Overview of vignettes for copy number estimation

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The workflow for copy number analyses in the crlmm package includes preprocessing and genotyping of the raw intensities followed by estimation of parameters for copy number estimation using crlmmCopynumber. Supported platforms are those for which a corresponding annotation package is available. Table **??** provides an overview of the available vignettes pertaining to copy number estimation. These vignettes are located in the inst/scripts subdirectory of the crlmm package. HapMap datasets are used to illustrate the workflow and are not provided as part of the crlmm package. Users wishing to reproduce the analysis should download the HapMap CEL files (Affymetrix) or the idat files (Illumina) and modify the paths to the raw data files as appropriate.

Vignette	Platform	Annotation package	Scope
Infrastructure	Affy/Illumina		The CNSet container / large data support using the ff package
AffyGW	Affy 5.0, 6.0	genomewidesnp5crlmml, genomewidesnp6Crlmm	Preprocessing, genotyping, CN estimation
IlluminaPreprocessCN	Illumina	several[†]	Preprocessing, genotyping, CN estimation

Table 1: Vignettes for copy number estimation. [†] See annotationPackages() for a complete listing of supported Illumina/Affy platforms

The Infrastructure vignette provides additional details on the *CNSet* container used to organize the processed data as well as a brief discussion regarding large data support through the ff package.