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Title

COMP-05. EVALUATION OF A DEEP LEARNING ARCHITECTURE FOR MRI PREDICTION OF IDH, 1p19q AND TERT IN GLIOMA PATIENTS

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tracking. Confounding effects of tumor infiltration and edema results in significant discordance between subcortical, intraoperative electrical stimulation (IES) and preoperative fiber track visualization. We hypothesized that tracking in peritumoral zone, which includes vasogenic edema and neoplastic infiltration, could be enhanced by using a bi-compartment diffusion modeling. Due to the known tendency of primary malignant tumors, glioblastoma, to infiltrate surrounding white matter (WM), the bi-compartment model will be validated to distinguish peritumoral tissue in gliomas versus secondary brain tumors (metastases). METHODS: Patients with tumors (88 gliomas and 50 metastates) underwent 30 direction DTI and were fitted with standard tensor and *Fernet*, a free-water-invariant bi-compartment tensor model. Deterministic tractography was performed on each subject. Five WM tracts (corticospinal tract, inferior fronto-occipital, inferior longitudinal, arcuate and uncinate fasciculi) were extracted bilaterally in each patient using a shape-based clustering algorithm. For each subject, percentage change of edema volume was compared between standard and *Fernet* tensor models. RESULTS: *Fernet*-based tractography showed average increase in edema coverage of 87 +/- 25% (t=6.9, p CONCLUSIONS: Results show fiber tractography in peritumoral region is significantly improved with better diffusion modeling of peritumoral tissue microstructure. Additionally, difference in tracking between metastases and glioblastomas is representative of tracking being affected differentially due to infiltration in peritumoral regions. CLINICAL IMPLICATIONS: Our peritumoral tissue modeling incorporates edema and infiltration, leading to superior tracking, and hence robust surgical planning. In future, the peritumoral tissue maps could be used to elucidate differences in radiological diagnosis, surgical risk stratification, response to therapy, tumor invasion and tumor genetics, and neuroplasticity.

COMP-03. TUMOR CONNECTOME: INSIGHT INTO THE IMPACT OF CNS NEOPLASIA AND THERAPY ON THE BRAIN NETWORK

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PURPOSE: Although surgical planning tools are aimed at avoiding damage to eloquent tracts, resection as well as treatment like radiation, may alter the structural connectivity of the whole brain. This may lead to subtle cognitive deficits in the future. The aim of this work is to present a paradigm to create a Tumor Evaluation Connectome, which is a map of the brain that shows how the regions are connected to each other. Although, connectomes are routinely used in various studies these days, it is extremely challenging to create one in the presence of tumor or a resection cavity. Thus a tumor connectome will enable the quantitative evaluation of structural connectivity between brain regions. METHODS: The Tumor Evaluation Connectome was created as follows: the T1 images were parcellated into 153 anatomical regions, using multi-atlas tools. 119 gray matter regions were retained to build the connectome after the parcellations were manually assessed for mislabeling of unhealthy tissue. The DTI data was denoised, eddy and motion corrected. The anatomical labels in the T1 image were transferred to the DTI data, through a deformable registration method. 1 million streamlines were generated using deterministic tracking from mrtrix, seeded from voxels with fractional anisotropy exceeding 0.3. The Tumor Evaluation Connectome was defined with the 119 GM regions as nodes and the streamline count between them as the strength of the connection. These tumor connectomes will be used to generate network measures of deficit / change, as z-score from controls in the following pre-defined subnetworks: motor, visual, language, attention, memory, social cognition, cognitive control. CLINICAL IMPLICATIONS: Connectomes are an unmet need to refine tools for surgical planning, enhance recovery after brain tumor surgery, and assess the effects of therapeutic interventions is a specific, sensitive, and reproducible measure of the brain connectome.

