

iChip: A Package for Analyzing Multi-platform ChIP-chip data with Various Sample Sizes

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1 Introduction

This package implements the models proposed by Mo and Liang (2010a, b) for ChIP-chip data analysis. The package can be used to analyze ChIP-chip data from multiple platforms (e.g. Affymetrix, Agilent, and NimbleGen) with various genomic resolutions and various sample sizes. Mo and Liang (2010a,b) proposed Bayesian Hierarchical models to model ChIP-chip data in which the spatial dependency of the data is modeled through ferromagnetic high-order or standard Ising models. Briefly, without loss of generality, the proposed methods let each probe be associated with a binary latent variable $X_i \in (0,1)$, where i denotes the ID for the probe, and $X_i = 1$ denotes that the probe is an enriched probe, and 0 otherwise. In the first stage, conditioning on the latent variable, the probe enrichment measurements for each state (0 or 1) are modeled by normal distributions. Here, the probe enrichment measurement could be any appropriate measurement for comparison of

IP-enriched and control samples. For example, the measurement could be a log2 ratio of IP-enriched and control samples for a single replicate, or a summary statistic such as t-like statistic or mean difference for multiple replicates. In the second stage, the latent variable is modeled by ferromagnetic Ising models. The Gibbs sampler and Metropolis algorithm are used to simulate from the posterior distributions of the model parameters, and the posterior probabilities for the probes in the enriched state ($X_i = 1$) are used for statistical inference. A probe with a high posterior probability of the enriched state will provide strong evidence that the probe is an enriched probe. For further details, we refer the user to Mo and Liang's papers.

2 Agilent and Affymetrix ChIP-chip Data

A subset of the Oct4 (Boyer et al., 2005) and the p53 (Cawley et al, 2004) data are used for the purpose of illustration. The average genomic resolutions for the Oct4 and p53 data are about 280 bps and 35 bps, respectively. Both the Oct4 and p53 data have been log2 transformed and quantile-normalized. Note iChip software doesn't provide functions for data normalization. The users should normalize their data before using iChip software. For one-color and two-color data, one can use the quantile method (e.g., see the function *normalize.quantiles()* in the **affy** package). For two-color data, one can also use the *loess* method (e.g., see the function *normalizeWithinArrays()* in the **limma** package). The full Oct4 data can be obtained from

http://jura.wi.mit.edu/young_public/hESregulation/Data_download.html.

The full p53 data can be obtained from

http://www.gingeras.org/affy_archive_data/publication/tfbs/.

3 Example1 — Analyzing the Agilent Promoter Array Data

Let's start analyzing the low resolution Oct4 data. First, we need to calculate the enrichment measurement for each probe. Although the enrichment measurement could be any appropriate measurement for comparison of IP-enriched and control samples, we suggest using the empirical Bayes t-statistic for multiple replicates, which can be easily calculated using the **limma** package (Smyth, 2004). Here, we call the empirical Bayes t-statistic limma t-statistic. For the users who are not familiar with limma t-statistic, we provide a wrapper function **lmtstat** for the calculation.

There are two replicates for the Oct4 data. The enriched DNA was labeled with Cy5 (red) dye and the control DNA was labeled with Cy3 (green) dye.

```
> library(iChip)
> data(oct4)
> head(oct4,n=3L)
```

	chr	position	green1	green2	red1	red2
1	20	70312	6.969102	6.847819	6.808445	7.063581
2	20	70601	6.625190	6.176981	6.996920	6.391692
3	20	70873	10.334613	11.072903	9.521095	10.785880

To use the `iChip1` and `iChip2` function, the data must be sorted, firstly by chromosome then by genomic position. It may be a good habit to sort the data at the beginning, although function `lmtstat` doesn't require the data to be sorted.

```
> oct4 = oct4[order(oct4[,1],oct4[,2]),]
```

Calculate the enrichment measurements — two-sample limma t-statistics.

```
> oct4lmt = lmtstat(oct4[,5:6],oct4[,3:4])
```

Here, we treat the IP-enriched and control data as independent data although both the IP-enriched and control samples were hybridized to the same array. This is because the quantile-normalization method was applied to the oct4 data. If the data are normalized using *loess* method, the resulting data are in log ratio format (e.g., $\log_2(\text{IP-enriched}/\text{control})$). In this case, one can calculate the paired limma t-statistics. Suppose a matrix called `log2ratio` are the loess-normalized data, where each column corresponds to a sample, the paired limma t-statistics can be calculated using `lmtstat(log2ratio)`.

