

## General R Functions:

Function	Package	Purpose
<code>aes</code>	<i>ggplot2</i>	Defines “aesthetics” for a <i>ggplot2</i> object
<code>all</code>	<i>base</i>	Returns <b>TRUE</b> if all the values of a vector are <b>TRUE</b>
<code>alpha</code>	<i>scales</i>	Changes the opacity of a color
<code>arrange</code>	<i>dplyr</i>	Sorts rows of a <b>data.frame</b> based on a variable
<code>as.data.frame</code>	<i>base</i>	Coerces an object to a <b>data.frame</b>
<code>basename</code>	<i>base</i>	Extracts the name of a file from a file path
<code>biocLite</code>	<i>BiocInstaller</i>	Install Bioconductor packages
<code>boxplot</code>	<i>base</i>	Plots a box and whisker plot
<code>brewer_pal</code>	<i>scales</i>	Creates a palette of colors from ColorBrewer
<code>c</code>	<i>base</i>	Combines elements into a vector
<code>cbind</code>	<i>base</i>	Performs binding by column
<code>class</code>	<i>base</i>	Returns the class of an object
<code>colMeans</code>	<i>base</i>	Performs the column means on a matrix/ <b>data.frame</b>
<code>cut</code>	<i>base</i>	Separates a vector into a factor based on a set of breaks
<code>data.frame</code>	<i>base</i>	Creates a <b>data.frame</b> object
<code>density</code>	<i>base</i>	Estimates a kernel density estimate from a vector
<code>desc</code>	<i>dplyr</i>	A helper function, used with <b>arrange</b> to specify descending sorting
<code>dim</code>	<i>base</i>	Gets the dimensions of an object
<code>do.call</code>	<i>base</i>	Performs a call to a specific function with a list of arguments
<code>example</code>	<i>base</i>	Runs the code in the example section of a function’s help file
<code>file.exists</code>	<i>base</i>	Tests whether a file exists on the hard disk
<code>file.path</code>	<i>base</i>	Pastes directories and file names together to form a file path
<code>file.remove</code>	<i>base</i>	Removes files from the hard disk
<code>floor</code>	<i>base</i>	Rounds numbers down to the nearest integer
<code>format_sci</code>	<i>knitr</i>	Formats numbers using scientific notation
<code>geom_line</code>	<i>ggplot2</i>	Adds a line layer to a ggplot
<code>ggplot</code>	<i>ggplot2</i>	Creates a <b>ggplot2</b> plot object
<code>gradient_n_pal</code>	<i>scales</i>	Creates a palette of colors based on a number of gradients
<code>gray</code>	<i>base</i>	Returns colors based on white to black in grayscale
<code>grep</code>	<i>base</i>	Searches a string for a regular expression and returns the index of characters that contain that string
<code>group_by</code>	<i>dplyr</i>	Groups a <b>data.frame</b> by sets of factors
<code>head</code>	<i>base</i>	Prints the first set of elements of an object
<code>hi_latex</code>	<i>knitr</i>	Highlighter for LaTeX
<code>hist</code>	<i>base</i>	Calculates and plots a histogram of a vector
<code>image</code>	<i>graphics</i>	Plots a 2-D grid of an image
<code>install_github</code>	<i>devtools</i>	Command that can install packages from GitHub
<code>install.packages</code>	<i>base</i>	General installer for CRAN and other packages.
<code>is.numeric</code>	<i>base</i>	Test whether a vector is numeric or not
<code>lapply</code>	<i>base</i>	Apply a function to each element of a list and return a list
<code>length</code>	<i>base</i>	Returns the number of elements in an object
<code>library</code>	<i>base</i>	Loads a package into memory so functions can be used.
<code>lines</code>	<i>base</i>	Adds lines to a base R plot
<code>list</code>	<i>base</i>	Constructs a list object
<code>list.files</code>	<i>base</i>	Returns a list of files from a path based on a file pattern
<code>mapply</code>	<i>base</i>	Multi-apply function for running functions over linked lists
<code>matrix</code>	<i>base</i>	Constructs a matrix object
<code>max</code>	<i>base</i>	Calculates the maximum over a vector
<code>names</code>	<i>base</i>	Extracts the names of an object
<code>options</code>	<i>base</i>	Set global options in R
<code>pandoc.table</code>	<i>pander</i>	Prints out tables nicely for HTML slides
<code>par</code>	<i>base</i>	Set of parameters relevant to plotting
<code>paste</code>	<i>base</i>	Concatenates strings together, separated by spaces by default
<code>paste0</code>	<i>base</i>	Concatenates strings together, separated by nothing by default
<code>plot</code>	<i>base</i>	General plotting function for the R base
<code>print</code>	<i>base</i>	Shows an object
<code>quantile</code>	<i>base</i>	Estimates the quantiles of a vector, based on the probabilities given, otherwise the standard quantiles
<code>range</code>	<i>base</i>	Returns the min and maximum values

