MIA - Medical Imaging Analysis tools

I. PACKAGE

FOLDERS	SUBFOLDERS & FILES	DESCRIPTION
impro		**utility functions for image handling (both list and raster formats)**
	impro.R	implements rasterize.voi(), which creates an array-frepresentation of the tumor volume object
ellmod		**implementations of functions used for ellipsoidal-model-based structural analysis**
	hetE.R	core functions for monotonic and bitonic analyses, incl. a plot function
	data/	VOIs for two sarcoma case studies (Case_A_tumor.tsv and Case_B_tumor.tsv, typical AMIDE output)
root		**root directory**
	demo_script.R	demo script…

II. DESCRIPTION OF CORE FUNCTIONS

ellmod	plot.profile	plot function…
	project	weighted projection of 3D data based on eigendecomposition
	iso.reg	performs stepwise isotonic uptake profile fit
	grad	calculation of gradient for objective function
	hetE	implements the core heterogeneity analysis
	unismooth	performs stepwise bitonic uptake profile fit
	unismooth.sp	performs smoothed bitonic uptake profile fit
	struct.quant	generates metabolic gradient quantitations from bitonic uptake profile fit

III. DESCRIPTION OF UTILITY FUNCTIONS

impro	rasterize.voi	creates an array-frepresentation of the tumor volume object
root	demo_script.R	displays mid-volume views of the VOIs and outputs structural analysis for 2 case studies