Prepare the data for `iChip2` function.

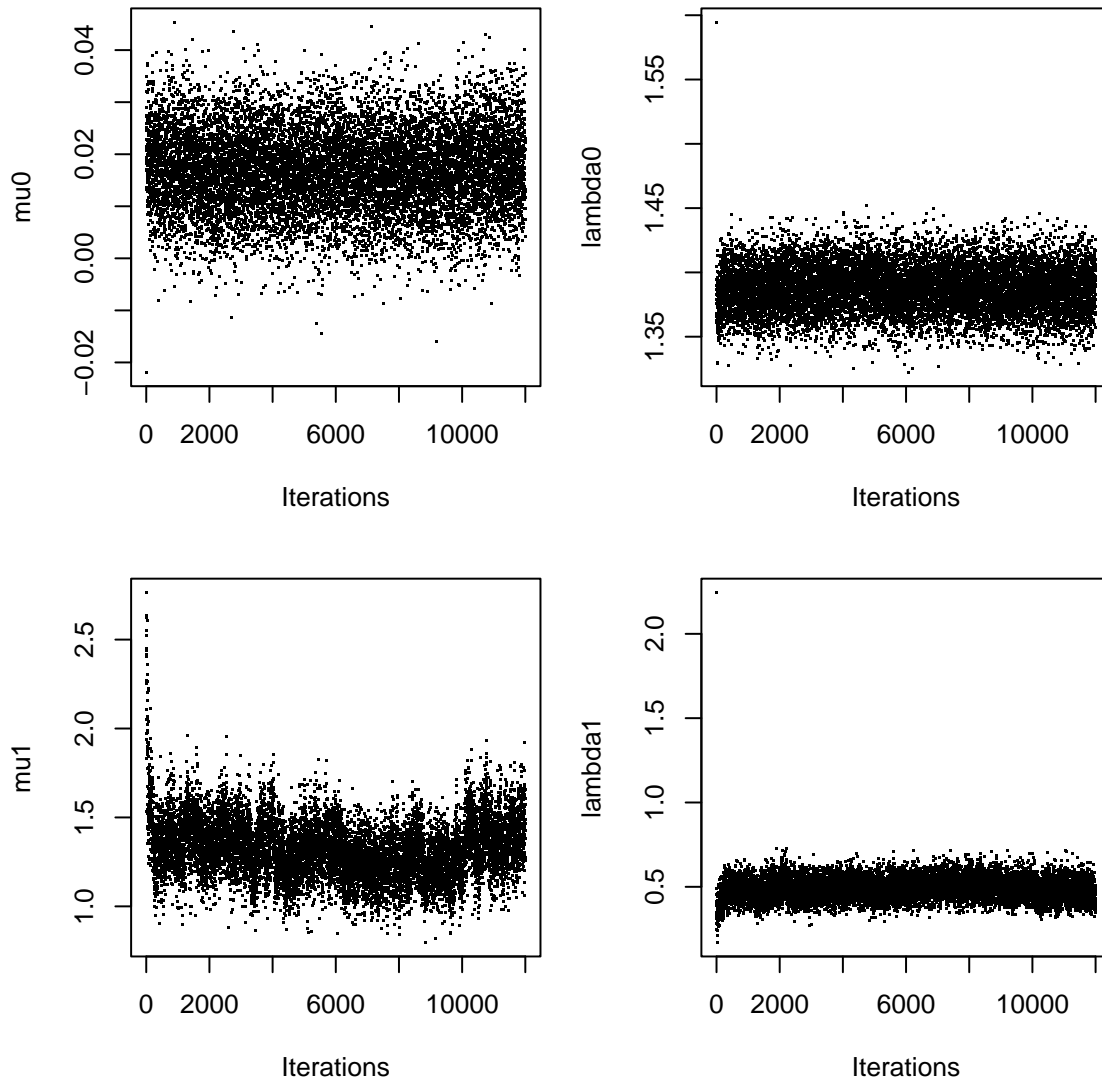
```
> oct4Y = cbind(oct4[,1],oct4lmt)
```

