

	N	Chi.squared.1.df	Chi.squared.2.df	P.1df	P.2df
rs7909677	800	0.024965308	0.5845936	0.8744535	0.7465469
rs12773042	800	0.226052327	0.2264178	0.6344665	0.8929641
rs11253563	800	0.388716924	2.0141873	0.5329746	0.3652791
rs4881552	800	0.007942575	2.6072584	0.9289856	0.2715445
rs10904596	800	0.468290808	2.2064007	0.4937745	0.3318075

```
> imp[1:5]
```

	N	N.r2	Chi.squared.1.df	Chi.squared.2.df	P.1df	P.2df
rs7909677	800	542.1618	0.02214562	0.6768491	0.8817004	0.7128926
rs12773042	800	799.9997	0.21439133	0.2148980	0.6433471	0.8981223
rs11253563	800	755.3733	0.38175013	1.9588770	0.5366681	0.3755219
rs4881552	800	774.3374	0.01098225	2.6324536	0.9165375	0.2681452
rs10904596	800	748.0431	0.49760870	2.2442143	0.4805527	0.3255930

There are small discrepancies due to the genotype assignment probabilities not being stored to full accuracy. However these should have little effect on power of the tests and no effect on the type I error rate.

Note that the ability of `snpStats` to store imputed genotypes in this way allows alternative programs to be used to generate the imputed genotypes. For example, the file "mach1.out.mlprob.gz" (which is stored in the `extdata` sub-directory of the `snpStats` package) contains imputed SNPs generated by the MACH program, using the `-mle` and `-mldetails` options. In the following commands, we find the full path to this file, read it, and inspect one the imputed SNP in column 50:

```
> path <- system.file("extdata/mach1.out.mlprob.gz", package = "snpStats")
> mach <- read.mach(path)
```

```
Reading MACH data from file /home/Hin-Tak/Rlibs/snpStats_1.13.0/extdata/mach1.out.mlprob.gz
Reading SnpMatrix with 500 rows and 178 columns
```

```
> plotUncertainty(mach[, 50])
```

	N	Chi.squared.1.df	Chi.squared.2.df	P.1df	P.2df
rs7909677	800	0.024965308	0.5845936	0.8744535	0.7465469
rs12773042	800	0.226052327	0.2264178	0.6344665	0.8929641
rs11253563	800	0.387874127	1.9881639	0.5334190	0.3700630
rs4881552	800	0.007800641	2.6079225	0.9296214	0.2714544
rs10904596	800	0.487591969	2.2351447	0.4850034	0.3270728

```
> imp[1:5]
```

	N	N.r2	Chi.squared.1.df	Chi.squared.2.df	P.1df	P.2df
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rs11253563	800	755.3733	0.38175013	1.9588770	0.5366681	0.3755219
rs4881552	800	774.3374	0.01098225	2.6324536	0.9165375	0.2681452
rs10904596	800	748.0431	0.49760870	2.2442143	0.4805527	0.3255930

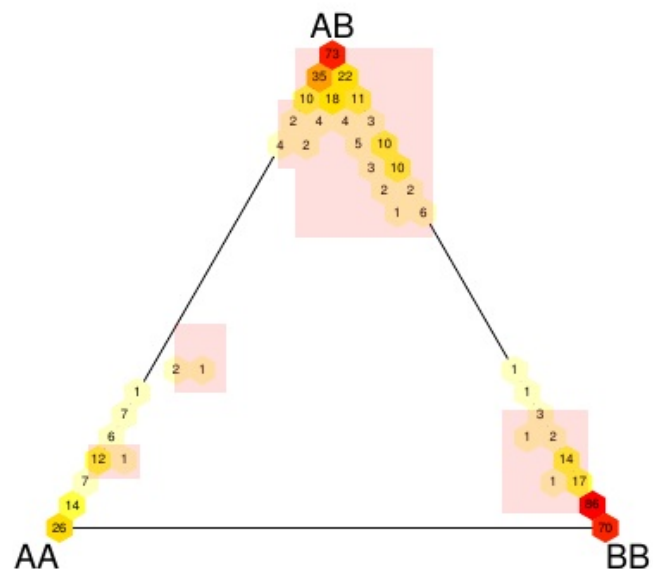
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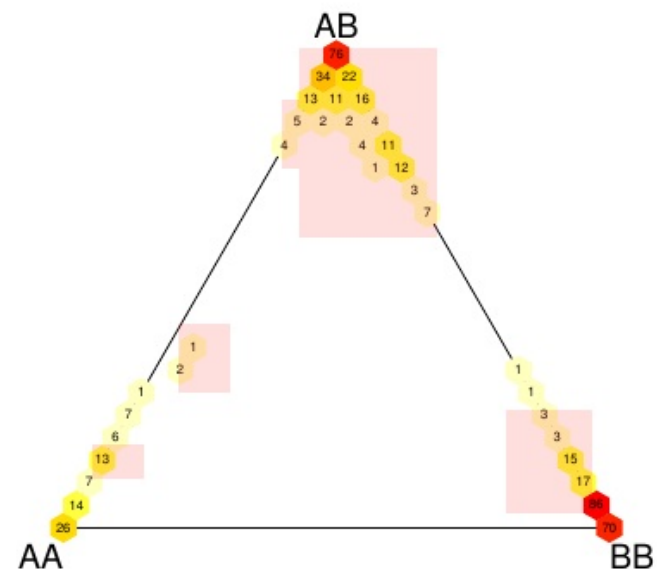
```
Reading MACH data from file /home/Hin-Tak/Rlibs/snpStats_1.13.0.6/extdata/mach1.out.mlprob.gz
Reading SnpMatrix with 500 rows and 178 columns
```

```
> plotUncertainty(mach[, 50])
```



Meta-analysis

As stated at the beginning of this document, one of the main reasons that we need imputation is to perform meta-analyses which bring together data from genome-wide studies which use different platforms. The `snpStats` package includes a number of tools to facilitate this. All the tests implemented in `snpStats` are "score" tests. In the 1 df case we calculate a score defined by the first derivative of the log likelihood function with respect to the association parameter of interest at the parameter value corresponding to the null hypothesis of no



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