# Integration with the crlmm package for copy number inference

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March 22, 2012

We load a portion of chromosome 8 from 2 HapMap samples that were processed using the *crlmm* package.

```
> library(oligoClasses)
> library(VanillaICE)
> library2(crlmm)
> library2(SNPchip)
> library2(IRanges)
> data(cnSetExample, package="crlmm")
```

The data `cnSetExample` is an object of class `CNSet`. We coerce the `CNSet` objectf to an object of class `oligoSnpSet` containing log R ratios and B allele frequencies.

```
> oligoSet <- as(cnSetExample, "oligoSnpSet")
```

Next, we fit a 6-state hidden markov model from estimates of the B allele frequency and log R ratios.

```
> res <- hmm(oligoSet, p.hom=0, TAUP=1e8)
```

The `TAUP` parameter scales the transition probability matrix. Larger values of `TAUP` makes it more expensive to transition from the normal copy number state to states with altered copy number. In the following code chunk, we use a lattice multi-panel display to plot each of the altered stated. We frame each alteration by plotting a genomic interval of 200kb on each side (using the `frame=200e3` argument):

```
> rd <- res[!state(res)%in%c(3,4), ]
> fig <- SNPchip:::xyplotLrrBaf(rd[1:2, ], oligoSet,
+                               frame=200e3,
+                               panel=SNPchip:::xypanelBaf,
+                               scales=list(x="free"),
+                               par.strip.text=list(cex=0.6),
+                               pch=".")
```

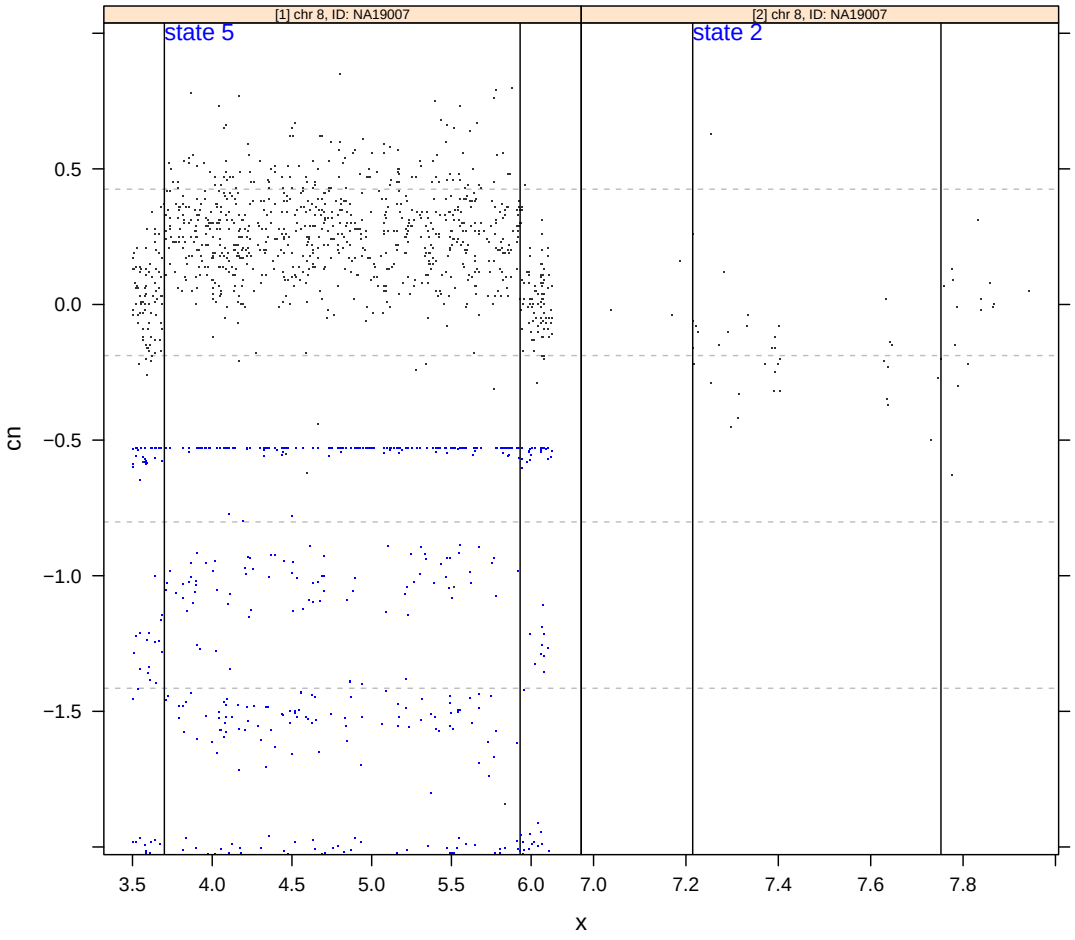


Figure 1: Plot of log R ratios (grey) and B allele frequencies (blue). The B allele frequencies have a range of 0-1 and were rescaled for ease of viewing alongside the log R ratios. Each panel displays one region with a copy number alteration predicted from the 6-state HMM.