Methylation Project

Check the types of distributions of methylation signals

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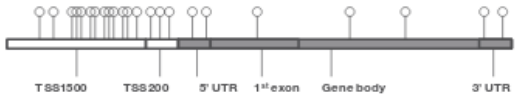
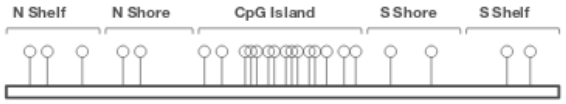
Figure 2: HumanMethylation450 BeadChip Provides Coverage Throughout Gene Regions



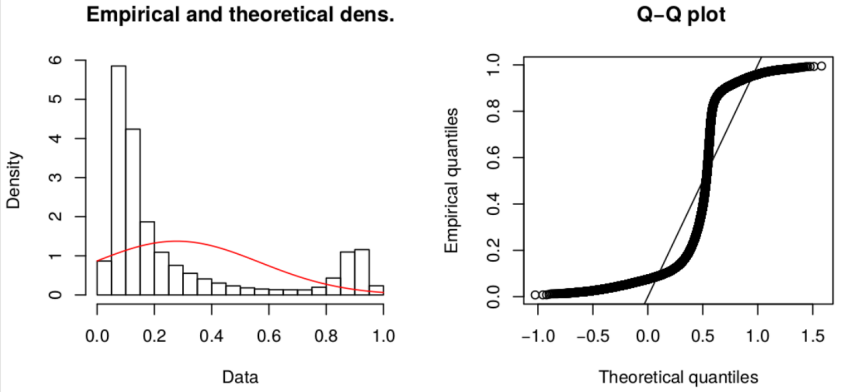
Feature Type	Genes Mapped	Percent Genes Covered	Number of Loci on Array
NM_TSS200	14895	0.79	2.56
NM_TS1500	17820	0.94	3.41
NM_5'UTR	13865	0.78	3.34
NM_1stExon	13127	0.80	1.62
NM_3'UTR	13042	0.72	1.02
NM_GeneBody	17071	0.97	8.97
NR_TSS200	1967	0.65	1.84
NR_TSS1500	2672	0.88	2.92
NR_GeneBody	2345	0.77	5.34



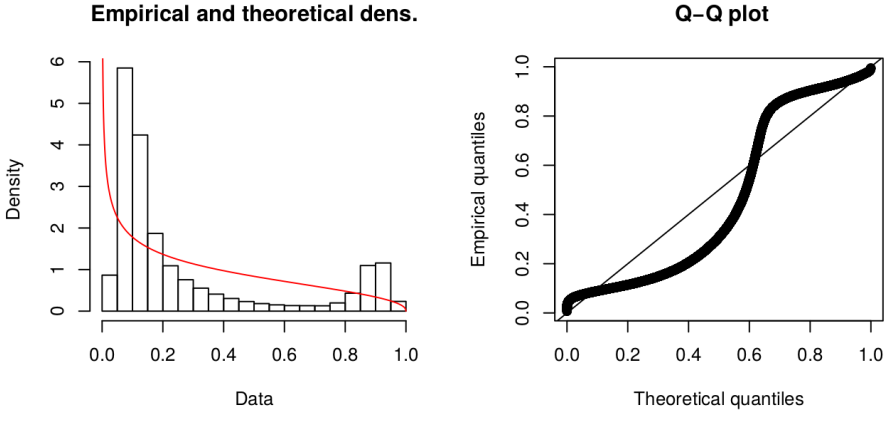
Feature Type	Islands Mapped	Percent Islands Covered	Average Number of Locion Array
Island	26153	0.94	5.08
N_Shore	25770	0.93	2.74
S_Shore	25614	0.92	2.66
N_Shelf	23896	0.86	1.97
S_Shelf	23968	0.86	1.94

