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-format representation of the tumor volume object
ellmod	----------	**implementation of the ellipsoidal model of volumetric PET tracer uptake distribution**
	hetE.R	core functions for monotonic and bitonic analyses, incl. a plot function
	hetE_demo.R	demo script for hetE() functions: run hetE.demo()
	data/	VOIs for two sarcoma case studies (Case_A_ROI.rda and Case_B_ROI.rda, typical AMIDE output)

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
ellmod	hetE.demo()	displays mid-volume views of the VOIs and outputs structural analysis for 2 case studies