)

image_in_magickimageformat_combined_with_layers_observ <- image_mosaic(image_layer_list_observ)

# HUOM. EI TARVITSE HETI HUOLESTUA, JOS TÄMÄ R-KONSOLIN TULOSTEKUVA NÄYTTÄÄ PELKÄLTÄ MUSTALTA, SILLA
KUN TALLENTAA TUON KUVAN ALLA HETKEÄ MYÖHEMMIN KUVAILLULLA KOMENNOLLA PNG-KUVATIEDOSTOON NIIN
TUOSTA VARSINAISESTA 1024x1024-kokoisesta KUVASTA ZOOMATTUNA VOI USEIMMITEN ONNEKSI NÄHDÄ TULEVAAN ESIIN
HARMAASÄVYLLÄ PIIRTYVIÄ YKSITYISKOHTIA

plot(image_in_magickimageformat_combined_with_layers_observ)



# tulostetaan pelkkä maskedpix-kuva (eli maskialueella olevat hermostokuvan pikselit)

# pois:  filepath_of_image_for_output_temp <- filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined
```

```
# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_maskedpix", ".png", sep="" )


# HUOM. NYT TÄRKEÄÄ KÄYTTÄÄ ALLA OLEVAA TALLENNUSKOMENTOA JOTTA LAYERED-MAGICIMAGEFORMAT-KUVA TALLENTUISI PARHAALLA TERÄVYYDELLÄ JA NIIN ETTÄ ALKUPERÄISEN KUVAN PORTAITTAISIET SÄVYT (SIIS NE SÄVYT JOTKA OLI OTETTU MASKIN RAJAUKSESSA MUKAAN TIETYN THRESHOLDIN YLITTÄVINÄ SÄVYARVOINA) TULEVAT NÄKYVIIN JA LISÄKSI PIKSELIN TARKASTI OVAT MASKIIN KUULUVAT PIKSELIJOUKOT JA YKSITTÄISETKIN PIKSELIIT NÄKYVISSÄ ILMAN ANTIALIASINGIA TAI MUUTA BLURRAUTUMISTA

image_write(image_in_magickimageformat_combined_with_layers_observ, path = filepath_of_image_for_output_temp, format = "png")


#  EDELLÄ OLEVALLA SAATIIN ILMEISESTI TOIMIVAT TULOKSET GENEROIDUKSI, MIKÄ ON ILAHDUTTAVAA




# lisays20210927a_lop




# lisays20210927: ladataan maskedpix-kuva tiedostosta käyttäen ebimage-tiedostoavaamiskomentoa readImage(), millä varmistetaan, että ladattava tiedosta avataan juuri ebimage-muotoiseen muutujaan:


# uusi20210728:

filepath_of_image_for_input_maskedpix_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_maskedpix", ".png", sep="" )

c2_gray_masked_pixels <- readImage( filepath_of_image_for_input_maskedpix_temp )

plot(c2_gray_masked_pixels)


# lisays20210927: korvattiin seuraavassa muuttuja c2_gray ilmaisulla c2_gray_masked_pixels, jotta saadaan tarkasteluun juuri maskedpix-kuva:


c2_gray_eval_brightnessabovethresholdvalue <- c2_gray_masked_pixels > brightness_thresholdvalue # apply simple threshold

plot( c2_gray_eval_brightnessabovethresholdvalue )




# uusi20210728:

max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed <- analysis_list_of_max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed[ counter_index_for_max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed ]


filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f', digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  ), "_areg",  gsub("\\.", "dot", max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), ".png", sep="" )


#  20220129: TALLENNETAAN seuraavalla komennolla NYT brightnessabovethresholdvalue_cnt-KUVAN OUTPUT-TIEDOSTONIMI KÄYTETTÄVÄKSI MYÖHEMMIN INPUT-TIEDOSTONIMENÄ, JOTTA VOIDAAN MYÖHEMMIN LADATA TÄMÄ KUVA, JOTTA VOIDAAN GENEROIDA TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVA:
# EI ENÄÄ VOIMASSA: JA JOTTA brightnessabovethresholdvalue_cnt-KUVAN TIEDOSTONIMEN POHJALTA VOIDAAN GENEROIDA UUSI TIEDOSTONIMI TUOLLE TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVALLE

filepath_output_c2_gray_eval_brightnessabovethresholdvalue_cnt <- filepath_of_image_for_output_temp
```

```
c2_gray_eval_brightnessabovethresholdvalue_cnt_initial <- bwlabel(  c2_gray_eval_brightnessabovethresholdvalue  ) # count the 'regions'



# next category is shapes
# these a calculated from the thresholded image
fts_initial <- computeFeatures.shape( c2_gray_eval_brightnessabovethresholdvalue_cnt_initial )

# 20210818 harhaanjohtavuuden vähentämiseksi lauri vaihtoi regions-elementin nimeksi region_index


area_initial <- fts_initial[,1]  # select first column from object called fts

df_area_element_candidates_initial <- area_initial

c2_gray_eval_brightnessabovethresholdvalue_cnt <- rmObjects( c2_gray_eval_brightnessabovethresholdvalue_cnt_initial , which(
df_area_element_candidates_initial <= max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed     ) )

                        plot( c2_gray_eval_brightnessabovethresholdvalue_cnt  )



fts_initial_testingifnoelements <- computeFeatures.shape( c2_gray_eval_brightnessabovethresholdvalue_cnt )


if (   not(  is.null( fts_initial_testingifnoelements )  )  )  {


# HUOM. ERITTÄIN OLENNAISTA KÄYTTÄÄ ALLA OLEVAA MÄÄRETTÄ type="cairo" JOLLOIN KUVAT TALLENTUVAT
PARHAALLA TERÄVYYDELLÄ ILMAN HARMAASÄVY-ANTIALIASINGIA, SILTÄ VAIKUTTAA

png(filename = filepath_of_image_for_output_temp, dim(c2_gray)[1] , dim(c2_gray)[2] , type="cairo" )

par(mar = c(0, 0, 0, 0))

# 20211215 POIS KÄYTÖSTÄ:   plot(c2_gray_eval_brightnessabovethresholdvalue)

                        plot( c2_gray_eval_brightnessabovethresholdvalue_cnt  )

dev.off()



# 20211215 POIS KÄYTÖSTÄ:   c2_gray_eval_brightnessabovethresholdvalue_cnt <- bwlabel(  c2_gray_eval_brightnessabovethresholdvalue  ) #
count the 'regions'



c2_gray_eval_brightnessabovethresholdvalue_cnt_withcolorlabels <- colorLabels( c2_gray_eval_brightnessabovethresholdvalue_cnt )


plot( c2_gray_eval_brightnessabovethresholdvalue_cnt_withcolorlabels )



# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial,
"_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f',
digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  ), "_areg",  gsub("\\.", "dot",
max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_reg_colorlabels",  ".png", sep="" )


# HUOM. ERITTÄIN OLENNAISTA KÄYTTÄÄ ALLA OLEVAA MÄÄRETTÄ type="cairo" JOLLOIN KUVAT TALLENTUVAT
PARHAALLA TERÄVYYDELLÄ ILMAN HARMAASÄVY-ANTIALIASINGIA, SILTÄ VAIKUTTAA

png(filename = filepath_of_image_for_output_temp, dim(c2_gray)[1] , dim(c2_gray)[2] , type="cairo" )

par(mar = c(0, 0, 0, 0))
```

```
plot ( c2_gray_eval_brightnessabovethresholdvalue_cnt_withcolorlabels )

dev.off()



