Name/Acronym	Acquisition information	Punchy Sentence
FiberCup / Tractometer	b-values: 650, 1500, and 2000 s/mm², 64 diffusion-weighted measurements and 1 b=0 image., Synthetic	Online system scoring tractography pipelines via valid/invalid connections and bundles using diverse estimation techniques.
DiSCo Challenge	Numerical phantoms via Monte Carlo, 12,000 fibers.	Numerical phantoms assess connectivity methods, demonstrating accurate ROI connection strength estimation.
ISMRM 2015 Tractography Challenge	Simulated human brain diffusion-weighted dataset.	Simulated brain challenge reveals tractography struggles with spatial overlap and false positives in bundle reconstruction.
VOTEM3: Anisotropic Diffusion Phantom	16 pathways, Phantom	Physical phantom validates tractography accuracy against manually drawn tracts in a controlled geometry.
BigMac	PLI: 4 μm in-plane resolution, Macaque	Macaque BigMac integrates PLI and MRI for comprehensive brain mapping.
IronTract Challenge	515 directions, bmax = 40,000 s/mm², Two monkey brains, Macaque, Data resampled via NUFFT.	Monkey brain challenge robustly tests tractography across seed areas using high angular resolution dMRI.
VOTEM1: Ex vivo Macaque	0.25 mm isotropic resolution, 7 volumes b=0, 114 directions, b-value 4000 s/mm^2, Macaque	Macaque dMRI & tracer validation: region-to-region connectivity at high resolution.
VOTEM2: Ex vivo Squirrel Monkey	31 sampling directions, Squirrel Monkey	Squirrel monkey dMRI & tracer: validating both region-to-region and voxel-wise connectivity.
TraCED	Scan-rescan dataset, two scanners, five repetitions per session, single subject.	TraCED: empirically assessing tractography reproducibility across scans and scanners.
Penthera3T	3T diffusion MRI, 30 subjects, 1.0mm isotropic resolution.	Penthera3T: demonstrating high reproducibility of TractoFlow pipeline outputs.
Tractostorm	Gold standard generated by voting from 80 segmentations.	Tractostorm: optimizing dissection reproducibility through protocol dissemination and voting-based gold standard.
MASiVar	319 diffusion scans, 14 adults and 83 children, multi-site/scanner.	MASiVar: multi-site DWI dataset revealing variability increase from intra- to inter-subject.
Digital Brain Bank	Varies depending on the dataset, 45 brains	Digital Brain Bank: web-accessible MRI & microscopy data spanning neuroanatomy to neuropathology.
TractoInferno	dMRI: single-shell, b-values around 1000 s/mm², 284 samples, Human	TractoInferno: large human dMRI database powering machine learning for tractography.

Tool Name	Processing Steps	Interface	Punchy Sentence
DIPY	Pre-processing, reconstruction, tractography, post-processing, tractometry, visualization	Code Library, CLI, GUI	Python library for comprehensive diffusion MRI analysis, emphasizing readability and integrating classic and advanced methods.
MRtrix3	Voxel-level modeling (DTI, CSD), tractography (deterministic, probabilistic, anatomically-constrained), connectomics, visualization	CLI	Fast and flexible C++ framework for diffusion MRI, offering advanced modeling, tractography, and connectomics via the command line.
FSL	Modeling (bedpostx), tractography (probtrackx), segmentation (xtract)	CLI	Widely used C/C++ software suite for diverse MRI analysis, including robust diffusion MRI preprocessing and registration, accessible via the command line.
Camino	Reconstruction, tractography, Connectomics statistics	CLI	Java toolkit with Unix-style CLI for a complete diffusion MRI pipeline from raw data to statistics, emphasizing flexibility and transparency.
Diffusion Toolkit	Reconstruction, fiber tracking, analysis, visualization	GUI	Cross-platform C++ package with a GUI for a full diffusion MRI workflow, from reconstruction to visualization, including TrackVis.
ExploreDTI	Processing, analysis, interactive display & manipulation	GUI	MATLAB toolbox focused on interactive diffusion MRI data exploration and manipulation through a user-friendly GUI.
DSI Studio	Advanced reconstruction, tractography, segmentation, connectomics	GUI & CLI	Software providing advanced diffusion MRI reconstruction and tractography, outputting in versatile file formats.
Scilpy	dMRI & tractography, post-tractography analysis, bundle segmentation, Tractometry, connectomics	CLI & Code Library	Python library with user-friendly CLI scripts for dMRI and advanced post-tractography processing, leveraging DIPY
Spinal Cord Toolbox	Preprocessing, atlas-based analysis, cord-specific quantification	CLI	Python toolbox specialized for spinal cord MRI processing, offering preprocessing, atlas-based analysis, and cord quantification via command line.
SlicerDMRI	General image computing, diffusion MRI processing, Tractography	GUI	Open-source C++ extension to 3DSlicer with a rich GUI for image computing, including versatile diffusion MRI analysis tools and visualization.