COMP-04. R TOOLS FOR EXPLORATORY ANALYSIS OF PUBLICLY AVAILABLE DATA: HPAANALYZE AND BEYOND

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BACKGROUND: The Human Protein Atlas (HPA) is a comprehensive resource for exploration of human proteome which contains a vast amount of proteomics and transcriptomics data generated from antibody-based tissue micro-array profiling and RNA deep-sequencing. Data from the HPA are freely available via proteinatlas.org, allowing scientists to access and incorporate the data into their research. Previously, the R package *hpar* has been created for fast and easy programmatic access of HPA data. Here, we introduce *HPAanalyze*, an R package aims to simplify exploratory data analysis from those data, as well as provide other complementary functionality to *hpar*. RESULTS: *HPAanalyze* is an R package for retrieving and performing exploratory data analysis from HPA. It provides functionality for importing data tables and xml files from HPA, exporting and visualizing data, as

well as download all staining images of interest. The package is free, open source, and available via Github. CONCLUSIONS: *HPAanalyze* intergrates into the R workflow via the *tidyverse* philosophy and data structures, and can be used in combination with Bioconductor packages for easy analysis of HPA data.

COMP-05. EVALUATION OF A DEEP LEARNING ARCHITECTURE FOR MRI PREDICTION OF IDH, 1p19q AND TERT IN GLIOMA PATIENTS

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Recent studies have highlighted the importance of using molecular biomarkers (IDH, 1p19q, TERT) to group gliomas that have similar clinical behavior, response to therapy, and outcome. An emerging hypothesis is that glioma specific genetic and/or molecular alterations manifest as specific observable changes in MR anatomical imaging. Morphologic and texture features, originating from anatomical MRI, have been investigated as imaging biomarkers to predict MGMT and glioma group status. These texture or morphologic based approaches pose several challenges including requirements for several preprocessing steps such as intensity standardization, skull stripping, and tumor segmentation. Deep learning is an important evolving technology in many different fields, including anatomic imaging, and can be used to empirically identify important features in a variety of modalities, including MRI. Importantly deep learning precludes the need for extensive pre-processing. We describe a convolutional neural network, evaluating resnet50, vgg16, inception and xception neural network architectures, that can predict IDH, 1p19q and TERT status utilizing conventional T2 weighted MRI imaging with intensity normalization and nonuniform intensity normalization (N4) bias corrections. The dataset consisted of 432 images (340 for training and 92 for validation) from patients published by Eckel-Passow et al *New England Journal of Medicine* (2015). The system achieved a weighted f1 score of 0.901, 0.937 and 0.924 for IDH, 1p19q and TERT prediction on the test dataset, respectively. IDH status was misclassified in 9 out of 92 patients, while 1p19q and TERT status was misclassified in 6 and 7 patients respectively. Our results demonstrate the potential of deep learning architectures applied to conventional MRI to predict molecular glioma groups.

COMP-06. GLIOBLASTOMA DEVELOPMENT MIRRORS THE DEVELOPING BRAIN

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Intratumoral and interpatient heterogeneity are characteristics of glioblastoma and constitute important challenges in overcoming treatment resistance and developing new, more effective therapies. Using single-cell RNA sequencing, we characterized 60 933 cells from 4 developing fetal brains and 8 glioblastomas. By using fetal brain development as a road map, we show a tri-lineage (astrocytic, oligodendrocytic, and neuronal) hierarchical organization in all glioblastomas. In each patient, a population of progenitor cancer cells was found at the apex of this hierarchy. These cells were enriched in our patient-derived glioma stem cell samples, and, like progenitors in the developing brain, were the main dividing cell population within the cancer. Using expression signatures obtained from single-cell RNA-sequencing, we isolated progenitor cancer cells and compared them to other glioblastoma cell types. We showed the progenitors are the most resistant to chemotherapy and the most tumorigenic in mouse xenograft models. This newly found conserved developmental organization points to the cell of origin and suggests new therapeutic approaches.

COMP-07. COMPARATIVE MOLECULAR LIFE HISTORY OF SPONTANEOUS CANINE AND HUMAN GLIOMA

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