# lisäys 20211026, osio 4: tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä

c2_gray_original_nonblurred_image <- readImage( filepath_of_image_for_input_original_nonblurred_images_combined )


plot(c2_gray_original_nonblurred_image)


c2_gray_original_nonblurred_image_gray = channel(c2_gray_original_nonblurred_image, 'gray')

plot(c2_gray_original_nonblurred_image_gray)




 #  uusi20210728:
# POISTETAAN 20210730 AIEMPI MUOTOILU:

ftb <- computeFeatures.basic(  c2_gray_eval_brightnessabovethresholdvalue_cnt , c2_gray_original_nonblurred_image_gray )

# POISTETAAN 20210730 AIEMPI MUOTOILU:

ftb_moment <- computeFeatures.moment(  c2_gray_eval_brightnessabovethresholdvalue_cnt , c2_gray_original_nonblurred_image_gray )






head(ftb, 10)


par(mar = c(0, 0, 0, 0))

# tärkeää asettaa parametriarvot: xaxs="i", yaxs="i", jotta poistuvat tyhjät valkoiset marginaalialueet kuvaajan pisteiden ja x-akselin välistä sekä kuvaajan pisteiden ja y-akselin välistä
#   https://stackoverflow.com/questions/12300622/remove-spacing-around-plotting-area-in-r
#   https://stackoverflow.com/a/12300673
#  There is an argument in function plot that handles that: xaxs (and yaxs for the y-axis). As default it is set to xaxs="r" meaning that 4% of the axis value is left on each side. To set this to 0: xaxs="i". See the xaxs section in ?par for more information.

plot(NULL, xlim=c(0,  dim(c2_gray)[1] ), ylim=c(0,  dim(c2_gray)[2] ), xaxs="i", yaxs="i")

# käännetään vain y-akselin osata ylösalaisin olleet koordinaatti arvot oikein päin
# numeroinnin lukuväli on ilmaistu lausekkeellla lukuvälin_alkupää:lukuvälin_loppupää

text(x= ftb_moment[,1] , y= (  dim(c2_gray)[2]  - ftb_moment[,2] ) ,labels=1:(length( ftb_moment[,1] )) )



# päivitetty20210728_tiedostonimet:

# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial,
"_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f',
digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  ), "_areg",  gsub("\\.", "dot",
max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_reg_numberlabels",  ".png", sep="" )

#  HUOM_2. SEURAAVASSA TEXT()-KOMENTO PIIRTÄÄ PELKÄT ALUEIDEN NUMEROINTIA KOSKEVAT TEKSTIT NIIN, ETTÄ Y-AKSELIN SUHTEEN KOORDINAATIT OVAT OIKEIN PÄIN:

png(filename = filepath_of_image_for_output_temp,  dim(c2_gray)[1] , dim(c2_gray)[2]  , type="cairo" )

par(mar = c(0, 0, 0, 0))
```

```
# tärkeää asettaa parametriarvot: xaxs="i", yaxs="i", jotta poistuvat tyhjät valkoiset marginaalialueet kuvaajan pisteiden ja x-akselin välistä sekä kuvaajan pisteiden ja y-akselin välistä
#   https://stackoverflow.com/questions/12300622/remove-spacing-around-plotting-area-in-r
#   https://stackoverflow.com/a/12300673
#  There is an argument in function plot that handles that: xaxs (and yaxs for the y-axis). As default it is set to xaxs="r" meaning that 4% of the axis value is left on each side. To set this to 0: xaxs="i". See the xaxs section in ?par for more information.

plot(NULL, xlim=c(0, dim(c2_gray)[1] ), ylim=c(0, dim(c2_gray)[2] ), xaxs="i", yaxs="i")

# käännetään vain y-akselin osata ylösalaisin olleet koordinaatti arvot oikein päin
# numeroinnin lukuväli on ilmaistu lausekkeellla lukuvälin_alkupää:lukuvälin_loppupää

text(x= ftb_moment[,1] , y= (  dim(c2_gray)[2]  - ftb_moment[,2] ) ,labels=1:(length( ftb_moment[,1] )) )

dev.off()




library(ggplot2)



#   VALITETTAVASTEI TULI VIRHEILMOITUS KAIKETI MUISTIN TÄYTTYMISESTÄ:
#   > fts <- computeFeatures.shape(c2_gray.t.cnt)
#   Error: protect(): protection stack overflow
#   >

#   LAURI TOTETTI TÄMÄN ONNISTUNEESTI WINDOWSIN KOMENTOKEHOTEIKKUNASSA, JA TÄMÄN JÄLKEEN EI TULLUT EM. ONGELMAA MUISTIN LOPPUMISESTA:

#   Microsoft Windows [Version 10.0.18362.959]
#   (c) 2019 Microsoft Corporation. All rights reserved.

#   C:\Users\Lauri>cd C:\R\R-4.0.1\bin\x64

#   C:\R\R-4.0.1\bin\x64>ls
#   R.dll  RSetReg.exe  Rcmd.exe  Rgraphapp.dll  Riconv.dll   Rscript.exe  open.exe
#   R.exe  Rblas.dll    Rfe.exe   Rgui.exe       Rlapack.dll  Rterm.exe

#   C:\R\R-4.0.1\bin\x64>
#   C:\R\R-4.0.1\bin\x64>
#   C:\R\R-4.0.1\bin\x64>Rgui.exe --max-ppsize=500000

#   C:\R\R-4.0.1\bin\x64>

#   EM. KOMENNOLLA PITÄISI KÄYNNISTYÄ UUSI KONSOLI-IKKUNA NIIN, ETTÄ SE ON VARANNUT TAVALLISTA ENEMMÄN MUISTIA KÄYTTÖÖNSÄ (
#   https://stat.ethz.ch/R-manual/R-devel/library/base/html/Memory.html
#   The command-line option --max-ppsize controls the maximum size of the pointer protection stack. This defaults to 50000, but can be increased to allow deep recursion or large and complicated calculations to be done. Note that parts of the garbage collection process goes through the full reserved pointer protection stack and hence becomes slower when the size is increased. #   Currently the maximum value accepted is 500000.
#   )

#   YRITETÄÄN NYT UUDESTAAN, ONNISTUUKO LASKEA TULOS SEURAAVALLA KOMENNOLLA (
#   fts <- computeFeatures.shape(c2_gray.t.cnt)




# to get a vector of the mean intensities
# there is one value for each shape...

average_signal_per_pixel_of_region <- ftb[,1]


# next category is shapes
# these a calculated from the thresholded image
fts <- computeFeatures.shape( c2_gray_eval_brightnessabovethresholdvalue_cnt )
```

```
# 20210818 harhaanjohtavuuden vähentämiseksi lauri vaihtoi regions-elementin nimeksi region_index


area <- fts[,1]  # select first column from object called fts
perimeter <- fts[,2] # select second colum from object called fts


# put the data into a dataframe (a different kind of R object)
# df <- as.data.frame(m.intent)

df <- as.data.frame(average_signal_per_pixel_of_region)

df$area <- area


signal_per_area_of_region <- average_signal_per_pixel_of_region * area

df$signal_per_area_of_region <- df$average_signal_per_pixel_of_region * df$area


df$region_index <- seq(1:nrow(df))




#  talletetaan before-tilanteen arvot talteen, niin vanhoja muuttujanimiä voidaan käyttää ohjelmalistausta kierrättäen after-tilanteen analysointiin


df_situation_current <- df


area_situation_current <- area

average_signal_per_pixel_of_region_situation_current <- average_signal_per_pixel_of_region

signal_per_area_of_region_situation_current <- signal_per_area_of_region


# määritellään lukuluettelo, joka ilmaisee region_index-ominaisuutta
region_index_situation_current <- c(1:(length(area_situation_current)))


ftb_situation_current <- ftb

fts_situation_current <- fts




w_list_of_outlineregions_masscenterpoint_coordpoints = cbind( ftb_moment[,1], ftb_moment[,2] )




