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# Extract the DTI files for the subject and name them using the NIfTI format
library(neurobase)
library(rcamino)
outfiles <- result$output_files
names(outfiles) <- neurobase::nii.stub(basename(outfiles))

# Specify the B-values and B-vectors used in the HCP database for further processing:
camino_fsl2scheme(bvecs = outfiles[["bvecs"]], bvals = outfiles[["bvals"]],
  outfile = "hcp.scheme")

# Convert the diffusion data from NIfTI to Camino format:
camino_image2voxel(infile = outfiles[["data"]], outfile = "dwi.Bfloat")

# Fit the diffusion tensor imaging model:
camino_modelfit(infile = "dwi.Bfloat", outfile = "dt.Bdouble",
  scheme = "hcp.scheme", gradadj = outfiles[["grad_dev"]],
  model = "ldt", mask = outfiles[["nodif_brain_mask"]])

# Produce the FA and MD maps from the fitted tensor data:
fa <- camino_fa_img(infile = "dt.Bdouble", inputmodel = "dt", header = outfiles[["data"]])
md <- camino_md_img(infile = "dt.Bdouble", inputmodel = "dt", header = outfiles[["data"]])

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