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## ► To cite this version:

Tristan Moreau, Bernard Gibaud. A pipeline for automatic semantic annotation of human connectomics revealed by diffusion tractography. International Conference on Brain Informatics, 2015, London, United Kingdom. hal-01899824

**HAL Id: hal-01899824**

**<https://hal.science/hal-01899824>**

Submitted on 19 Oct 2018

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# A pipeline for automatic semantic annotation of human connectomics revealed by diffusion tractography

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## INTRODUCTION

Different non-invasive neuroimaging modalities and multi-level analysis of human connectomics datasets yield a great amount of heterogeneous data which are hard to integrate into an unified representation. Biomedical ontologies can provide a suitable integrative framework for domain knowledge as well as a tool to facilitate information retrieval, data sharing and data comparisons across scales, modalities and species [1]. Especially, it is urgently needed to fill the gap between neurobiology and in vivo human connectomics in order to better take into account the reality highlighted in Magnetic Resonance Imaging (MRI) and relate it to existing brain knowledge. However, none of the current ontologies addressing cerebral connectivity relationships can be used to represent connectivity assessed by diffusion tractography (the only neuroimaging modality that can reconstruct white matter fiber bundles in a non invasive way in the living brain).

The main contribution reported in this paper is a pipeline dedicated to automatic semantic annotation of human connectomics revealed by tractography [2].

## MATERIAL AND METHOD

The pipeline for semantic annotations takes as inputs: (1) atlas-based segmentation results delineating different gray matter regions [3] and major white matter fiber bundles [4], (2) binary connectivity matrices assessed by tractography. Finally, the pipeline generates a set of RDF annotations referring to the terms of the Human Connectomics Ontology (HCO) [2] represented in OWL.

## RESULTS

Each gray matter region is represented as an instance of the “hco:Gray\_matter\_part” class. If the gray matter region is a cortical parcel, then the cortical parcel is related to the instance of the overlapping gyrus using a part-whole relationship.

Binary connectivity matrices provide the information about connections revealed by tractography. First, the two gray matter regions corresponding to the row and column of a connectivity matrix are represented as instances of the “hco:MR\_Node” class and are related together using the “hco:mr\_connection” relationship. Second, an instance of the “hco:MR\_Route” class is created and related to the two corresponding instances of the “hco:MR\_Node” using the “hco:tracto\_connects” relationship. If the route of the connexion is part of a white matter fiber bundle, then this is encoded using a part-whole relationship.

## DISCUSSION AND CONCLUSION

This pipeline for automatic annotations is not entirely generic, since it depends on a specific data structure representing segmentation results and connectivity matrices. However, it can be easily adapted to other situations.

This approach can facilitate both data sharing and comparison of data across individuals and neuroimaging modalities.

## References

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- [2] **Moreau, et al. (2015)**. *Ontology-based approach for in vivo human connectomics: the medial Brodmann area 6 case study.* Front Neuroinform.
- [3] **Daducci, et al. (2012)**. *The connectome mapper: an open-source processing pipeline to map connectomes with MRI.* PLoS One.
- [4] **Hua, et al. (2008)**. *Tract probability maps in stereotaxic spaces: analyses of white matter anatomy and tract-specific quantification.* Neuroimage.