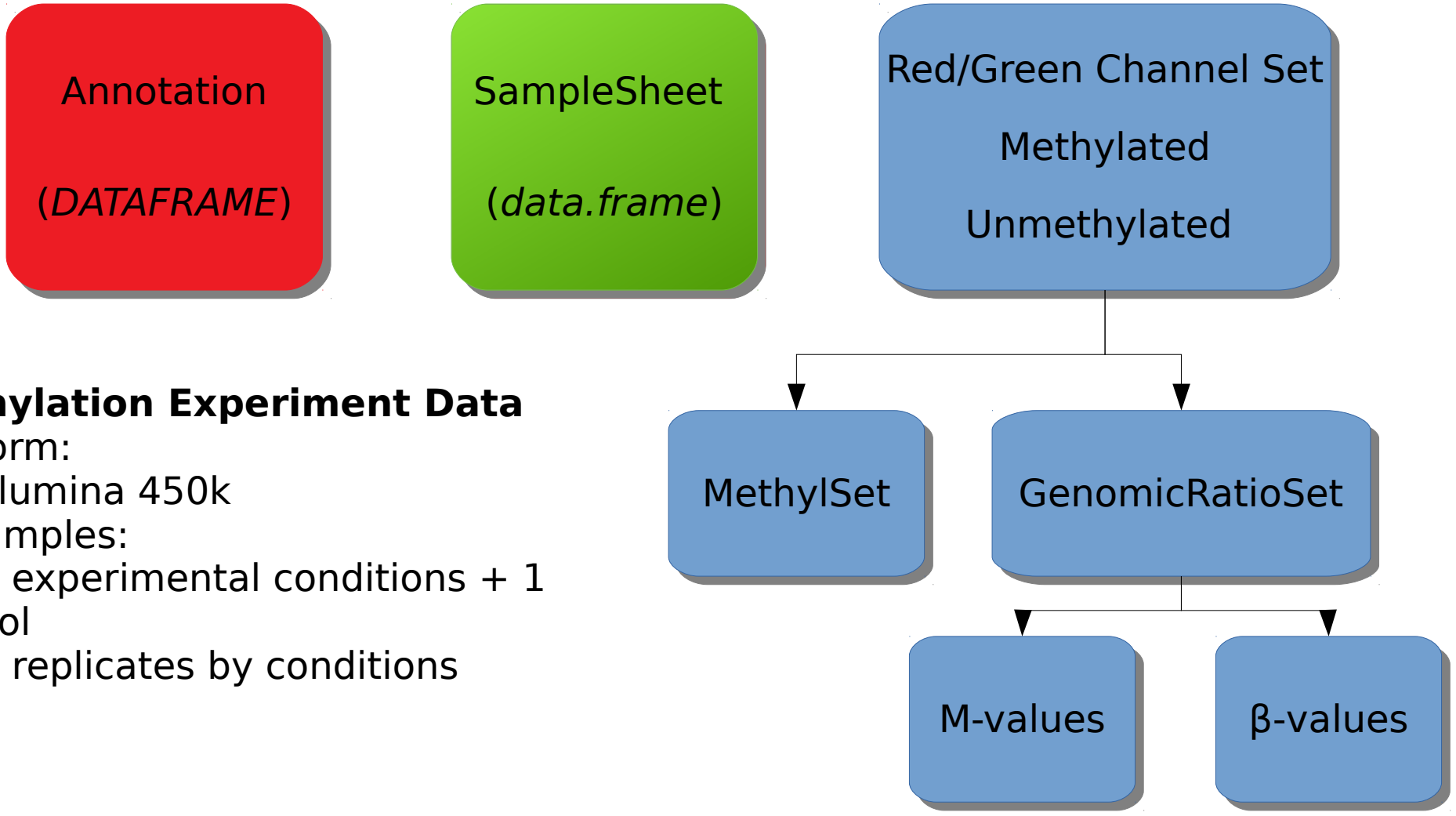
https://cancergenome.nih.gov/abouttcga/aboutdata/platformdesign/illuminamethylation450

Normal fit



Beta fit





Methylation Experiment Data

Platform:

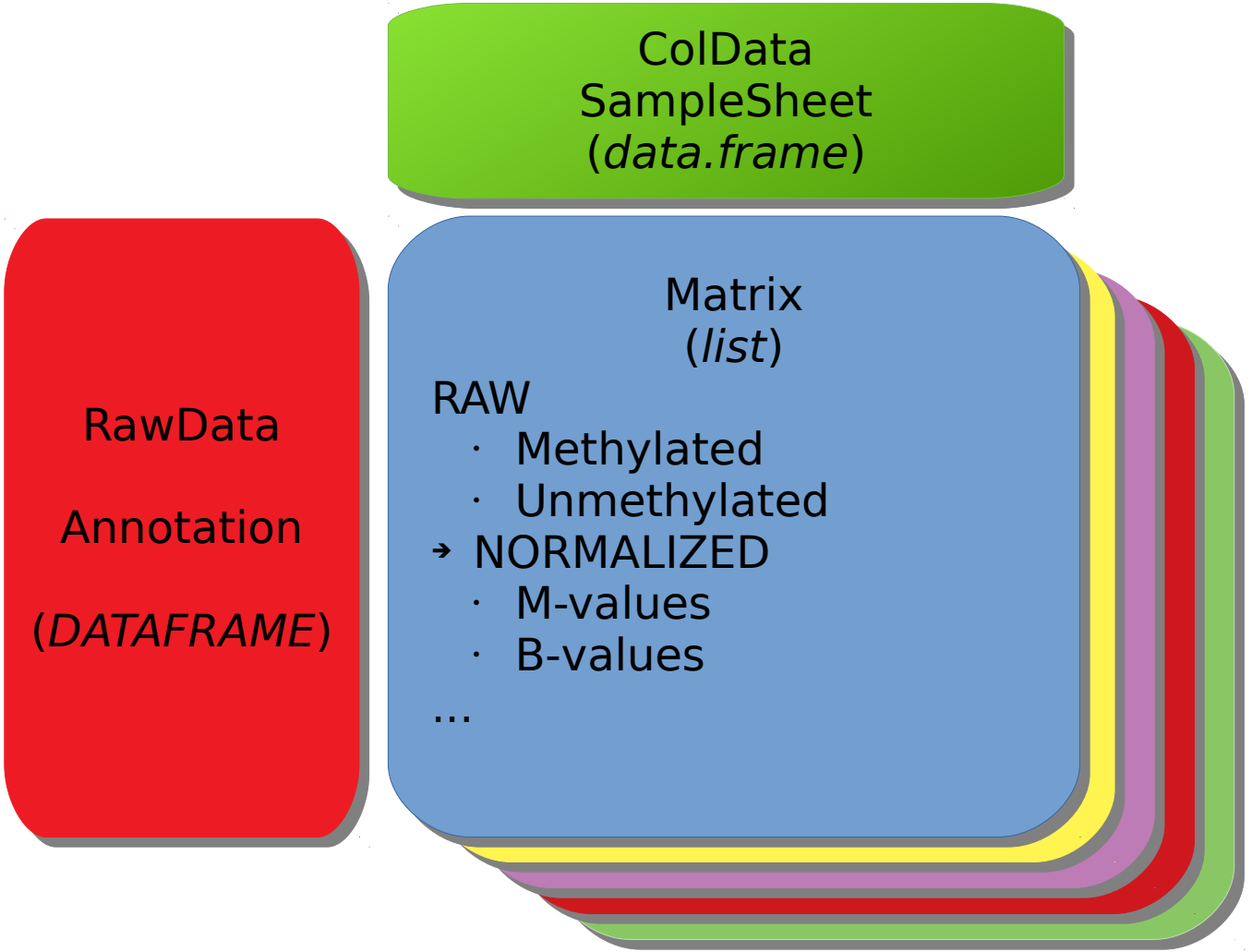
Illumina 450k

12 samples:

2 experimental conditions + 1 control

4 replicates by conditions

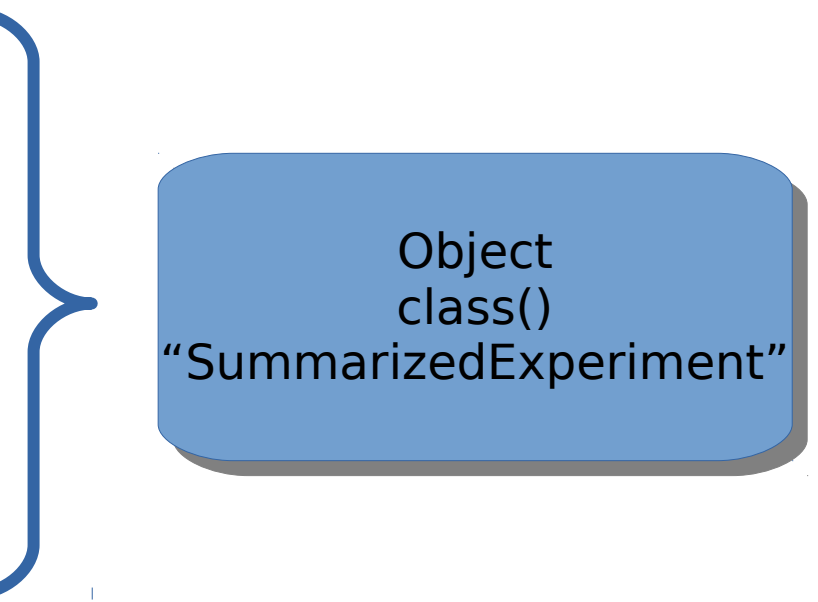
Object of class *SummarizedExperiment*

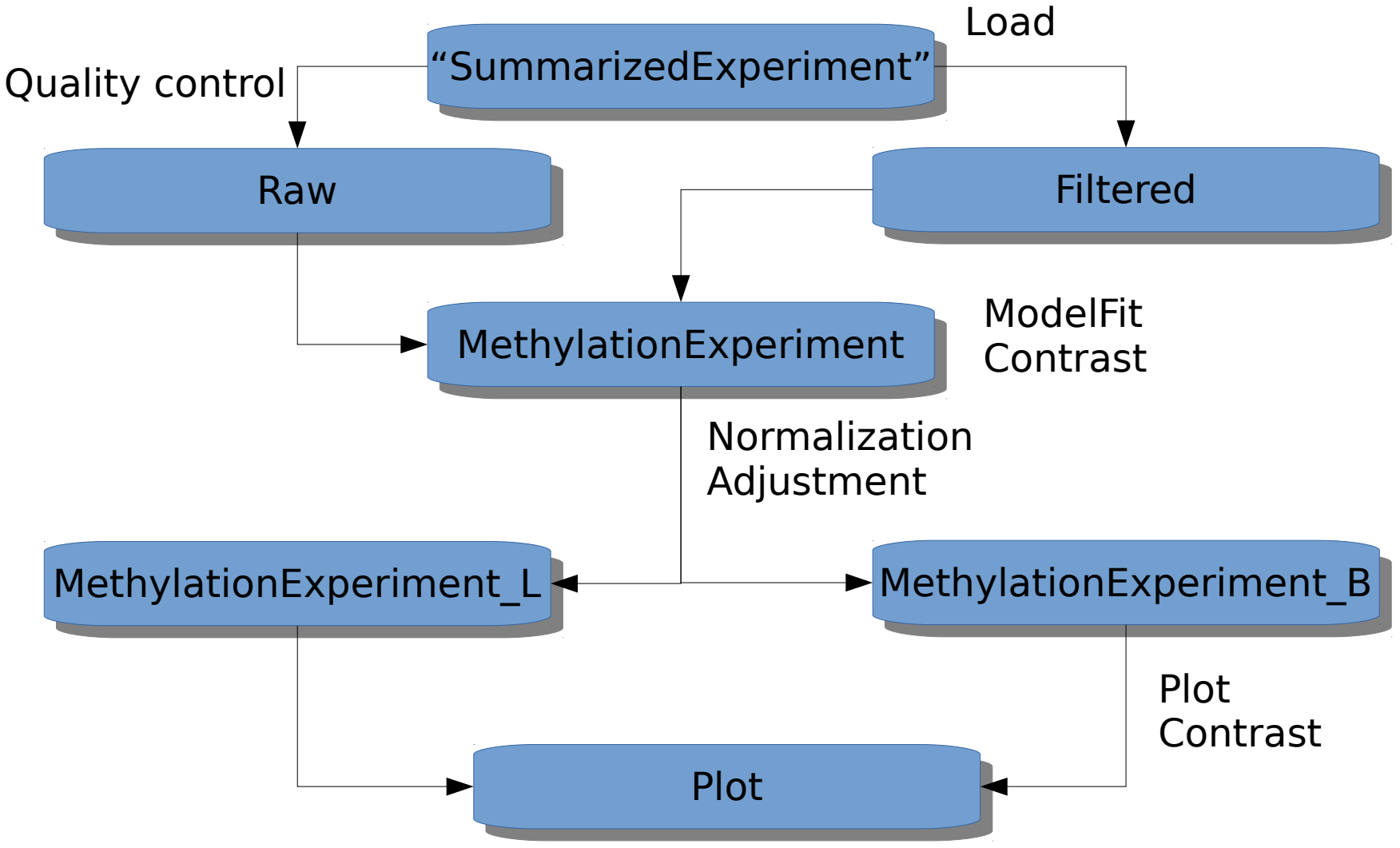


How to access the *SummarizedExperiment*?

Functions:

- Load
- Quality_Control
  - Detection
  - Filter
    - Sample
    - X, Y
    - Detection_by_probe
    - Cross_reactivity
- Normalization
- Ajustment
  - Limma
  - Beta
- Plot
- Contrast




Load
Quality control
“SummarizedExperiment”
Raw
Filtered
MethylationExperiment
ModelFit
Contrast
Normalization
Adjustment
MethylationExperiment_L
MethylationExperiment_B
Plot
Contrast
Plot