Apply the second-order Ising model to the ChIP-chip data by setting `winsize = 2`. According to our experience, a balance between high sensitivity and low FDR can be achieved when `winsize = 2`. The critical value of the second-order Ising model is about 1.0. For low resolution data, the value of `beta` could be around the critical value. In general, increasing `beta` value will lead to less enriched regions, which amounts to setting a stringent criterion for detecting enriched regions.

```
> set.seed(777)
> oct4res2 = iChip2(Y=oct4Y,burnin=2000,sampling=10000,winsize=2,
+   sdcut=2,beta=1.25,verbose=FALSE)
```

Plot the model parameters to see whether they converge. In general, the MCMC chains have converged when the parameters fluctuate around the modes of their distributions. If there is an obvious trend(e.g. continuous increase or decrease), one should increase the number of iterations in the burn-in phase. If this doesn't work, one can adjust the parameter `beta` to see how it affects the results.

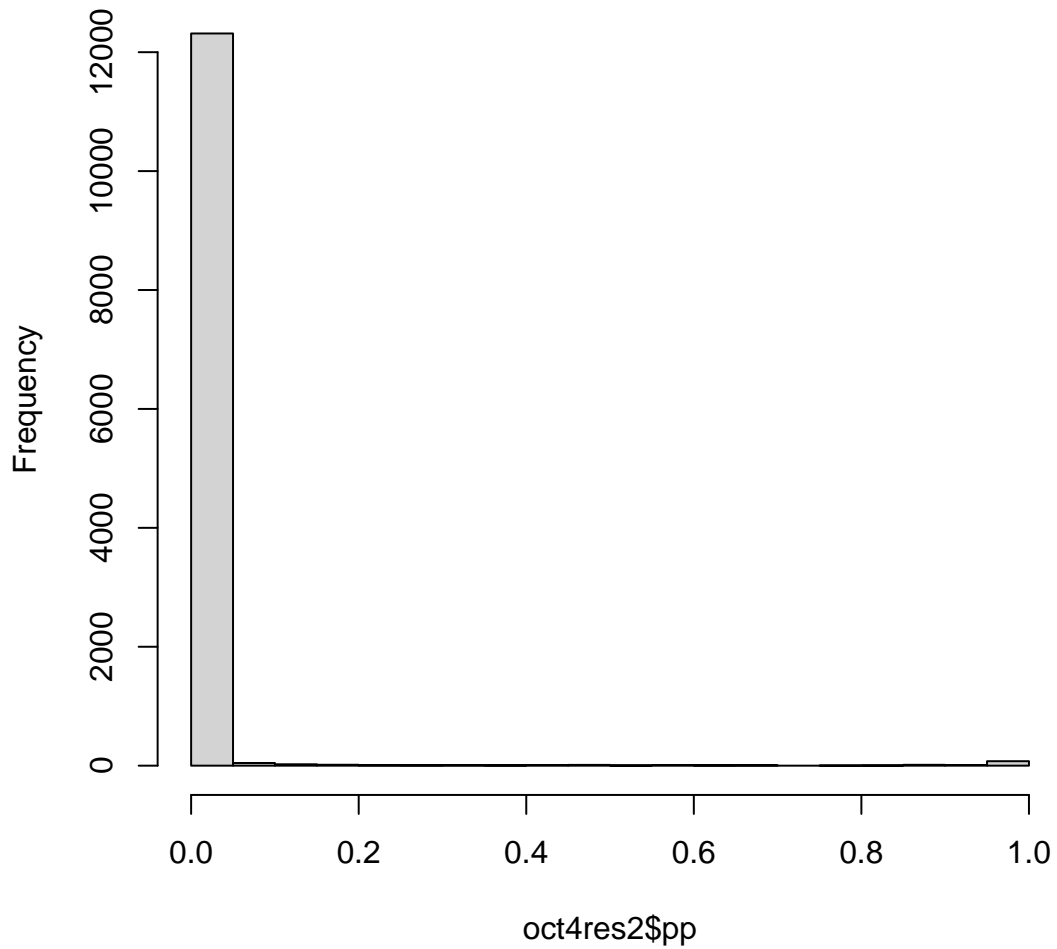
```
> par(mfrow=c(2,2), mar=c(4.1, 4.1, 2.0, 1.0))
> plot(oct4res2$mu0, pch=".", xlab="Iterations", ylab="mu0")
> plot(oct4res2$lambda0, pch=".", xlab="Iterations", ylab="lambda0")
> plot(oct4res2$mu1, pch=".", xlab="Iterations", ylab="mu1")
> plot(oct4res2$lambda1, pch=".", xlab="Iterations", ylab="lambda1")
```