# huom. ei nyt käytätä _yaxisdirectionchagedtoopposite-versioita

regions_x_coord = w_list_of_outlineregions_masscenterpoint_coordpoints[, 1]

regions_y_coord = w_list_of_outlineregions_masscenterpoint_coordpoints[, 2]
```

```
area_specialcol = c(0, (dim(c2_gray)[1]) , 0, (dim(c2_gray)[2]))


area_specialcol

names(area_specialcol) = c("xl", "xu", "yl", "yu")

area_specialcol


# huom. seuraavassa as.numeric-komentoa EI KOHDISTETA ELEMENTTIIN area_specialcol JOTTA EI MENETETÄ EDELLÄ JUURI LISÄTTYJÄ NAMES-LISUKKEITA

# ON NYT KÄYTÖSSÄ:
# HUOM. TÄMÄ KOMENTO AIHEUTTAA Y-AKSELIN KOORDINAATTIEN NÄKYMISEN OIKEINPÄIN, TULOSTUVA KUVA ON SIIS NYT OIKEIN PÄIN, eli nyt y-akseli kasvaa oikeaan suuntaan
list_test_as_numeric_new = list(  x = as.numeric(regions_x_coord), y= as.numeric(  (dim(c2_gray)[2]) -  regions_y_coord), area = area_specialcol)

#   str(list_test_as_numeric_new)

list_test_as_numeric_new_as_ppp = as.ppp(list_test_as_numeric_new)
#  > list_test_as_numeric_new_as_ppp = as.ppp(list_test_as_numeric_new)
#  NYT 20210818 EI TULLUTKAAN SEURAAVAA VIRHEILMOITUSTA DUBLIKKAATIPISTEISTÄ:
#  Warning message:
#  data contain duplicated points
#  >

# plot(list_test_as_numeric_new_as_ppp, main=NULL)


# huom. alustusarvona ei enää NA vaan nolla eli 0
# ei enää:  w <- matrix(NA, x_axis_length ,y_axis_length)
# vaan on:  w <- matrix(0, x_axis_length ,y_axis_length)

 w_func <- matrix(0, (dim(c2_gray)[1]) , (dim(c2_gray)[2]) )


# voidaan yhtä hyvin käyttää tässä  length(list_test_as_numeric_new_as_ppp$x )  TAI
# length(list_test_as_numeric_new_as_ppp$x )   JA NYT VALITTIIIN KÄYTTÖÖN $x

looping_endvalue = length(list_test_as_numeric_new_as_ppp$x )

#  w_matriisiin_tulostamisen_rivi <- 1


for (n_looping in 1:looping_endvalue){

w_func[ list_test_as_numeric_new_as_ppp$x[n_looping],      (  (dim(c2_gray)[2])  -   list_test_as_numeric_new_as_ppp$y[n_looping]  )   ] = 1


#   w[w_matriisiin_tulostamisen_rivi] <-  output_report_string

#  w_matriisiin_tulostamisen_rivi <- w_matriisiin_tulostamisen_rivi + 1

}



display(w_func, method="raster")




# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f', digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  ), "_areg",  gsub("\\.", "dot", max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_reg_masscenterp",  ".png", sep="" )


#  POIS KÄYTÖSTÄ:    writeImage(nuclei_copyversion_step007_onlykeepingelementswithcertainsize, filepath_of_image_for_output_temp, quality=100);


png(filepath_of_image_for_output_temp, width= (dim(c2_gray)[1]) , height= (dim(c2_gray)[2]) );   # define png handling device
```

```
par(mar=c(0, 0, 0, 0));

# päivitetty20210729:
# tämä seuraava plot-tulostuskomento plot(w_func) tuottaa hämmenntävästi vain yhden pisteen näkyviin, onkohan huolestuttavaa
# toisaalta hieman alempana oleva komento display(w_func, method="raster") (20210729poisto: tässä oli aiemmin mainittuna image-komento) tuntuu tuottavan ihan mielekkään ja vivahteikkaamman tulostuksen
#  POISTETTU KÄYTÖSTÄ: plot(w_func)

display(w_func, method="raster")

dev.off();   # close png handling device




#  uusi TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt_outlineandinsideareawithdifferentcolors-osio 20220129 alkaa tästä

# lisays20210927:
# tulostetaan TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-kuva (eli punaisella värillä määrätään läpikuultavasti brightnessabovethresholdvalue_cnt-kuva niin, että sen läpi kuultaa alkuperäinen kuva taustalla)

# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt

# EI KÄYTÖSSÄ: # uusi20210728, päivitetty 20220129:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_masktr", ".png", sep="" )

# EI KÄYTÖSSÄ:   filepath_of_image_for_output_temp <- paste( filepath_output_c2_gray_eval_brightnessabovethresholdvalue_cnt, "_tr", ".png", sep="" )

#  20220129_lisämuutos_1/2: KÄYTETÄÄN NYT TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVAN TALLENTAMISESSA OUTPUT-TIEDOSTONIMENÄ SELLAISTA MUOTOILUA, JOKA ON ALKUOSA SIITÄ MUOTOILUSTA, JOTA ON EDELLÄ KÄYTETTY OUTPUT-TIEDOSTONIMENÄ, KUN ON TALLENNETTU brightnessabovethresholdvalue_cnt-KUVA, siis nyt käytetään samaa alkuosaa ja sen perään lisätään string ”_trdc”:

filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f', digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  ), "_areg",  gsub("\\.", "dot", max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_trdc", ".png", sep="" )



# HUOM. NYT TÄRKEÄÄ KÄYTTÄÄ ALLA OLEVAA TALLENNUSKOMENTOA JOTTA LAYERED-MAGICIMAGEFORMAT-KUVA TALLENTUISI PARHAALLA TERÄVYYDELLÄ JA NIIN ETTÄ ALKUPERÄISEN KUVAN PORTAITTAISIET SÄVYT (SIIS NE SÄVYT JOTKA OLI OTETTU MASKIN RAJAUKSESSA MUKAAN TIETYN THRESHOLDIN YLITTÄVINÄ SÄVYARVOINA) TULEVAT NÄKYVIIN JA LISÄKSI PIKSELIN TARKASTI OVAT MASKIIN KUULUVAT PIKSELIJOUKOT JA YKSITTÄISETKIN PIKSELIIT NÄKYVISSÄ ILMAN ANTIALIASINGIA TAI MUUTA BLURRAUTUMISTA

# EI KÄYTÖSSÄ: image_write(image_test_in_magickimageformat_observ2, path = filepath_of_image_for_output_temp, format = "png")

# HUOM. KÄYTETTÄVÄ NIMENOMAAN EBImage-kirjaston mukaisia tiedostojen lukemis- ja kirjoittamis- yms. komentoja (ks. https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf)


#  EI KÄYTÖSSÄ:   maskimage_in_ebimageformat = readImage( filepath_of_image_for_output_temp )

# EI KÄYTÖSSÄ:  maskimage_in_ebimageformat = readImage( filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined )


#  20220129_lisämuutos_2/2: HYÖDYNNETÄÄN NYT INPUT-TIEDOSTONIMENÄ EDELLLÄ AIEMMIN TALLENNETTU brightnessabovethresholdvalue_cnt-KUVAN OUTPUT-TIEDOSTONIMI, JOTTA VOIDAAN NYT SITÄ KÄYTTÄEN NYT KOHTA GENEROIDA TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVA:

maskimage_in_ebimageformat = readImage( filepath_output_c2_gray_eval_brightnessabovethresholdvalue_cnt )


maskimage_in_ebimageformat_gray = channel(maskimage_in_ebimageformat, 'gray')

maskimage_thresholded = thresh(maskimage_in_ebimageformat_gray, 10, 10, 0.05)
```

