

# CRAN and Bioconductor packages for Microarray data analysis

Analysis Step	Agilent 2-color	Agilent 1-color	Affymetrix	Illumina Methylation
Raw Data	limma::read.maimages	limma::read.maimages	affy::justRMA	minfi::read.metharray.exp
QC	arrayQualityMetrics::arrayQualityMetrics	arrayQualityMetrics::arrayQualityMetrics	yaqcaffy::yaqc	shinyMethyl
Probe Quality Estimation	Custom function(); by using signal distribution of negative control probes	Custom function(); by using signal distribution of negative control probes	NA	minfi::detectionP
Sample and/or Array Variation Diagnostics	limma::plotDensities, limma::plotMD, boxplot	limma::plotDensities, boxplot	limma::plotDensities, boxplot	minfi::densityPlot, boxplot
Normalization	limma::normalizeBetweenArrays, limma::normalizeQuantiles, limma::normalizeVSN, limma::normalizeCyclicLoess	limma::normalizeQuantiles, limma::normalizeVSN, limma::normalizeCyclicLoess, limma::normalizeBetweenArrays	Handled by justRMA (Raw Data)	minfi::preprocessRaw, minfi::preprocessSWAN, minfi::preprocessRaw, minfi::preprocessQuantile, minfi::preprocessIllumina, minfi::preprocessFunnorm, minfi::preprocessNoob

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Batch Effect Estimation		swamp::confounding, swamp::prince, swamp::prince.plot, limma:::plotMDS	swamp::confounding, swamp::prince, swamp::prince.plot, limma:::plotMDS	swamp::confounding, swamp::prince, swamp::prince.plot, limma:::plotMDS	swamp::confounding, swamp::prince, swamp::prince.plot, limma:::plotMDS
Batch Effect Mitigation	Known	Custom function(); employs sva::ComBat to iteratively isolate and correct each batch	Custom function(); employs sva::ComBat to iteratively isolate and correct each batch	Custom function(); employs sva::ComBat to iteratively isolate and correct each batch	Custom function(); employs sva::ComBat to iteratively isolate and correct each batch
	Unknown	1. sva::sva for identification of unknown sources of variation; 2. Estimation of surrogate variable effect via diagnostic plots; 3. Batch surrogate variables correction by sva::ComBat	1. sva::sva for identification of unknown sources of variation; 2. Estimation of surrogate variable effect via diagnostic plots; 3. Batch surrogate variables correction by sva::ComBat	1. sva::sva for identification of unknown sources of variation; 2. Estimation of surrogate variable effect via diagnostic plots; 3. Batch surrogate variables correction by sva::ComBat	1. sva::sva for identification of unknown sources of variation; 2. Estimation of surrogate variable effect via diagnostic plots; 3. Batch surrogate variables correction by sva::ComBat

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Annotation	Array design specific annotation from eArray OR intrinsic annotation from raw data	Array design specific annotation from eArray OR intrinsic annotation from raw data	Array design specific annotation from brainarray; Installable from user interface	IlluminaHumanMethylation450kanno.ilmn12.hg19, IlluminaHumanMethylationEPICanno.ilm10b2.hg19 (from Bioconductor)
Differential Analysis	limma::makeContrasts, limma::lmFit, limma::eBayes, limma::topTable	limma::makeContrasts, limma::lmFit, limma::eBayes, limma::topTable	limma::makeContrasts, limma::lmFit, limma::eBayes, limma::topTable	limma::makeContrasts, limma::lmFit, limma::eBayes, limma::topTable
Data Exploration	1. Differential sets intersection VennDiagram::venn.diagram, UpSetR::upset; 2. Volcano plot via ggplot2::ggplot; 3. Expression values inspection via multi-gene/multi-probe, multi-sample/group facteted ggplot2::ggplot; 4. Highly differential gene set heatmap via made4::made4::heatmap	1. Differential sets intersection VennDiagram::venn.diagram, UpSetR::upset; 2. Volcano plot via ggplot2::ggplot; 3. Expression values inspection via multi-gene/multi-probe, multi-sample/group facteted ggplot2::ggplot; 4. Highly differential gene set heatmap via made4::made4::heatmap	1. Differential sets intersection VennDiagram::venn.diagram, UpSetR::upset; 2. Volcano plot via ggplot2::ggplot; 3. Expression values inspection via multi-gene/multi-probe, multi-sample/group facteted ggplot2::ggplot; 4. Highly differential gene set heatmap via made4::made4::heatmap	1. Differential sets intersection VennDiagram::venn.diagram, UpSetR::upset; 2. Volcano plot via ggplot2::ggplot; 3. Expression values inspection via multi-gene/multi-probe, multi-sample/group facteted ggplot2::ggplot; 4. Highly differential gene set heatmap via made4::made4::heatmap