The histogram of the posterior probabilities should be dichotomized, either 0 or 1. For transcription factor binding site studies, the histogram should be dominated by 0.

```
> hist(oct4res2$pp)
```

Histogram of oct4res2\$pp



Call the enriched regions detected by iChip2 using a posterior probability (pp) cutoff of 0.9.

```
> reg1 = enrichreg(pos=oct4[,1:2],enrich=oct4lmt,pp=oct4res2$pp,
+   cutoff=0.9,method="ppcut",maxgap=500)
> print(reg1)
```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	20	3944132	3946241	1415	1427	3946061	0.96	1	13
2	20	20291072	20291658	3293	3295	20291658	0.96	1	3
3	20	20292352	20294499	3296	3304	20293941	1.00	1	9
4	20	21441187	21450238	3441	3477	21445231	0.99	1	37
5	20	22519126	22519690	3545	3547	22519406	1.00	1	3
6	20	28137489	28138889	4307	4312	28137489	1.00	1	6

7	20	34633143	34633770	6132	6134	34633506	0.98	1	3
8	20	44034352	44034352	8313	8313	44034352	1.00	1	1
9	20	54633181	54635934	9703	9713	54633459	0.99	1	11

Call the enriched regions detected by iChip2 using a FDR cutoff of 0.01. The FDR is calculated using a direct posterior probability approach (Newton et al., 2004).

```
> reg2 = enrichreg(pos=oct4[,1:2],enrich=oct4lmt,pp=oct4res2$pp,
+   cutoff=0.01,method="fdrcut",maxgap=500)
> print(reg2)
```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	20	3944132	3946241	1415	1427	3946061	0.96	1	13
2	20	20291344	20291658	3294	3295	20291658	0.98	1	2
3	20	20292352	20294499	3296	3304	20293941	1.00	1	9
4	20	21441187	21449717	3441	3475	21445231	1.00	1	35
5	20	22519126	22519690	3545	3547	22519406	1.00	1	3
6	20	28137489	28138889	4307	4312	28137489	1.00	1	6
7	20	34633143	34633770	6132	6134	34633506	0.98	1	3
8	20	44034352	44034352	8313	8313	44034352	1.00	1	1
9	20	54633181	54635934	9703	9713	54633459	0.99	1	11

BED file can be easily made using the output from function **enrichreg**, which can be used for motif discovery and visualized in the UCSC genome browser. For example,

```
> bed1 = data.frame(chr=paste("chr",reg2[,1],sep=""),reg2[,2:3])
> print(bed1[1:2,])
```

	chr	gstart	gend
1	chr20	3944132	3946241
2	chr20	20291344	20291658

Alternatively, one may create a BED file using the peak position of the enriched regions. For example,

```
> bed2 = data.frame(chr=paste("chr",reg2[,1],sep=""),gstart=reg2[,6]-100,
+   gend=reg2[,6]+100)
> print(bed2[1:2,])
```