```
# lisäys 20220129 (tavallaan lisäys 20211026, osio 5extra20220129): tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä

c2_gray_original_nonblurred_image <- readImage( filepath_of_image_for_input_original_nonblurred_images_combined )


plot(c2_gray_original_nonblurred_image)


c2_gray_original_nonblurred_image_gray = channel(c2_gray_original_nonblurred_image, 'gray')

plot(c2_gray_original_nonblurred_image_gray)



#  huom. muuttujassa c2_gray_original_nonblurred_image_gray on jo aiemmin nimenomaanomaan EBImage-muodossa ladattu alkuperäinen harmaasävykuva, jota EI OLE BLURRATTU (SITÄ EI SIIS OLE PEHMENNETTY)


# transp_overl_kokeilu_1/2: yritetään ensimmäisenä kokeiluna harmaasävykuvien avulla, mutta tällöin ei saada värillisiä transparent_overlay-merkintöjä näkyviin:

#  EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded_gray , c2_gray_original_nonblurred_image_gray  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))

#  EI KÄYTÖSSÄ:     display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title=' output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')



# transp_overl_kokeilu_2/2: yritetään toisena kokeiluna värikuvien (eli ei vain harmaasävykuvien) avulla, yritetään saada värillisiä transparent_overlay-merkintöjä näkyviin:

# ilmeisesti tärkeää erikseen antaa komento c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image ) JOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN (ks. https://stackoverflow.com/questions/45660935/add-color-elements-to-single-frame-greyscale-image), JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT
#  MUTTA SEN SIJAAN TUOTTAISI ONGELMIA (eli harmaasävyt näytettäisiin vain punaisen kanavan muodossa esitettyinä punasävyinä) KÄYTTÄÄ KOMENTOA: c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')
# SIIS KOMENTO c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )
#  AUTTAA SIINÄ, ETTÄ saadaan ebimage-muodossa oleva kuva käsitellyksi värikuvamuodossa, jotta saadaan harmaasävyisen alkuperäiskuvan päälle värillisiä transp_overl_merkintöjä; alun perin ebimagen lukemiskomento tuntuu (ehkä muistin säästämiseksi) lataavan kuvan harmaasävymuodossa, ks. esim. tuloste:
#  EI KÄYTÖSSÄ:  > c2_gray_original_nonblurred_image
#  EI KÄYTÖSSÄ:  Image
#  EI KÄYTÖSSÄ:    colorMode    : Grayscale
#  EI KÄYTÖSSÄ:   storage.mode : double
#  EI KÄYTÖSSÄ:    dim          : 1024 1024
#  EI KÄYTÖSSÄ:    frames.total : 1
#  EI KÄYTÖSSÄ:    frames.render: 1
#  EI KÄYTÖSSÄ:
#  EI KÄYTÖSSÄ:  imageData(object)[1:5,1:6]
# joten lienee käytettävä komentoa  z = Image(m, colormode='Color')  (ks. https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf )


# EI KÄYTÖSSÄ:   c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')

# EI KÄYTÖSSÄ:   plot(c2_gray_original_nonblurred_image_incolormode)

# TÄLLÄ KOMENNOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN, JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT:

c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )

plot(c2_gray_original_nonblurred_image_incolormode_keepinggrayshades)


# HUOM. MUUTTUJALLA maskimage_thresholded ON storage.mode : integer JA MUUTTUJALLA maskimage_in_ebimageformat_gray ON storage.mode : double
# KUITENKIN TUNTUISI SILTÄ, ETTÄ TÄSTÄ EROSTA HUOLIMATTA VOIDAAN MOLEMPIA KÄYTTÄÄ PaintObject-komennossa parametreina MUTTA KUITENKIN LAURI HUOMASI, ETTÄ EDELLÄ TAPAHTUNEESSA MUUTTUJAN maskimage_thresholded
```

MÄÄRITTELELYSSÄ EI SAATU KOROSTUNEEKSTI TULEVAAN ÄÄRISIVIIVOJEN RAJAAMAA ALUETTA VALITUKSI SITEN KUIN LAURIN KOKEILUSSA

```
# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt
#
#  > nuc = readImage(system.file('images', 'nuclei.tif', package='EBImage'))
#  >
#  > nmask = thresh(nuc, 10, 10, 0.05)
#  >
#  > plot( nuc )
#  >
#  > plot( nmask )
# JOKA POHJAUTUU ESIMERKKIIN  (https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf JA ) JA TÄTEN LAURI PÄÄTYI KÄYTTÄMÄÄN MUUTTUJAAN EDELLÄ TEHTYÄ MÄÄRITTELYÄ, JOTTA LAURI SAA TRANSPARENT_LAYERIN-GENEROIDUKSI NIMENOMAAN ALUEEN (JA MYÖS ÄÄRIVIIVAN) MAALATEN, EIKÄ VAIN ÄÄRILAITOJEN JA ÄÄRILAITAVIIVAN SISÄOSION (SIIS EI ÄÄRIVIIVOEN RAJAAMANA ALUEEN, VAAN ÄÄRIVIVAN SISÄOSION) VÄRITYKSEEN TYYTYEN, KUTEN NÄYTTÄISI KÄYVÄN MUUTTUJALLA PaintObject-komentoa SUORITETTAESSA, SIIS YHTEENVETONA: LAURI PÄÄTYI KÄYTTÄMÄÄN KOMENTOA: maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))
#
# TAUSTATARKASTELUA:
#  > maskimage_thresholded
#  Image
#    colorMode    : Grayscale
#    storage.mode : integer
#    dim          : 1024 1024
#    frames.total : 1
#    frames.render: 1
#
#  imageData(object)[1:5,1:6]
#       [,1] [,2] [,3] [,4] [,5] [,6]
#  [1,]    0    0    0    0    0    0
#  [2,]    0    0    0    0    0    0
#  [3,]    0    0    0    0    0    0
#  [4,]    0    0    0    0    0    0
#  [5,]    0    0    0    0    0    0
#  >
#  > maskimage_in_ebimageformat_gray
#  Image
#    colorMode    : Grayscale
#    storage.mode : double
#    dim          : 1024 1024
#    frames.total : 1
#    frames.render: 1
#
#  imageData(object)[1:5,1:6]
#       [,1] [,2] [,3] [,4] [,5] [,6]
#  [1,]    0    0    0    0    0    0
#  [2,]    0    0    0    0    0    0
#  [3,]    0    0    0    0    0    0
#  [4,]    0    0    0    0    0    0
#  [5,]    0    0    0    0    0    0
#  >

# EI KÄYTÖSSÄ, KOSKA EI SAADA ÄÄRIVIIVOJEN RAJAAMAA ALUETTA KUNNOLLA MAALATUKSI, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))


#  KÄYTÖSSÄ, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# huom. määritellään väri ja läpikuultavuus sekä ääriviivalle että sen raajamalle alueelle käyttäen vektorimuodossa olevia kahden elementin c(arvo1, arvo2)-luetteloita:
# aiemmin käytössä OUTLINEred_INSIDEgreen: col=c('#ff0000', '#00ff00'), opac=c(0.1, 0.1)
# aiemmin käytössä OUTLINEpurple_INSIDEyellow: col=c('#ff00ff', '#ffff00'), opac=c(0.1, 0.1)
# aiemmin käytössä OUTLINEpurple_INSIDEgreen: col=c('#ff00ff', '#00ff00'), opac=c(0.1, 0.1)

maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#00ff00'), opac=c(0.1, 0.1) )


plot( maskimage_transparentlyoverlayed_over_orginalnonblurredimage )