<code>return</code>	<i>base</i>	Used in making functions, determines what the function should output
<code>rm</code>	<i>base</i>	Removes objects from memory in R
<code>rownames</code>	<i>base</i>	Extract the row names of an object (matrix or data.frame)
<code>sapply</code>	<i>base</i>	Apply a function to each element of a list and return a simplified object if possible
<code>seq</code>	<i>base</i>	Generates a sequence of numbers
<code>source</code>	<i>base</i>	Loads in an R script
<code>strsplit</code>	<i>base</i>	Splits a character vector by a splitting string
<code>system.file</code>	<i>base</i>	Returns the paths of files on the hard disk for installed packages
<code>t</code>	<i>base</i>	Transposes a matrix/vector
<code>table</code>	<i>base</i>	Performs a simple tabulations of the unique values of a vector
<code>tally</code>	<i>dplyr</i>	Counts the number of rows in a <code>data.frame</code> , usually used with <code>group_by</code>
<code>text</code>	<i>base</i>	Adds text to a base plot
<code>unique</code>	<i>base</i>	Returns the unique values of a vector
<code>which</code>	<i>base</i>	Returns the indices that are <code>TRUE</code> from an object, also can return array indices

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## Imaging Specific Functions:

Function	Package	Purpose
<code>applyEmptyImageDimensions</code>	<i>neurobase</i>	Applies indices to drop dimensions from <code>getEmptyImageDimensions</code>
<code>bias_correct</code>	<i>extrantsr</i>	Performs N3 or N4 Bias-field correction
<code>check_nifti</code>	<i>neurobase</i>	Ensures the output is a <code>nifti</code> object or list of <code>nifti</code> objects
<code>dicom2nifti</code>	<i>oro.dicom</i>	Converts a list of <code>dicom</code> files to a <code>nifti</code> object
<code>dicomTable</code>	<i>oro.dicom</i>	Converts a list of <code>dicom</code> headers into a <code>data.frame</code>
<code>dim</code>	<i>base</i>	Gets the dimensions of an object
<code>double_ortho</code>	<i>neurobase</i>	Plots 2 orthographic images side-by-side
<code>download_img_data</code>	<i>WhiteStripe</i>	Downloads example image data for <code>whitestripe</code>
<code>dropEmptyImageDimensions</code>	<i>neurobase</i>	Drops empty image dimensions from a <code>nifti</code> object, combines <code>getEmptyImageDimensions</code> and <code>applyEmptyImageDimensions</code>
<code>fast</code>	<i>fslr</i>	Performs tissue-class segmentation using the FAST algorithm
<code>fslbet</code>	<i>fslr</i>	Runs the brain extraction tool (BET) from FSL
<code>fslbet_robust</code>	<i>extrantsr</i>	Runs neck removal, bias correction, BET, re-estimates a center of gravity, then BET again
<code>get_image_filenames_list_by_subject</code>	<i>ms.lesion</i>	Returns a list of file names for images by subject. Different types returns different files
<code>get_t1_filenames</code>	<i>kirby21</i>	Returns a list of file names for T1 images from Kirby21
<code>have_fsl</code>	<i>fslr</i>	Logical test to see if FSL is installed, useful for examples
<code>image.nifti</code>	<i>graphics</i>	Plots a slice of a <code>nifti</code> . By default, plots all slices.
<code>install_dcm2nii</code>	<i>dcm2niiir</i>	Installs the <code>dcm2nii</code> binary for executing DICOM to NIfTI conversions
<code>malf</code>	<i>extrantsr</i>	Multi-atlas label fusion function for segmenting structures based on registration
<code>mask_vals</code>	<i>neurobase</i>	Returns the values of an image for voxels within a mask
<code>mass_images</code>	<i>malf.template.</i>	A set of template images and masks used for MALF
<code>multi_overlay</code>	<i>neurobase</i>	Takes a list of images and plots one slice of each image side-by-side
<code>nii.stub</code>	<i>neurobase</i>	Removes the <code>nii</code> or <code>nii.gz</code> extensions from a file name
<code>oMask</code>	<i>extrantsr</i>	Calls <code>getMask</code> from ANTsR to get a coarse mask
<code>ortho2</code>	<i>neurobase</i>	Plots an orthographic image, different defaults than <code>orthographic</code>
<code>orthographic</code>	<i>oro.nifti</i>	Plots an orthographic image
<code>otropos</code>	<i>extrantsr</i>	Runs Atropos k-means segmentation
<code>overlay</code>	<i>oro.nifti</i>	Displays a slice of an image overlaid with the slice of another
<code>plot.densities</code>	no package	Defined function we made to plot the densities of the tissue classes after normalization
<code>readDICOM</code>	<i>oro.dicom</i>	Reads in a DICOM image and returns a list of the header and image values
<code>readnii</code>	<i>neurobase</i>	Reads in NIfTI files
<code>robust_window</code>	<i>neurobase</i>	Calculates the min and 99.9 <sup>th</sup> quantiles and sets anything outside those values to those values
<code>slice</code>	<i>oro.nifti</i>	Similar to <code>image</code> for <code>nifti</code> objects, but only returns one slice by default
<code>voxres</code>	<i>oro.nifti</i>	Returns the 3 voxel dimensions in millimeters
<code>whitestripe</code>	<i>WhiteStripe</i>	Estimates the voxels within the White Stripe from an image
<code>whitestripe_norm</code>	<i>WhiteStripe</i>	Applies the White Stripe to an image to normalize it
<code>within_visit_registration</code>	<i>extrantsr</i>	Performs registration of a list of images to the first image, aka co-registration
<code>writenii</code>	<i>neurobase</i>	Writes a <code>nifti</code> object to a NIfTI file on hard disk
<code>xyz</code>	<i>neurobase</i>	Estimates the indices of the center of gravity of an image
<code>zscore_img</code>	<i>neurobase</i>	Performs z-score normalization, using the mean and standard deviation, by default