Prototype QTL Strategy: Phenotype bp in Cross hyper

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September 7, 2006

1 Overview

This document analyzes trait bp for dataset hyper using the 1-D and 2-D Bayesian genome scan routines that build on Markov chain Monte Carlo (MCMC) samples from a posterior for the genetic architecture of a trait. Below the generic `cross` is actually the cross passed by the user in a call to `qb.sweave`. This entire document was created automatically by a function call in `R`. The function is not yet part of `R/qtlbim`. The actual call was

```
> library(qtlbim)

Loading required package: lattice
Loading required package: coda
Loading required package: MASS

> qb.sweave(hyper, pheno.col = 1,
+  n.iter = 3000, n.draws = 64,
+  scan.type = "2logBF", hpd.level = 0.5,
+  threshold = c(upper = 2),
+  SweaveFile = "/tmp/Rinst1076266882/qtlbim/doc/hyperslide.Rnw",
+  SweaveExtra = "/tmp/Rinst1076266882/qtlbim/external/hyperpaperextra.Rnw",
+  PDFDir = "bpPDF",
+  remove.qb = TRUE)
```

At present, the `threshold` values are somewhat arbitrary, chosen for the hyper dataset to pick up apparently real QTL and previously detected epistasis.

This document automates a search for main and epistatic QTL. The main QTL positions are reliably estimated using `qb.scanone`. This pass also seems to capture the major chromosomes possibly involved in epistasis, although it does not provide very good estimates of positions of purely epistatic QTL within those chromosomes. Next we use `qb.scantwo` and to identify which pairs of QTL are epistatic, and to get initial estimates of their positions. We refine there positions with `qb.slice`. Along the way, we use generic `summary` and `plot` routines to view results.

Once we have reasonable estimates of QTL postions and effects, we use confirmatory ANOVA tools to refine the model. That is, we use R/qtl's simulation-based `fitqtl` followed by a stepwise backward fitting approach, using a new `step.fitqtl`, to confirm key QTL. That completes this automated analysis. It would be possible to add other, user-supplied refined analysis at the end of this document if desired.

2 Generating Samples

Here is a summary of the `cross` copy of the hyper object, followed by creation of 3000 MCMC samples.

```
> summary(cross)
```

```
    Backcross

    No. individuals:    250

    No. phenotypes:     1
    Percent phenotyped: 100

    No. chromosomes:    19
        Autosomes:      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

    Total markers:      170
    No. markers:        22 8 6 20 14 11 7 6 5 5 14 5 5 5 11 6 12 4 4
    Percent genotyped:  47.9
    Genotypes (%):      AA:50.1  AB:49.9
```

```
> cross <- qb.genoprob(cross,step=2)
> cross.qb <- qb.mcmc(cross, pheno.col = pheno.col
+   genoupdate=TRUE, n.iter = 3000, mydir = "bpPDF")
```

3 1-D Scans

Now a 1-D scan picks out the major effects. We could uxe `qb.scanone` directly. Instead, we use `qb.hpdone`, which gives us a profile scan as well as a scan of genotypic means.

```
> hpd.level
```

```
[1] 0.5
```

```
> cross.hpd <- qb.hpdone(cross.qb, hpd.level)
> sum.one <- summary(cross.hpd)
> sum.one
```

```
   chr n.qtl  pos lo.50% hi.50% 2logBF       A       H
1    1 0.694 64.5   64.5   69.9  6.796 103.604  99.073
4    4 3.460 29.5   25.1   31.7 11.347 104.561  98.026
6    6 1.107 59.0   56.8   66.7  6.179  99.606 102.924
15  15 0.341 17.5   17.5   17.5  6.032 101.940 100.692
```

