## 6th BigBrain Workshop - From microstructure to functional connectomics



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## Advanced neuroimaging at Croatian Institute for Brain Research

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For the last two decades, our research team has been working on applying histological and neuroradiological methods in studying the complex processes of proliferation, migration, and differentiation, all of which are key to understanding both normal and abnormal perinatal human brain development. We believe that it is possible to substantially improve the sensitivity and the specificity of the structural perinatal MR examination that looks for developmental disorders, particularly the ones which occur in the zones of intensive developmentals processes (sagittal strata, subplate zone, white matter crossroad zone). We anticipate a better interpretation of the structural MRI will help to identify developmental disorders even before the clinical onset of motor, sensory, and cognitive disorders. We are aware that the structural MRI has limitations and cannot reliably visualize the discrete structural and functional deviations which can have a significant impact on the neurodevelopmental outcome. Therefore, we expect that the use of state-of-the-art diffusion MR imaging and high-resolution T1 and T2 sequences will additionally increase the sensitivity and specificity of the perinatal MRI examination for disorders that cannot be visually detected (white matter microstructure and connectivity, intracortical myelination, cortex thickness, etc.). In our research, we use multi-shell diffusion sequences optimized for neonatal imaging with 106 gradient directions optimally divided between shells with b-values 0, 400, 1000 and 2600 s/mm 2 . Using the diffusion model of constrained spherical deconvolution (CSD) multiple fibre populations within each voxel could be reconstructed. High-resolution T1 and T2 sequences are used in the morphometric analysis (voxel size 0.8x0.8x0.8 mm). The sequences are processed using the Developing Human Connectome Project structural algorithm for MR image processing. This automated analysis system uses automatic processing the generate morphometric cortical parameters: surface on the border between the cortex and white matter, the surface on the border between the cortex and the pia mater, segmentation of the defined cortical structures (lobes and gyri), sulcus depth, gyrification index, intracortical myelination maps, cortex thickness.

The scientific and clinical objective of our research is to define structural and diffusion biomarkers of normal and abnormal brain development at perinatal MRI.

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