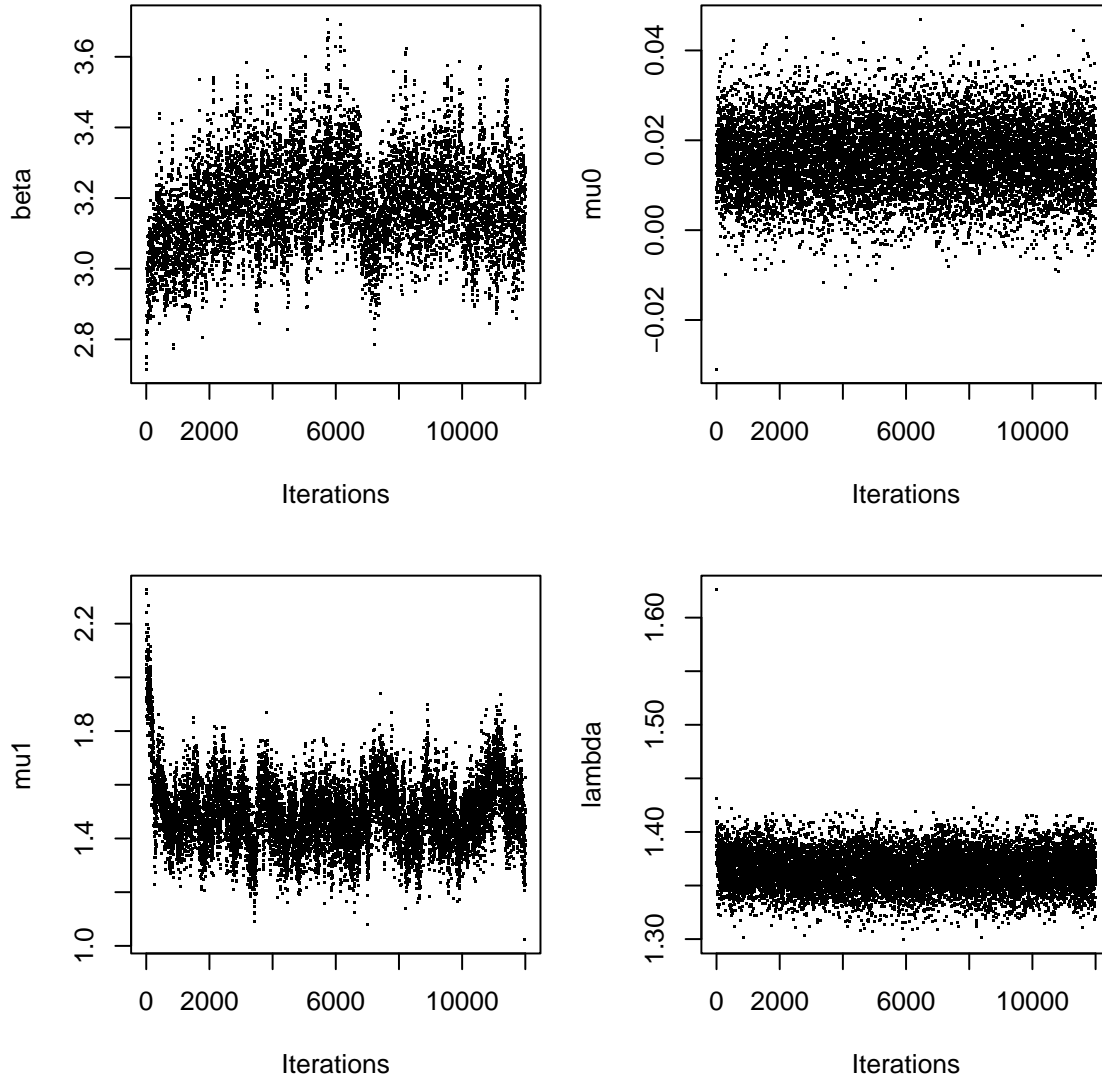
	chr	gstart	gend
1	chr20	3945961	3946161
2	chr20	20291558	20291758