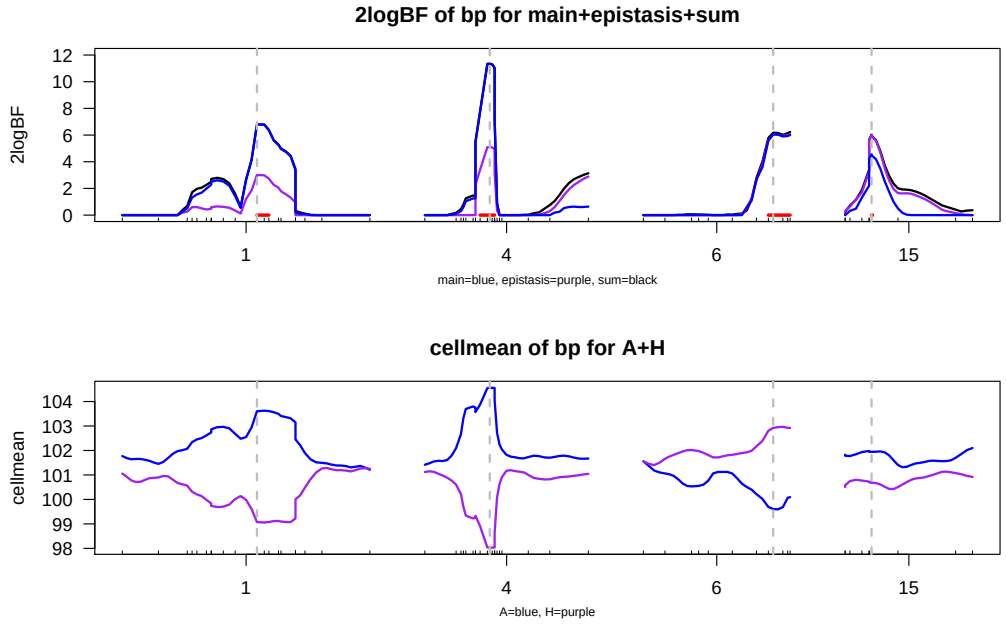
The `qb.hpdone` routine mostly automates the selection of peaks. We are still working on how to set reasonable thresholds, but for now a HPD level of 0.5 for the overall (`sum`) picks up the key features nicely for many phenotypes. The variable `hpd.level` was set in the call to `qb.sweave` that created this document. The new variables `chrs` and `pos` capture the chromosome numbers and main QTL positions, respectively.

```
> chrs <- as.vector(sum.one[, "chr"])
> pos <- sum.one[, "pos"]
> pos
```

```
   1    4    6   15
64.5 29.5 59.0 17.5
```

The following two figures highlight the selected chromosomes. In the top panel, the blue curve represents the `2logBF` (twice log of Bayes factor) score for the `main` effect of a QTL at each locus, while the purple curve shows the score for any `epistasis` between a locus and any other loci. The black curve shows the combination of main and epistatic effects. The second panel shows the marginal means, which are roughly symmetric about the phenotype mean of 101.

```
> plot(cross.hpd)
```



4 2-D Scan

Now a look at a 2-D scan reveals the strength of epistasis. The summary suggests some other epistases, but some of this may be spurious [i.e. we will want to look further!]. We consider a subset of this summary above the `upper` threshold of 2.

```
> two <- qb.scantwo(cross.qb, chr = chrs, type = scan.type)
> sum.two <- summary(two, threshold = threshold, refine = TRUE)
> sum.two

     chr1 chr2 n.qtl l.pos1 l.pos2 lower u.pos1 u.pos2 upper
6.15    6   15  1.08     59   17.5 3.531     59   17.5 3.502
```

Now let's extract the genetic architecture implied by this evidence for epistasis. The loci pairs thar show epistasis are indexed to the vector of main QTL. In addition we see the pairs of chromosomes involved in epistasis. Some effort is made to merge nearby QTL estimated positions in `qb.arch`.

```
> cross.arch <- qb.arch(sum.two, chrs, pos)
> cross.arch

main QTL loci:
       1    2  3    4
chr  1.0  4.0  6 15.0
pos 64.5 29.5 59 17.5

Epistatic pairs by qtl, chr, pos:
  qtla qtlb chra chrb posa posb
1    3    4    6   15   59 17.5
Epistatic chromosomes by connected sets:
6,15
```

5 ANOVA Model Fit

Here we want to merge the 1-D `chrs` and `pos` with the 2-D epistatic pairs to determine the chromosomes and positions to include in an ANOVA fit. We equate QTL that are within, say 10cM of each other. After fitting a (very) full model, we use `step.fitqtl`, a newly written routine, to step-by-step reduce the model to key main effects and interactions, preserving hierarchy.