#  EI KÄYTÖSSÄ:  display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title=' output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')
```

```
#  seuraavalla komennolla toteutetaan mask_transparent_overlay_over_original_image-kuvatiedoston tallentaminen tiedostoon:

writeImage(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, filepath_of_image_for_output_temp, quality=100);



#  uusi TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt_outlineandinsideareawithdifferentcolors-osio 20220129 loppuu tähän









#  uusi TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt_outlineandinsideareawithsamecolors-osio 20220129 alkaa tästä

# lisays20210927:
# tulostetaan TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-kuva (eli punaisella värillä määrätään läpikuultavasti brightnessabovethresholdvalue_cnt-kuva niin, että sen läpi kuultaa alkuperäinen kuva taustalla)

# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt

# EI KÄYTÖSSÄ: # uusi20210728, päivitetty 20220129:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_masktr", ".png", sep="" )

# EI KÄYTÖSSÄ:   filepath_of_image_for_output_temp <- paste( filepath_output_c2_gray_eval_brightnessabovethresholdvalue_cnt, "_tr", ".png", sep="" )

#  20220129_lisämuutos_1/2: KÄYTETÄÄN NYT TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVAN TALLENTAMISESSA OUTPUT-TIEDOSTONIMENÄ SELLAISTA MUOTOILUA, JOKA ON ALKUOSA SIITÄ MUOTOILUSTA, JOTA ON EDELLÄ KÄYTETTY OUTPUT-TIEDOSTONIMENÄ, KUN ON TALLENNETTU brightnessabovethresholdvalue_cnt-KUVA, siis nyt käytetään samaa alkuosaa ja sen perään lisätään string ”_trsc”:

filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial, "_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f', digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  ), "_areg",  gsub("\\.", "dot", max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_trsc", ".png", sep="" )



# HUOM. NYT TÄRKEÄÄ KÄYTTÄÄ ALLA OLEVAA TALLENNUSKOMENTOA JOTTA LAYERED-MAGICIMAGEFORMAT-KUVA TALLENTUISI PARHAALLA TERÄVYYDELLÄ JA NIIN ETTÄ ALKUPERÄISEN KUVAN PORTAITTAISIET SÄVYT (SIIS NE SÄVYT JOTKA OLI OTETTU MASKIN RAJAUKSESSA MUKAAN TIETYN THRESHOLDIN YLITTÄVINÄ SÄVYARVOINA) TULEVAT NÄKYVIIN JA LISÄKSI PIKSELIN TARKASTI OVAT MASKIIN KUULUVAT PIKSELIJOUKOT JA YKSITTÄISETKIN PIKSELIIT NÄKYVISSÄ ILMAN ANTIALIASINGIA TAI MUUTA BLURRAUTUMISTA

# EI KÄYTÖSSÄ: image_write(image_test_in_magickimageformat_observ2, path = filepath_of_image_for_output_temp, format = "png")

# HUOM. KÄYTETTÄVÄ NIMENOMAAN EBImage-kirjaston mukaisia tiedostojen lukemis- ja kirjoittamis- yms. komentoja (ks. https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf)


#  EI KÄYTÖSSÄ:   maskimage_in_ebimageformat = readImage( filepath_of_image_for_output_temp )

# EI KÄYTÖSSÄ:  maskimage_in_ebimageformat = readImage( filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined )


#  20220129_lisämuutos_2/2: HYÖDYNNETÄÄN NYT INPUT-TIEDOSTONIMENÄ EDELLLÄ AIEMMIN TALLENNETTU brightnessabovethresholdvalue_cnt-KUVAN OUTPUT-TIEDOSTONIMI, JOTTA VOIDAAN NYT SITÄ KÄYTTÄEN NYT KOHTA GENEROIDA TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVA:

maskimage_in_ebimageformat = readImage( filepath_output_c2_gray_eval_brightnessabovethresholdvalue_cnt )


maskimage_in_ebimageformat_gray = channel(maskimage_in_ebimageformat, 'gray')

maskimage_thresholded = thresh(maskimage_in_ebimageformat_gray, 10, 10, 0.05)
```

```
# lisäys 20220129 (tavallaan lisäys 20211026, osio 5extra20220129): tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä

c2_gray_original_nonblurred_image <- readImage( filepath_of_image_for_input_original_nonblurred_images_combined )


plot(c2_gray_original_nonblurred_image)


c2_gray_original_nonblurred_image_gray = channel(c2_gray_original_nonblurred_image, 'gray')

plot(c2_gray_original_nonblurred_image_gray)



#  huom. muuttujassa c2_gray_original_nonblurred_image_gray on jo aiemmin nimenomaanomaan EBImage-muodossa ladattu alkuperäinen harmaasävykuva, jota EI OLE BLURRATTU (SITÄ EI SIIS OLE PEHMENNETTY)


# transp_overl_kokeilu_1/2: yritetään ensimmäisenä kokeiluna harmaasävykuvien avulla, mutta tällöin ei saada värillisiä transparent_overlay-merkintöjä näkyviin:

#  EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded_gray , c2_gray_original_nonblurred_image_gray  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))

#  EI KÄYTÖSSÄ:     display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title='output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')



# transp_overl_kokeilu_2/2: yritetään toisena kokeiluna värikuvien (eli ei vain harmaasävykuvien) avulla, yritetään saada värillisiä transparent_overlay-merkintöjä näkyviin:

# ilmeisesti tärkeää erikseen antaa komento c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image ) JOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN (ks. https://stackoverflow.com/questions/45660935/add-color-elements-to-single-frame-greyscale-image), JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT
#  MUTTA SEN SIJAAN TUOTTAISI ONGELMIA (eli harmaasävyt näytettäisiin vain punaisen kanavan muodossa esitettyinä punasävyinä)
KÄYTTÄÄ KOMENTOA: c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')
# SIIS KOMENTO c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )
#  AUTTAA SIINÄ, ETTÄ saadaan ebimage-muodossa oleva kuva käsitellyksi värikuvamuodossa, jotta saadaan harmaasävyisen alkuperäiskuvan päälle värillisiä transp_overl_merkintöjä; alun perin ebimagen lukemiskomento tuntuu (ehkä muistin säästämiseksi) lataavan kuvan harmaasävymuodossa, ks. esim. tuloste:
#  EI KÄYTÖSSÄ:  > c2_gray_original_nonblurred_image
#  EI KÄYTÖSSÄ:  Image
#  EI KÄYTÖSSÄ:    colorMode    : Grayscale
#  EI KÄYTÖSSÄ:   storage.mode : double
#  EI KÄYTÖSSÄ:    dim          : 1024 1024
#  EI KÄYTÖSSÄ:    frames.total : 1
#  EI KÄYTÖSSÄ:    frames.render: 1
#  EI KÄYTÖSSÄ:
#  EI KÄYTÖSSÄ:  imageData(object)[1:5,1:6]
# joten lienee käytettävä komentoa  z = Image(m, colormode='Color')  (ks. https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf )


# EI KÄYTÖSSÄ:   c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')

# EI KÄYTÖSSÄ:   plot(c2_gray_original_nonblurred_image_incolormode)

# TÄLLÄ KOMENNOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN, JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT:

c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )

plot(c2_gray_original_nonblurred_image_incolormode_keepinggrayshades)
```

```
# HUOM. MUUTTUJALLA maskimage_thresholded ON storage.mode : integer JA MUUTTUJALLA maskimage_in_ebimageformat_gray ON storage.mode : double
# KUITENKIN TUNTUISI SILTÄ, ETTÄ TÄSTÄ EROSTA HUOLIMATTA VOIDAAN MOLEMPIA KÄYTTÄÄ PaintObject-komennossa parametreina MUTTA KUITENKIN LAURI HUOMASI, ETTÄ EDELLÄ TAPAHTUNEESSA MUUTTUJAN maskimage_thresholded MÄÄRITTELELYSSÄ EI SAATU KOROSTUNEEKSTI TULEVAAN ÄÄRISIVIIVOJEN RAJAAMAA ALUETTA VALITUKSI SITEN KUIN LAURIN KOKEILUSSA
# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt
#
#  > nuc = readImage(system.file('images', 'nuclei.tif', package='EBImage'))
#  >
#  > nmask = thresh(nuc, 10, 10, 0.05)
#  >
#  > plot( nuc )
#  >
#  > plot( nmask )
# JOKA POHJAUTUU ESIMERKKIIN  (https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf JA ) JA TÄTEN LAURI PÄÄTYI KÄYTTÄMÄÄN MUUTTUJAAN EDELLÄ TEHTYÄ MÄÄRITTELYÄ, JOTTA LAURI SAA TRANSPARENT_LAYERIN-GENEROIDUKSI NIMENOMAAN ALUEEN (JA MYÖS ÄÄRIVIIVAN) MAALATEN, EIKÄ VAIN ÄÄRILAITOJEN JA ÄÄRILAITAVIIVAN SISÄOSION (SIIS EI ÄÄRIVIIVOEN RAJAAMANA ALUEEN, VAAN ÄÄRIVIVAN SISÄOSION) VÄRITYKSEEN TYYTYEN, KUTEN NÄYTTÄISI KÄYVÄN MUUTTUJALLA PaintObject-komentoa SUORITETTAESSA, SIIS YHTEENVETONA: LAURI PÄÄTYI KÄYTTÄMÄÄN KOMENTOA: maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))
#
# TAUSTATARKASTELUA:
#  > maskimage_thresholded
#  Image
#    colorMode    : Grayscale
#    storage.mode : integer
#    dim          : 1024 1024
#    frames.total : 1
#    frames.render: 1
#
#  imageData(object)[1:5,1:6]
#       [,1] [,2] [,3] [,4] [,5] [,6]
#  [1,]    0    0    0    0    0    0
#  [2,]    0    0    0    0    0    0
#  [3,]    0    0    0    0    0    0
#  [4,]    0    0    0    0    0    0
#  [5,]    0    0    0    0    0    0
#  >
#  > maskimage_in_ebimageformat_gray
#  Image
#    colorMode    : Grayscale
#    storage.mode : double
#    dim          : 1024 1024
#    frames.total : 1
#    frames.render: 1
#
#  imageData(object)[1:5,1:6]
#       [,1] [,2] [,3] [,4] [,5] [,6]
#  [1,]    0    0    0    0    0    0
#  [2,]    0    0    0    0    0    0
#  [3,]    0    0    0    0    0    0
#  [4,]    0    0    0    0    0    0
#  [5,]    0    0    0    0    0    0
#  >

# EI KÄYTÖSSÄ, KOSKA EI SAADA ÄÄRIVIIVOJEN RAJAAMAA ALUETTA KUNNOLLA MAALATUKSI, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))


#  KÄYTÖSSÄ, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# huom. määritellään väri ja läpikuultavuus sekä ääriviivalle että sen raajamalle alueelle käyttäen vektorimuodossa olevia kahden elementin c(arvo1, arvo2)-luetteloita:
# aiemmin käytössä OUTLINEgreen_INSIDEgreen: col=c('#00ff00', '#00ff00'), opac=c(0.1, 0.1)
# aiemmin käytössä OUTLINEyellow_INSIDEyellow: col=c('# ffff00', '#ffff00'), opac=c(0.1, 0.1)
# aiemmin käytössä OUTLINEgreen_INSIDEgreen: col=c('#00ff00', '#00ff00'), opac=c(0.1, 0.1)

maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#00ff00', '#00ff00'), opac=c(0.1, 0.1)  )


plot( maskimage_transparentlyoverlayed_over_orginalnonblurredimage )
```

```
#  EI KÄYTÖSSÄ:  display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title='
output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')


#  seuraavalla komennolla toteutetaan mask_transparent_overlay_over_original_image-kuvatiedoston tallentaminen tiedostoon:

writeImage(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, filepath_of_image_for_output_temp, quality=100);



#  uusi TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt_outlineandinsideareawithsamecolors-osio 20220129 loppuu tähän









#  uusi TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt_outlinewithcolorandinsideareawithnocolor-osio 20220129 alkaa tästä

# lisays20210927:
# tulostetaan TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-kuva (eli punaisella värillä määrätään läpikuultavasti
brightnessabovethresholdvalue_cnt-kuva niin, että sen läpi kuultaa alkuperäinen kuva taustalla)

# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt

# EI KÄYTÖSSÄ: # uusi20210728, päivitetty 20220129:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial,
"_masktr", ".png", sep="" )

# EI KÄYTÖSSÄ:   filepath_of_image_for_output_temp <- paste( filepath_output_c2_gray_eval_brightnessabovethresholdvalue_cnt, "_tr", ".png",
sep="" )

#  20220129_lisämuutos_1/2: KÄYTETÄÄN NYT TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVAN
TALLENTAMISESSA OUTPUT-TIEDOSTONIMENÄ SELLAISTA MUOTOILUA, JOKA ON ALKUOSA SIITÄ MUOTOILUSTA, JOTA ON
EDELLÄ KÄYTETTY OUTPUT-TIEDOSTONIMENÄ, KUN ON TALLENNETTU brightnessabovethresholdvalue_cnt-KUVA, siis nyt käytetään
samaa alkuosaa ja sen perään lisätään string ”_truc”:

filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial,
"_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f',
digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot )  ), "_areg",  gsub("\\.", "dot",
max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_truc", ".png", sep="" )



# HUOM. NYT TÄRKEÄÄ KÄYTTÄÄ ALLA OLEVAA TALLENNUSKOMENTOA JOTTA LAYERED-MAGICIMAGEFORMAT-KUVA
TALLENTUISI PARHAALLA TERÄVYYDELLÄ JA NIIN ETTÄ ALKUPERÄISEN KUVAN PORTAITTAISIET SÄVYT (SIIS NE SÄVYT
JOTKA OLI OTETTU MASKIN RAJAUKSESSA MUKAAN TIETYN THRESHOLDIN YLITTÄVINÄ SÄVYARVOINA) TULEVAT
NÄKYVIIN JA LISÄKSI PIKSELIN TARKASTI OVAT MASKIIN KUULUVAT PIKSELIJOUKOT JA YKSITTÄISETKIN PIKSELIIT
NÄKYVISSÄ ILMAN ANTIALIASINGIA TAI MUUTA BLURRAUTUMISTA

# EI KÄYTÖSSÄ: image_write(image_test_in_magickimageformat_observ2, path = filepath_of_image_for_output_temp, format = "png")

# HUOM. KÄYTETTÄVÄ NIMENOMAAN EBImage-kirjaston mukaisia tiedostojen lukemis- ja kirjoittamis- yms. komentoja (ks.
https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf)


#  EI KÄYTÖSSÄ:   maskimage_in_ebimageformat = readImage( filepath_of_image_for_output_temp )

# EI KÄYTÖSSÄ:  maskimage_in_ebimageformat = readImage(
filepath_of_image_for_input_maskdefinedbywhiteregiononblackbackground_combined )


