

Connectomic Analysis

Connectomic analysis refers to the study and mapping of the brain's structural and functional networks using neuroimaging and computational tools. In the context of [neurosurgery](#) and [deep_brain_stimulation](#) (DBS), it enables the identification of specific fiber pathways and network hubs associated with clinical outcomes.

Techniques and Tools

Connectomic analysis integrates data from:

Diffusion-weighted imaging (DWI) and tractography — to reconstruct white matter fiber pathways

Resting-state fMRI — to examine functional connectivity

Normative connectomes — population-averaged brain networks

Patient-specific connectomes — derived from individual imaging data

Common platforms include:

Lead-DBS

MRtrix

FSL

BrainSuite

Applications in DBS

Allows clinicians and researchers to map volumes of activated tissue (VAT) onto brain networks.

Identifies fiber tracts whose modulation correlates with clinical response (e.g., the [ocd_response_tract](#) in [treatment-resistant_obsessive-compulsive_disorder](#)).

Supports target refinement and the concept of “sweet spots” in subcortical stimulation.

Advantages

Moves beyond anatomical landmarks to network-based neurosurgery.

Enables hypothesis-driven selection of DBS targets.

Can aid in personalized treatment planning by identifying individual network disruptions.

Limitations

Heavily reliant on image quality and accurate coregistration.

Normative connectomes may not capture patient-specific anatomy, especially in diseased brains.

Causal inferences from correlational data remain challenging.

Clinical Example

In the 2025 study by Coenen et al. (Mol Psychiatry), connectomic analysis was used to:

Compare the connectivity profiles of DBS targets (e.g., [anteromedial_subthalamic_nucleus](#), [superolateral_medial_forebrain_bundle](#)).

Demonstrate that the [ocd_response_tract](#) is embedded within sIMFB fibers.

Suggest that symptom improvement in OCD relates to modulation of convergent sub-networks projecting to the [dorsomedial_prefrontal_cortex](#).

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