The following uses R/qtl tools `calc.genoprob`, `sim.geno` and `makeqtl`, plus the new `step.fitqtl`, which calls `fitqtl` multiple times.

```
> cross.sub <- subset(cross, chr = cross.arch$qtl$chr)
> n.draws

[1] 64

> cross.sub <- sim.geno(cross.sub, n.draws = n.draws, step = 2,
+     error = 0.01)
> qtl <- makeqtl(cross.sub, cross.arch$qtl$chr, cross.arch$qtl$pos)
```

Now we run stepwise backward elimination, preserving hierarchy.

```
> cross.step <- step.fitqtl(cross.sub, qtl, pheno.col, cross.arch)

> summary(cross.step$fit)

Full model result
----------------------------------

       df        SS         MS      LOD     %var Pvalue(Chi2) Pvalue(F)
Model   5  5299.117 1059.82334 19.35588 29.99115            0         0
Error 244 12369.820   50.69598
Total 249 17668.936


Drop one QTL at a time ANOVA table:
----------------------------------
                   df Type III SS      LOD     %var F value Pvalue(F)
Chr1@64.5           1     905.142    3.834    5.123   17.85  3.37e-05 ***
Chr4@29.5           1    2736.837   10.851   15.490   53.98  3.03e-12 ***
Chr6@59             2    1475.392    6.117    8.350   14.55  1.07e-06 ***
Chr15@17.5          2    1346.262    5.608    7.619   13.28  3.36e-06 ***
Chr6@59:Chr15@17.5  1    1053.364    4.437    5.962   20.78  8.16e-06 ***
```

The final model may be more complicated than a model found 'by hand' using standard R/qtl tools. Hopefully that model is a subset of the automatically found model.