#  20220129_lisämuutos_2/2: HYÖDYNNETÄÄN NYT INPUT-TIEDOSTONIMENÄ EDELLLÄ AIEMMIN TALLENNETTU
brightnessabovethresholdvalue_cnt-KUVAN OUTPUT-TIEDOSTONIMI, JOTTA VOIDAAN NYT SITÄ KÄYTTÄEN NYT KOHTA
GENEROIDA TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt-KUVA:

maskimage_in_ebimageformat = readImage( filepath_output_c2_gray_eval_brightnessabovethresholdvalue_cnt )
```

```
maskimage_in_ebimageformat_gray = channel(maskimage_in_ebimageformat, 'gray')

maskimage_thresholded = thresh(maskimage_in_ebimageformat_gray, 10, 10, 0.05)



# lisäys 20220129 (tavallaan lisäys 20211026, osio 5extra20220129): tällä lisäyksellä kohdistetaan pikselikirkkauksien yms. mittaus nimenomaan alkuperäiseen kuvaan eikä blurred-kuvaan
# täten viitataan nyt uudella tavalla tiedostonimeen, joka on määriteltynä list-elementissä

c2_gray_original_nonblurred_image <- readImage( filepath_of_image_for_input_original_nonblurred_images_combined )


plot(c2_gray_original_nonblurred_image)


c2_gray_original_nonblurred_image_gray = channel(c2_gray_original_nonblurred_image, 'gray')

plot(c2_gray_original_nonblurred_image_gray)



#  huom. muuttujassa c2_gray_original_nonblurred_image_gray on jo aiemmin nimenomaanomaan EBImage-muodossa ladattu alkuperäinen harmaasävykuva, jota EI OLE BLURRATTU (SITÄ EI SIIS OLE PEHMENNETTY)


# transp_overl_kokeilu_1/2: yritetään ensimmäisenä kokeiluna harmaasävykuvien avulla, mutta tällöin ei saada värillisiä transparent_overlay-merkintöjä näkyviin:

#  EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded_gray , c2_gray_original_nonblurred_image_gray  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))

#  EI KÄYTÖSSÄ:     display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title='output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')



# transp_overl_kokeilu_2/2: yritetään toisena kokeiluna värikuvien (eli ei vain harmaasävykuvien) avulla, yritetään saada värillisiä transparent_overlay-merkintöjä näkyviin:

# ilmeisesti tärkeää erikseen antaa komento c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image ) JOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN (ks. https://stackoverflow.com/questions/45660935/add-color-elements-to-single-frame-greyscale-image), JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT
#  MUTTA SEN SIJAAN TUOTTAISI ONGELMIA (eli harmaasävyt näytettäisiin vain punaisen kanavan muodossa esitettyinä punasävyinä) KÄYTTÄÄ KOMENTOA: c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')
# SIIS KOMENTO c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )
#  AUTTAA SIINÄ, ETTÄ saadaan ebimage-muodossa oleva kuva käsitellyksi värikuvamuodossa, jotta saadaan harmaasävyisen alkuperäiskuvan päälle värillisiä transp_overl_merkintöjä; alun perin ebimagen lukemiskomento tuntuu (ehkä muistin säästämiseksi) lataavan kuvan harmaasävymuodossa, ks. esim. tuloste:
#  EI KÄYTÖSSÄ:  > c2_gray_original_nonblurred_image
#  EI KÄYTÖSSÄ:  Image
#  EI KÄYTÖSSÄ:    colorMode    : Grayscale
#  EI KÄYTÖSSÄ:   storage.mode : double
#  EI KÄYTÖSSÄ:    dim          : 1024 1024
#  EI KÄYTÖSSÄ:    frames.total : 1
#  EI KÄYTÖSSÄ:    frames.render: 1
#  EI KÄYTÖSSÄ:
#  EI KÄYTÖSSÄ:  imageData(object)[1:5,1:6]
# joten lienee käytettävä komentoa  z = Image(m, colormode='Color')  (ks. https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf )


# EI KÄYTÖSSÄ:   c2_gray_original_nonblurred_image_incolormode = Image( c2_gray_original_nonblurred_image , colormode='Color')

# EI KÄYTÖSSÄ:   plot(c2_gray_original_nonblurred_image_incolormode)

# TÄLLÄ KOMENNOLLA SAADAAN SAMAT HARMAASÄVYT KAIKKIIN RGB-KUVAN KOLMEEN VÄRIKANAVAAN, JOLLOIN UUDESSAKIN ESITYSMUODOSSA KUVA EDELLEEN ON HARMAASÄVYKUVA, KUN NUO KOLME VÄRIKANAVAA SUMMAUTUVAT:

c2_gray_original_nonblurred_image_incolormode_keepinggrayshades <- rgbImage(red = c2_gray_original_nonblurred_image, green = c2_gray_original_nonblurred_image, blue = c2_gray_original_nonblurred_image )

plot(c2_gray_original_nonblurred_image_incolormode_keepinggrayshades)
```

```
# HUOM. MUUTTUJALLA maskimage_thresholded ON storage.mode : integer JA MUUTTUJALLA maskimage_in_ebimageformat_gray ON storage.mode : double
# KUITENKIN TUNTUISI SILTÄ, ETTÄ TÄSTÄ EROSTA HUOLIMATTA VOIDAAN MOLEMPIA KÄYTTÄÄ PaintObject-komennossa parametreina MUTTA KUITENKIN LAURI HUOMASI, ETTÄ EDELLÄ TAPAHTUNEESSA MUUTTUJAN maskimage_thresholded MÄÄRITTELELYSSÄ EI SAATU KOROSTUNEEKSTI TULEVAAN ÄÄRISIVIIVOJEN RAJAAMAA ALUETTA VALITUKSI SITEN KUIN LAURIN KOKEILUSSA
# otetaan vaikutteita laurin toimivaksi kehittelemästä menetelmästä, jota kuvaillaan kansiossa Documents tiedostossa
#  menettely_aariviivojenjaniidensisallaolevienpikselialueiden_lapikuultavapiirtamiseen_r-kielella_lauri_lahti_20220129.txt
#
#  > nuc = readImage(system.file('images', 'nuclei.tif', package='EBImage'))
#  >
#  > nmask = thresh(nuc, 10, 10, 0.05)
#  >
#  > plot( nuc )
#  >
#  > plot( nmask )
# JOKA POHJAUTUU ESIMERKKIIN  (https://bioconductor.org/packages/devel/bioc/manuals/EBImage/man/EBImage.pdf JA ) JA TÄTEN LAURI PÄÄTYI KÄYTTÄMÄÄN MUUTTUJAAN EDELLÄ TEHTYÄ MÄÄRITTELYÄ, JOTTA LAURI SAA TRANSPARENT_LAYERIN-GENEROIDUKSI NIMENOMAAN ALUEEN (JA MYÖS ÄÄRIVIIVAN) MAALATEN, EIKÄ VAIN ÄÄRILAITOJEN JA ÄÄRILAITAVIIVAN SISÄOSION (SIIS EI ÄÄRIVIIVOEN RAJAAMANA ALUEEN, VAAN ÄÄRIVIVAN SISÄOSION) VÄRITYKSEEN TYYTYEN, KUTEN NÄYTTÄISI KÄYVÄN MUUTTUJALLA PaintObject-komentoa SUORITETTAESSA, SIIS YHTEENVETONA: LAURI PÄÄTYI KÄYTTÄMÄÄN KOMENTOA: maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))
#
# TAUSTATARKASTELUA:
#  > maskimage_thresholded
#  Image
#    colorMode    : Grayscale
#    storage.mode : integer
#    dim          : 1024 1024
#    frames.total : 1
#    frames.render: 1
#
#  imageData(object)[1:5,1:6]
#       [,1] [,2] [,3] [,4] [,5] [,6]
#  [1,]    0    0    0    0    0    0
#  [2,]    0    0    0    0    0    0
#  [3,]    0    0    0    0    0    0
#  [4,]    0    0    0    0    0    0
#  [5,]    0    0    0    0    0    0
#  >
#  > maskimage_in_ebimageformat_gray
#  Image
#    colorMode    : Grayscale
#    storage.mode : double
#    dim          : 1024 1024
#    frames.total : 1
#    frames.render: 1
#
#  imageData(object)[1:5,1:6]
#       [,1] [,2] [,3] [,4] [,5] [,6]
#  [1,]    0    0    0    0    0    0
#  [2,]    0    0    0    0    0    0
#  [3,]    0    0    0    0    0    0
#  [4,]    0    0    0    0    0    0
#  [5,]    0    0    0    0    0    0
#  >

