Object Types	*Description*
CMetadata	The CMetadata object describes metadata relevant to contents of the whole connectome file. We use relevant parts of the Dublin Core Metadata Terms specification (`dublincore.org`) to define the following tags: *title, creator, publisher, created, modified, license, rights, reference, relation, description.* We have extended the core metadata tags with *generator, species* and *email* tags. For each connectome object, a metadata tag can be added that expresses container-wide valid properties.
CNetwork	Networks of any sort can be stored. For MR structural connectomes, nodes represent brain regions and edges represent fiber tractography derived connections. The possibility of storing an arbitrary number of attributes per node and edge allows, for example, brain region nodes to point to ontologies that define them uniquely. Formats: GraphML, GEXF, NXGPickle, Other Types: Attribute Network, Dynamic Network, Hierarchical Network, Structural Network, Functional Network, Effective Network, ...
CVolume	Volumetric, voxel-based datasets are widely used in the neuroimaging community to store many different measurement modalities. Examples: Apart from acquired raw data, brain segmentations or probability maps are often stored as 3D volumes. Formats: Nifti1, Nifti2, MGH, Other Types: Segmentation, T1-weighted, T2-weighted, PD-weighted, fMRI, Probability map, ASL, MD, FA, LD, TD, FLAIR, MRA, MRS, PET, ...
CSurface	Surface-based datasets are usually stored as triangular meshes. They are often extracted from an underlying volumetric segmentation. Examples: Cortical maps for parcellations, thickness, or curvature information. Formats: Gifti, Other Types: Labeling, Surfaceset, Probability map, Surfaceset+Labeling, ...
CTrack	Deterministic tractography creates sets of single polygonal lines. Examples: Reconstructed fiber bundles from Diffusion MRI Formats: TrackVis, Other Types: FACT Tractography, ...
CData	Data of any type that does not fit into any other connectome object category. Examples: Phenotypic subject variables, assessment results Formats: NumPy, HDF5, XML, JSON, CSV, Pickle, TXT, Other Types: Fiber Labeling, Bval, Bvect, FPI-R, NEO-P-I-R, STAI, BIS-Test, I-S-T 2000R, ...
CScript	Visualization and analysis procedures in the form of executable scripts. They may serve as provenance information for processed data. Examples: Connectome Mapper configuration script, Nipype script Formats: TXT, Python, Bash, Matlab, Other Types: Statistical Analysis, rsfMRI Connectivity Mapping, ...
CTimeseries	There are plenty of time series related formats which makes it difficult to support a general one. We support generic data array containers that can store arbitrary time series data. Formats: HDF5, NumPy, Other Types: EEG Timeseries, MEG Timeseries, fNIRS, ...
CImagestack	Series of 2D images not simply representable in volume-based formats. Examples: Typical examples would be annotated slice-based atlases that represent areas as closed 2D polygons. Formats: PNG, JPG, TIFF, SVG, Other Types: Scalable Brain Atlas, ...

Table 1: **The variety of connectome objects the CFF supports.** The connectome objects are a wrapping mechanism, extending single data files by further annotations. *Formats* lists the file formats that are supported for reading and writing through the Connectome File Format Library. *Types* can in principle be freely choosen, but usually denotes the measurement modality.