6 2-D Epistasis Plots

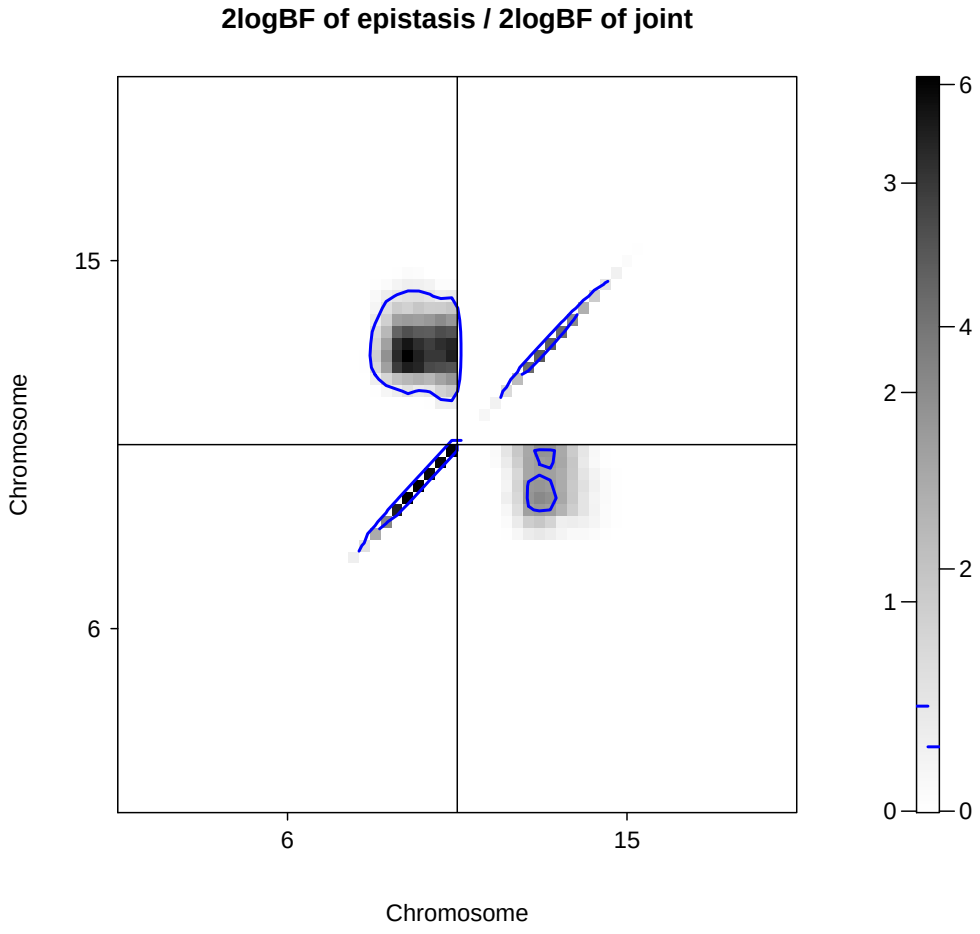
Should there be any evidence for epistasis that is confirmed by ANOVA, it can be useful to view 2-D plots similar to `scantwo`, but now using the marginal 2logBF. Here is the reduced, final genetic architecture:

```
> cross.arch <- cross.step$arch
> cross.arch

main QTL loci:
       1    2  3    4
chr  1.0  4.0  6 15.0
```

```
pos 64.5 29.5 59 17.5

Epistatic pairs by qtl, chr, pos:
  q1 q2 chra chrb posa posb
1  3  4    6   15   59 17.5
Epistatic chromosomes by connected sets:
6,15
```

Here are the plots by clique (if any).

```
> for(i in names(cross.arch$chr.by.set))
+   plot(two, chr = cross.arch$chr.by.set[[i]], smooth = 3,
+     col = "gray", contour = 3)
```