# EI KÄYTÖSSÄ, KOSKA EI SAADA ÄÄRIVIIVOJEN RAJAAMAA ALUETTA KUNNOLLA MAALATUKSI, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# EI KÄYTÖSSÄ:  maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_thresholded  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff00ff', '#ffff00'), opac=c(0.3, 0.3))


#  KÄYTÖSSÄ, KS. EDELLÄ TARKEMPAA PERUSTELUA:
# huom. määritellään väri ja läpikuultavuus sekä ääriviivalle että sen raajamalle alueelle käyttäen vektorimuodossa olevia kahden elementin c(arvo1, arvo2)-luetteloita:
# aiemmin käytössä OUTLINEgreen_INSIDEgreen: col=c('#00ff00', '#00ff00'), opac=c(0.1, 0.1)
# aiemmin käytössä OUTLINEyellow_INSIDEyellow: col=c('#ffff00', '#ffff00'), opac=c(0.1, 0.1)
# aiemmin käytössä OUTLINEgreen_INSIDEgreen: col=c('#00ff00', '#00ff00'), opac=c(0.1, 0.1)
# aiemmin käytössä OUTLINEpunaineneiläpinäkyvästi_INSIDEeimitäänmäärittelyäväristäeimäärittelyäläpinäkyvyydestä: col=c('#ff0000', NA), opac=c(1.0, NA)

maskimage_transparentlyoverlayed_over_orginalnonblurredimage = paintObjects( maskimage_in_ebimageformat_gray  , c2_gray_original_nonblurred_image_incolormode_keepinggrayshades  , col=c('#ff0000', NA), opac=c(1.0, NA) )
```

```
plot( maskimage_transparentlyoverlayed_over_orginalnonblurredimage )

#  EI KÄYTÖSSÄ:  display(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, title='
output_maskimage_transparentlyoverlayed_over_orginalnonblurredimage')


#  seuraavalla komennolla toteutetaan mask_transparent_overlay_over_original_image-kuvatiedoston tallentaminen tiedostoon:

writeImage(maskimage_transparentlyoverlayed_over_orginalnonblurredimage, filepath_of_image_for_output_temp, quality=100);



#  uusi TRANSPARENT_LAYERED_brightnessabovethresholdvalue_cnt_outlinewithcolorandinsideareawithnocolor-osio 20220129 loppuu tähän









list_test_as_numeric_new_as_ppp

list_test_as_numeric_new_as_ppp$x

list_test_as_numeric_new_as_ppp$y


list_test_as_numeric_new_as_ppp_situation_current <-  list_test_as_numeric_new_as_ppp


list_test_as_numeric_new_as_ppp_xcoord_situation_current <-  list_test_as_numeric_new_as_ppp$x

list_test_as_numeric_new_as_ppp_ycoord_situation_current <-  list_test_as_numeric_new_as_ppp$y


# vaihe B11: combining listings about region properties


# kootaan yhteen alueiden ominaisuuksia:

combination_of_properties_about_regions_situation_current <- cbind( region_index_situation_current, area_situation_current,
average_signal_per_pixel_of_region_situation_current,  signal_per_area_of_region_situation_current,
list_test_as_numeric_new_as_ppp_xcoord_situation_current, list_test_as_numeric_new_as_ppp_ycoord_situation_current    )


str( combination_of_properties_about_regions_situation_current  )

head( combination_of_properties_about_regions_situation_current , 10 )



combination_of_properties_about_regions_writeoutputformatting <- combination_of_properties_about_regions_situation_current

colnames(combination_of_properties_about_regions_writeoutputformatting)[1] <- "region_index"

colnames(combination_of_properties_about_regions_writeoutputformatting)[2] <- "area"

colnames(combination_of_properties_about_regions_writeoutputformatting)[3] <- "average_signal_per_pixel_of_the_region"

colnames(combination_of_properties_about_regions_writeoutputformatting)[4] <- "signal_per_area_of_the_region"

colnames(combination_of_properties_about_regions_writeoutputformatting)[5] <- "x_coordinate_of_the_region_s_mass_center_point"

colnames(combination_of_properties_about_regions_writeoutputformatting)[6] <- "y_coordinate_of_the_region_s_mass_center_point"

head( combination_of_properties_about_regions_writeoutputformatting, 10 )



# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial,
"_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f',
```

```
digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot ) ), "_areg",  gsub("\\.", "dot",
max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_reg_statmeasures",  ".txt", sep="" )



write.table(combination_of_properties_about_regions_writeoutputformatting, filepath_of_image_for_output_temp,sep="\t", row.names=FALSE,
quote=F,fileEncoding="UTF-8", append=FALSE)



  } else {  #  HUOM. TÄSSÄ ON IF-ELSE-TAITEKOHTA EHDOLLE   if (   not(  is.null( fts_initial_testingifnoelements ) ) ) {


combination_of_properties_about_regions_writeoutputformatting_simplenotationthat_theanalysis_didnotidentify_regions_basedonthegivenconditions
<- "The analysis did not identify regions based on the given conditions,"

# uusi20210728:
filepath_of_image_for_output_temp <- paste( filepath_of_image_for_output_folder_initial, filepath_of_image_for_output_filename_initial,
"_maskedpix_brig",  gsub("\\.", "dot", formatC( brightness_thresholdvalue ,format='f',
digits=brightness_thresholdvalue_toensureshowingtrailingzeros_numberofdigitsshownafterdecimaldot ) ), "_areg",  gsub("\\.", "dot",
max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed), "_reg_statmeasures",  ".txt", sep="" )



write.table(
combination_of_properties_about_regions_writeoutputformatting_simplenotationthat_theanalysis_didnotidentify_regions_basedonthegivenconditions
, filepath_of_image_for_output_temp,sep="\t", row.names=FALSE, quote=F,fileEncoding="UTF-8", append=FALSE)


}    #  HUOM. TÄSSÄ ON LOPPUAALTOSULKU EHDOLLE   if (   not(  is.null( fts_initial_testingifnoelements ) ) ) {


        }    #  HUOM. TÄSSÄ ON LOPPUAALTOSULKU EHDOLLE for( counter_index_for_brightness_thresholdvalue in
1:length(analysis_list_of_brightness_thresholdvalue) ) JOSSA TEHDÄÄN ANALYYSIA


        }    #  HUOM. TÄSSÄ ON LOPPUAALTOSULKU EHDOLLE for(
counter_index_for_max_number_of_pixels_in_segment_so_that_this_segment_still_needs_to_be_removed) ) JOSSA TEHDÄÄN ANALYYSIA



}    #  HUOM. TÄSSÄ ON LOPPUAALTOSULKU EHDOLLE for( counter_index_for_analysis in 1:length(analysis_list_of_filenames_initial) )
JOSSA TEHDÄÄN ANALYYSIA



#  xxxxxxxxxxxxxxxxxxxxxxxxxxx
```