Plotting Q1:Getting familiar with the available in BoutrosLab.plotting.general

INTRO: BoutrosLab.plotting.general

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This series of questions is designed to help teach the basics of using BoutrosLab.plotting.general.

1. Familiarize yourself with the functions available in BoutrosLab.plotting.general.

-These are easily viewable at
http://bpg.oicr.on.ca/API/BoutrosLab.plotting.general/5.3.4/index.html

-Note the scope and customizability of the different functions

-Think about what data-types would be most appropriate for the different plot-types

- append.footnote: Appends Footnotes to Grid Objects.
- CNA: Copy number aberration (CNA) data from colon cancer patients.
- color.gradient: Creates a colour gradient.
- colour.gradient: Creates a colour gradient. This is the same with color.gradient.
- covariates.grob: Create one or more covariate bars.
- create.barplot: Make a barplot. It is good for discrete data and allows for quick comparison of values for different samples. Limitation is that for plots with a high number of samples, and covariates are able to be expressed in a graph.
- create.boxplot: Make a boxplot. Boxplots can be created for individual variables or for variables that are divided into groups. It is good for displaying the central tendency and spread of each group.
- create.colorkey: Create Colourkey. It is good for generating and placing a colour key and use in multiplots when a smaller colour key is desired.
- create.colourkey: Create Colourkey. This is the same with create.colorkey.
- create.dendrogram: Generate a dendrogram. A dendrogram (or tree diagram) is a network structure which displays the groups formed by hierarchical clustering. It takes a matrix and creates a row-wise or column-wise dendrogram.
- create.densityplot: Make a density plot. A Density plot is used to visualize the distribution of a numerical variable. It is a good job for determining the distribution shape.
- create.dotmap: Make a dotmap with coloured background. A dotmap is good for comparison of multiple characteristics across variables by coupling the dot size and colors to the magnitude of each feature. However, the dotmap has the disadvantages of seeing small discrepancies in magnitude between sample measurements.

- <u>create.heatmap</u>: Make a heatmap. A heatmap is one of the great ways to visualize hierarchical clustering and to use color and binning for visualizing large clusters of samples and features. This function could create a heatmap with a key like legend - used to show a range of continuous variables. It is also able to make diverse heatmap graphs with covariates.grob, create.dendrogram, and legend.grob.
- <u>create.hexbinplot</u>: Make a hexagonally binned plot. Hexbin plots are shown as an alternative to the standard scatter plots. It summarizes high-density data with the data points grouped into bins.
- <u>create.histogram</u>: Make a histogram. It is convenient to graph continuous variables with variable arguments. The diverse types such as colour change and line type are available when using this function.
- <u>create.manhattanplot</u>: Make a Manhattan plot. It is used to display data with many data-points and with a distribution of higher-magnitude values. In bioinformatics it is used in genome-wide association studies (GWAS) to display significant SNPs. The mantahhan.plot function can provide many options for annotating different parts of your plot by different colors and labeled with their label name.
- <u>create.multiplot</u>: Joins plots together. This merges together multiple plots in the specified layout. Covariates can be created using this create.multiplot function.
- <u>create.polygonplot</u>: Make a polygonplot. It is useful for highlighting striking differences between groups and limited in scope.
- <u>create.qqplot.comparison</u>: Make a quantile-quantile plot of two samples. It shows whether two data sets come from populations with a common distribution. The QQ plot is also used to compare two distributions based on a sample from each.
- <u>create.qqplot.fit</u>: Make a quantile-quantile plot of a sample. The function takes a sample and creates a qq plot against a theoretical distribution, possibly conditioned on other variables.
- <u>create.qqplot.fit.confidence.interval</u>: Create the confidence bands for a one-sample qq plot.
- <u>create.scatterplot</u>: Make a scatterplot. It displays data as a collection of points that shows the linear relation between those two continuous variables. It enables us to use correlation to perform regression analysis or assess the strength of the relationship.
- <u>create.segplot</u>: Make a segplot. It is a form of scatter plots using only 1 expression where the data is represented as a line. This function is available to colour each sample with coloured background.
- <u>create.stripplot</u>: Make a strip-plot. It produces one dimensional scatter plots of the given data. These plots are a good alternative to boxplots when sample sizes are small.
- <u>create.violinplot</u>: Make a violin plot. A violin plot is similar to box plots, except that they visualize the kernel probability density of the data at different values.
- <u>default.colors</u>: Provides default colour schemes. The requested qual colour scheme has a length of 12 colours.
- <u>default.colours</u>: Provides default colour schemes. It is the same with <u>default.colors</u>.
- <u>display.colors</u>: Function to display R colors, as well as corresponding R grey colours.
- <u>display.colours</u>: Function to display R colors, as well as corresponding R grey colours. It is the same with <u>display.colors</u>.

- display.statistical.result: Utility function to display statistical result in a plot
- dist: Distance Matrix Computation.
- force.color.scheme: Based on predefined colour schemes, returns a vector of corresponding colours. Available schemes are "annovar.annotation", "annovar.annotation.collapsed", etc.
- force.colour.scheme: Based on predefined colour schemes, returns a vector of corresponding colours. It is the same with force.color.scheme.
- GarbageCollect: Force Garbage Collection to help ensure as much memory as necessary is returned.
- generate.at.final: Generates alternative default tick mark locations for create.densityplot() and create.scatterplot().
- generate.filename: Generate a filename in the lab standard.
- get.corr.key: Correlation Key. This is for adding correlation key legends to scatterplots.
- get.correlation.p.and.corr: Calculate a correlation and its statistical significance.
- get.defaults: Get operating system specific default properties.
- get.line.breaks: Get line breaks. Main use intended to be in row.lines arguments to create.heatmap.
- ks.test.critical.value: Critical Value for Kolmogorov-Smirnov Test.
- legend.grob: Generate a legend grob. It takes a list and generates a grob representing one or more legends.
- ls.objects: List of objects.
- microarray: Microarray dataset of colon cancer patients.
- panel.BL.bwplot: A lattice::panel.bwplot replacement that fixes colouring issues.
- patient: Dataset describing qualities of 58 colon cancer patients.
- recode.vector: Recode Vector.
- save.session.profile: Save Session Profile.
- scientific.notation: Use scientific notation in plots.
- show.available.palettes: Display the available colour palettes.
- SNV: Single nucleotide variant (SNV) data from colon cancer patients.
- write.metadata: Writes Metadata.
- write.plot: Simplifies plotting by standardizing and centralizing all output-handling.