pyAFQ	Tractography, bundle classification, tract profile extraction	CLI & Code Library	Python library for automated fiber quantification, providing reproducible tractometry analysis via API and CLI, built upon DIPY.
Tractome	Tractography analysis, dissimilarity representations, cluster-based segmentation	GUI	Python tool for advanced tractography analysis using dissimilarity representations and clustering algorithms for fiber organization.
Tracula	Tool for tract reconstruction, and statistical analyses	CLI	Tool for dMRI and tractography within Freesurfer
WMQL	Tract segmentation based on ROIs and parcellations	CLI	No streamline reconstruction, only segmentation based on a specific nomenclature tied to a brain parcellation

Name	Underlying Technologies/Languages	Scaling/Compatibilities	Key Steps
BrainSuite	BrainSuite CLI, FSL, AFNI, Nipype (Python), R	Participant/Group level, Parallel processing (Nipype), Reuses prev. outputs	Anatomical (T1w), Diffusion (dMRI + FSL eddy), Functional (fMRI + FSL, AFNI, BrainSuite, HCP space)
Connectome Mapper 3	Python3, Nipype, FSL, FreeSurfer, ANTS, Dipy, MRtrix3, AFNI, MNE	Linux, macOS, Windows, HPC, Multi-modal, Hierarchical connectomes, BIDS output	Anatomical (sMRI + FreeSurfer), Diffusion (dMRI), fMRI (rfMRI), EEG (source-level)
DeepPrep	Deep Learning (FastCSR, SUGAR, SynthMorph, FastSurferCNN), Nextflow	Scalable, Portable, Efficient, Local, HPC, Cloud, BIDS App	Anatomical (Deep Learning enhanced FreeSurfer), Functional (Motion, Slice-timing, Susceptibility correction), Visual & Summary Reports
dMRIPrep	Integrative platform with GUI	Part of BIDS Apps ecosystem	dMRI Preprocessing & Reconstruction, Data for pyAFQ
MaPPeRTrac	Bash, Neuroimaging scripts	HPC environments, Rapid prototyping	Motion/Artifact Correction, Non-brain removal, Diffusion Anisotropy, Grey matter connectivity matrix, EDI
Micapipe	XTract, MRtrix3, Ants, Freesurfer. Mix of Bash and Python	Macroscale brain models, Structural/Functional connectivity, Geodesic distance, Microstructural similarity, Validated datasets	Subcortical/Cortical/Cerebellar Segmentations, Inter-regional feature matrices (connectomes, covariance, geodesic distance)
nf-neuro	Nextflow (DSL2), nf-core framework	Infrastructure-agnostic, Collaborative, Reusable modules, Community-driven	Collaborative framework, Validation focus, Maintenance centralization
PreQual	MRtrix3, FSL, ANTs	From Raw dMRI data to fully preprocessed with complete QC report.	Denoising, Intensity Normalization, Concatenation, Artifact Correction, Susceptibility Correction, Tensor Model Fitting, Quality Assessment
QSIPrep	BIDS metadata, FSL, DSI Studio, DIPY, ANTs, MRtrix3	Unified dMRI platform, Robust, Interoperable format	BIDS-metadata driven Preprocessing, Advanced Reconstruction/Tractography, Visual Reports, Standardized Methods
TractoFlow Suite	Nextflow, scilpy, dipy, mrtrix3, ANTs, FSL,	Large databases, Easy to use, Reproducible, Fast	TractoFlow: dMRI Preprocessing, DTI/CSD, Tractography, T1

	FreeSurfer		Registration; tractometryflow: Tract Metrics, Tract Profiles; connectoflow: Connectivity Matrices; bstflow: Bundle-Specific Tracking