

Making aCGH object

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Contents

Please download and utilize example1. This code will also work if the complete example was run from the load.in.example1 data and the smoothing example was also performed on load.in.example1 data.

We have implemented the idea of an aCGHroster object and an aCGH object. The aCGHroster is a complete listing of all samples. This may be all samples for a particular lab or user, etc. An aCGH object is created off the aCGHroster. The aCGH object may consist of all or a subset of samples in the roster object.

For our example of 200 samples we will begin with an aCGH object of all samples:

```
> load("RData/aCGHroster.RData")
> aCGH = make.aCGH(aCGHroster, sampleDX = NA, mapping.data = "RData/HB4.5K.HG18.RData",
+   LGR.label = "array.images$smooth2D.noDesign$Mxy.default",
+   Flagmat.label = NA, min.rep = 1, vrb = T, saveFlag = T, saveName = "RData/aCGH.RData")
```

If we wanted to take a subset of samples we would specify a sampleDX. Lets create an aCGH object consisting of just the samples that are created off the load.specs.24 file.

```
> load("RData/aCGHroster.RData")
> indx = which(aCGHroster$inventory$load.specs == "config.files/load.specs.24")
> aCGHsub = make.aCGH(aCGHroster, sampleDX = indx, mapping.data = "RData/HB4.5K.HG18.RData",
+   LGR.label = "array.images$smooth2D.noDesign$Mxy.default",
+   Flagmat.label = NA, min.rep = 1, vrb = T, saveFlag = T, saveName = "RData/aCGHsub.RData")
```

Lets look at the second example a little closer: The following may be said:

- only the samples that used the load.specs.24 file make up this aCGH object
- The mapping file used to map the samples was "RData/HB4.5K.HG18.RData"
- The values that will be pulled from each sample's image file that will be considered as the log2 ratios came were taken from the smooth2D output.
- no spots will be flagged and values exclude from log ratios

- samples need to only have 1 replicate to be included in analysis
- the aCGH object made will be saved in the RData directory as aCGH-subset

One important aspect to mention is the mapping.data object that may be specified. aCGH objects consist of samples that use the same mapping file. The samples should be all mapped to the same values so that samples may be compared. If samples have a different default.map or when created have a different map then given as the argument mapping.data, the samples will be remapped to this given file.

For example, if we did the following code:

```
load("RData/aCGHroster")
indx = which(aCGHroster$inventory$load.specs=="load.specs.24")

aCGHsub = make.aCGH(aCGHroster,sampleDX=indx,
                    mapping.data="RData/HB19Kv2.HG18.RData",
                    LGR.label="array.images$smooth2D.noDesign$Mxy.default",
                    Flagmat.label=NA,min.rep=1, vrb=T, saveFlag=T,
                    saveName="RData/aCGHsubset.RData")
```

All the samples for this aCGH object will be re-mapped using the 19K human genome build rather than the 4.5K human genome build.

The aCGH object will have indices to sample image, mapping, and design files, will list what objects were used to create the aCGH object, will list the given samples' inventory entries, and will give the samples' log2 ratios at each spot (BAC/Probe).