**Preparation**
- Probe sequence remapping,
- Creation of a new bpmap file

**Preprocessing**
- Data import, Quality Control Normalization

**High Level Analysis**
- Visualization,
- Summary statistics

**Peak Finding**
- CMARRT algorithm,
- Ringo method

**Correlation Analysis**
- Relate mean binding intensities and, e.g., expression levels

**Profile Summaries**
- Alignment of binding profiles along genomic features

**FASTA, BPMAP** → Preparation

**CEL, ndf, pos, pair.txt** → Preprocessing

**GFF annotation** → High Level Analysis

**ExpressionSet, probeAnno, GFF** → Profile Summaries