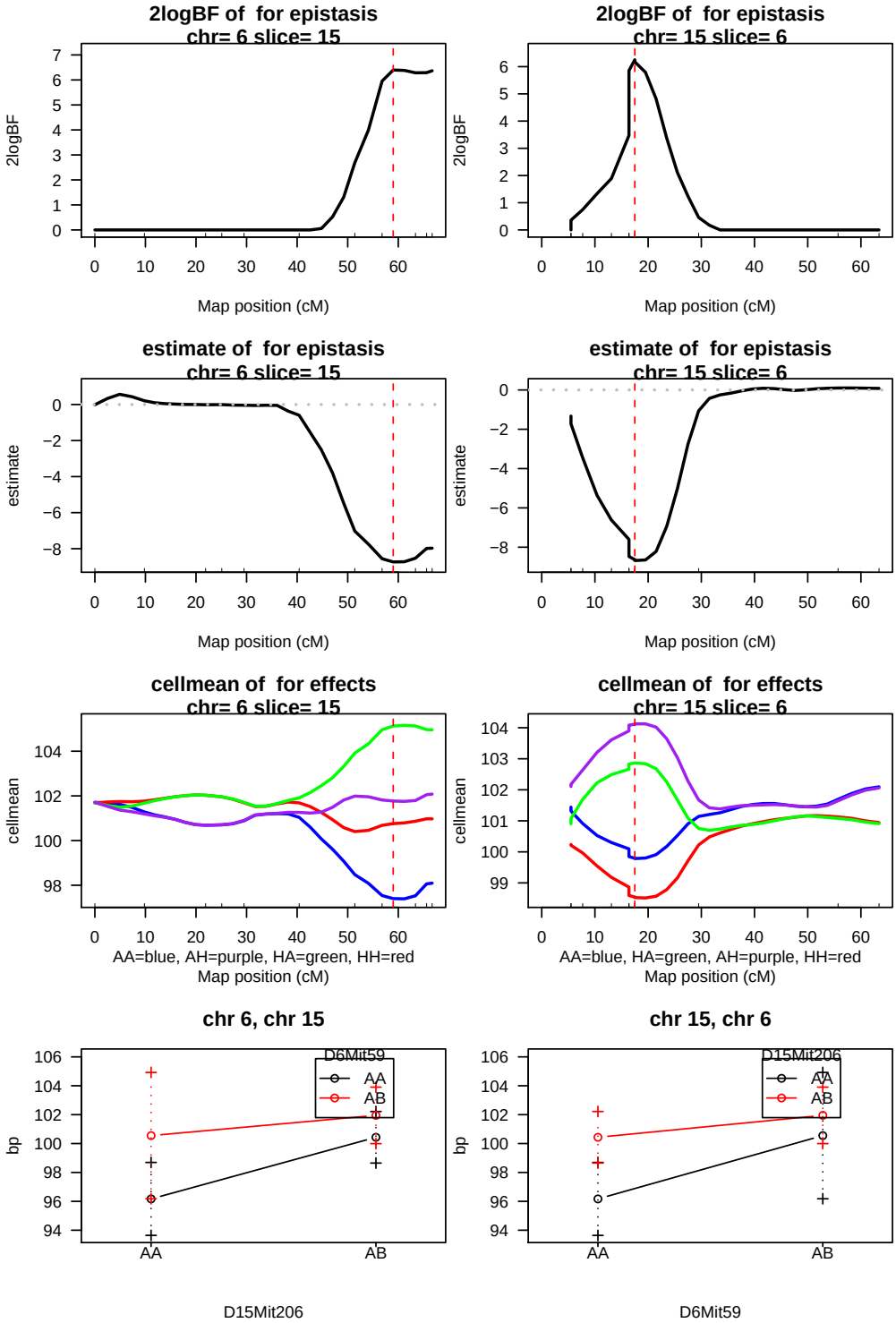


7 1-D Epistasis Slices

We then examine 1-D slices through the 2-D surface for epistatic pairs in the reduced model, to focus on epistasis for those identified pairs. We show 1-D slices of the LOD and the epistatic effects. In addition, we show interaction plots at the nearest markers.

```
> if(!is.null(cross.arch$pair.by.chr)) {
+  for(i in seq(nrow(cross.arch$pair.by.chr$chr))) {
```

```
+     chri <- cross.arch$pair.by.chr$chr[i,]
+     posi <- cross.arch$pair.by.chr$pos[i,]
+     plot(qb.slicetwo(cross.qb, chri, posi, scan.type), byrow = FALSE)
+   }
+}
```



8 User Customized Section

We know from previous work that there are main QTLs on chromosomes 1 and 4, and epistatic pairs involving 6 and 15, and 7 and 15. Here we pick the nested model that contains these QTL.

```
> arch3 <- qb.arch(cross.step, main = c(1, 4), epistasis = data.frame(q1 = c(6,
+     7), q2 = rep(15, 2)))
> arch3
> cross.step2 <- step.fitqtl(cross.sub, qtl, pheno.col, arch3)

> summary(cross.step2$fit)
```

Now we do a formal comparison of this reduced model with the fuller model we automatically uncovered. It appears that the fuller model is a much better fit.

```
> anova(cross.step, cross.step2)
```

9 Cleaning Up

That completes the template. Now the penultimate task is to remove the objects created by `R/qtlbim`, if this is desired by the user.

```
> remove.qb

[1] FALSE

> if (remove.qb) {
+     qb.remove(cross.qb)
+     rm(cross, cross.sub, pheno.col, threshold, n.iter, n.draws,
+         remove.qb)
+ }
```

Finally, externally rename file hyperslide.tex to bp.tex and run pdflatex twice on it. Use a free Acrobat reader to view.

```
> file.rename("hyperslide.tex", "bp.tex")
> invisible(system("pdflatex bp.tex",intern=TRUE))
>  invisible(system("pdflatex bp.tex",intern=TRUE))
```