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Editorial: Data science in neuro- and onco-biology

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Editorial on the Research Topic Data science in neuro- and onco-biology

In many fields of biomedical research the development and use of breakthrough technologies often produce a huge amount of heterogeneous, multi-scale data ranging from molecular genomic data to images describing the function and structure of tissues [1, 2]. In contrast, at a clinical level the need for real-time, minimally-invasive, and cost-effective measurements often reduces the quality of the recorded data rendering them to be noisy and incomplete [3].

Data science approaches based on robust mathematical and statistical methods have proven themselves to be of crucial importance in both these scenarios. For example, machine learning and data mining approaches can be used for patients classification and modeling of disease progression [4, 5]. Similarly, computational models and simulations may be used to build a patient's digital twin opening the possibilities for highly personalized therapeutic plans [6].

The purpose of this Research Topic is to review and present recent mathematical and statistical developments in the analysis of biomedical data. To this end, we focused on two specific biomedical fields, namely neuroscience and oncology, motivated by the fact that cancer and various neurodegenerative dementias, e.g., due to Alzheimer's and Parkinson's diseases, are among the leading causes of death worldwide¹.

The Research Topic features two Reviews and three Original Research articles that are briefly summarized below.

Ioannides et al. reviewed two families of numerical approaches for dimensionality reduction of complex systems, based on principal component analysis and graph clustering theory, respectively. The reviewed methods are illustrated on two neuroscientific studies: (i) the study of correlations between sleep stages and brain activity; (ii) the characterization of brain response to median nerve stimulation. In both scenarios, magnetoencephalography and electroencephalography were used for monitoring brain activity. To prove the flexibility of the reviewed methods, the authors also considered a problem rising from astrophysics, namely clustering of ultraluminous infrared galaxies based on their spectral energy distribution.

1 <https://www.who.int/data/gho/data/themes/mortality-and-global-health-estimates>

Righetti et al. revised recent mechanistic models developed for modeling at a molecular-scale the homeostasis of α -synuclein, one of the key drivers of Parkinson's disease pathogenesis [7]. Specifically they grouped the considered models in two families: single-pathway chemical kinetic model of α -synuclein aggregation, and multiple-pathway models accounting for both α -synuclein aggregation and degradation. Possible applications of such models toward quantitative system pharmacologic are discussed.

Reconstructing high quality magnetic resonance images is a first crucial step in many modern quantitative approaches for cancer precision medicine, including radiogenomics [8]. Motivated by this consideration, Di Cola et al. proposed to combine Rudin-Osher-Fatemi (ROF) total variation minimization with an histogram-matching (HM) approach for magnetic resonance image denoising. Different combinations of various implementations of both the ROF denoising algorithm and the HM approach were tested and validated on simulated data extracted from a publicly available database.

Nieus et al. present a multi-class logistic regression algorithm with l1 penalization to infer sparse connectivity networks within large populations of neurons from their voltage tracers. The authors proved the robustness of the proposed methods with respect to different parameters (such as presence of noise, network size, and limited data availability) by simulating realistic networks comprising both excitatory and inhibitory neurons. Overall, this work is motivated by the spread of emerging techniques capable of simultaneously recording spikes and post-synaptic-potential from large populations of neurons. Such techniques comprise genetically encoded voltage indicators [9] or proper combination of different optical recording techniques [10].

Sapienza et al. performed an experimental study on the impact of parameter initialization on the performance and training time of a modern autoencoder architecture, called deep image prior (DIP) [11]. Specifically, they focused on the application of DIP for denoising x-ray (sparse) computed tomography (CT) images. First, they used natural RGB images and gray-scaled CT images of a phantom to select a set of best initial configuration. Then, the selected initial configurations were applied for artifact removal on the CT images of a coronavirus (COVID-19) patient's lungs.

Author contributions

All authors contributed to the article and approved the submitted version.

Conflict of interest

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