

Figure 1:

| Data | Preprocessing | Segmentation | Visualization |
|---|--|---|---|
| Copy number data (+ allele frequencies) | Outlier handling <i>winsorize(...)</i> Missing value imputation <i>imputeMissing(...)</i> | Individual segmentation of one or more samples <i>pcf(...)</i> Joint segmentation of multiple samples <i>multipcf(...)</i> Segmentation of SNP-array data <i>aspcf(...)</i> | Whole-genome plots <i>plotHeatmap(...)</i> <i>plotGenome(...)</i> <i>plotCircle(...)</i> <i>plotFreq(...)</i> Chromosome plots of data and segments <i>plotSample (...)</i> <i>plotChrom (...)</i> <i>plotAllele(...)</i> Diagnostic plot <i>plotGamma (...)</i> |



Analysis pipeline