Model the oct4 data using the first-order Ising model.

```
> oct4res1 =iChip1(enrich=oct4lmt,burnin=2000,sampling=10000,sdcut=2,beta0=3,
+   minbeta=0,maxbeta=10,normsd=0.1,verbose=FALSE)
```

Plot the model parameters to see whether they converge.

```
> par(mfrow=c(2,2), mar=c(4.1, 4.1, 2.0, 1.0))
> plot(oct4res1$beta, pch=".", xlab="Iterations", ylab="beta")
> plot(oct4res1$mu0, pch=".", xlab="Iterations", ylab="mu0")
> plot(oct4res1$mu1, pch=".", xlab="Iterations", ylab="mu1")
> plot(oct4res1$lambda, pch=".", xlab="Iterations", ylab="lambda")
```



Call the enriched regions detected by iChip1.

```
> enrichreg(pos=oct4[,1:2], enrich=oct4lmt, pp=oct4res1$pp, cutoff=0.9,
+           method="ppcut", maxgap=500)
```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	20	3944132	3946241	1415	1427	3946061	1.00	1	13

```

2  20 20291072 20291658 3293 3295 20291658 0.96 1 3
3  20 20292352 20294805 3296 3305 20293941 0.99 1 10
4  20 21441187 21449717 3441 3475 21445231 0.99 1 35
5  20 22519126 22519690 3545 3547 22519406 1.00 1 3
6  20 28137489 28138889 4307 4312 28137489 0.99 1 6
7  20 34632735 34633770 6131 6134 34633506 0.97 1 4
8  20 54633181 54636203 9703 9714 54633459 0.99 1 12

> enrichreg(pos=oct4[,1:2],enrich=oct4lmt,pp=oct4res1$pp,cutoff=0.01,
+           method="fdrcut",maxgap=500)

```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	20	3944132	3946241	1415	1427	3946061	1.00	1	13
2	20	20291072	20291658	3293	3295	20291658	0.96	1	3
3	20	20292352	20294805	3296	3305	20293941	0.99	1	10
4	20	21441187	21449717	3441	3475	21445231	0.99	1	35
5	20	22519126	22519690	3545	3547	22519406	1.00	1	3
6	20	28137489	28138889	4307	4312	28137489	0.99	1	6
7	20	34632735	34633770	6131	6134	34633506	0.97	1	4
8	20	54633181	54636203	9703	9714	54633459	0.99	1	12

4 Example2 — Analyzing the Affymetrix Tiling Array Data

Now, let's analyze the high resolution p53 data.

```

> data(p53)
> head(p53,n=3L)

```

	chr	position	CON	CON	CON	CON	CON	CON
783581	22	27980300	9.576077	10.90728	9.585894	11.14744	10.23070	11.01191
783582	22	27980347	9.941713	10.66333	10.031774	10.86761	10.23361	10.81113
783583	22	27980372	9.932955	10.63290	9.995038	10.42966	10.02872	10.39427
	IP	IP	IP	IP	IP	IP	IP	IP
783581	9.70315	10.64889	10.53961	9.376407	9.869731	10.89024		
783582	10.32478	10.39944	10.39757	10.602358	10.544956	10.24796		
783583	10.27690	10.28804	10.27836	10.244013	9.961192	10.18641		

```

> # sort the p53 data by chromosome and genomic position
> p53 = p53[order(p53[,1],p53[,2]),]
> p53lmt = lmtstat(p53[,9:14],p53[,3:8])
> p53Y = cbind(p53[,1],p53lmt)

```

For high resolution data, beta could be set to a relatively large value (e.g. 2–4). In general, increasing beta value will lead to less enriched regions, which amounts to setting a stringent criterion for detecting enriched regions.

```

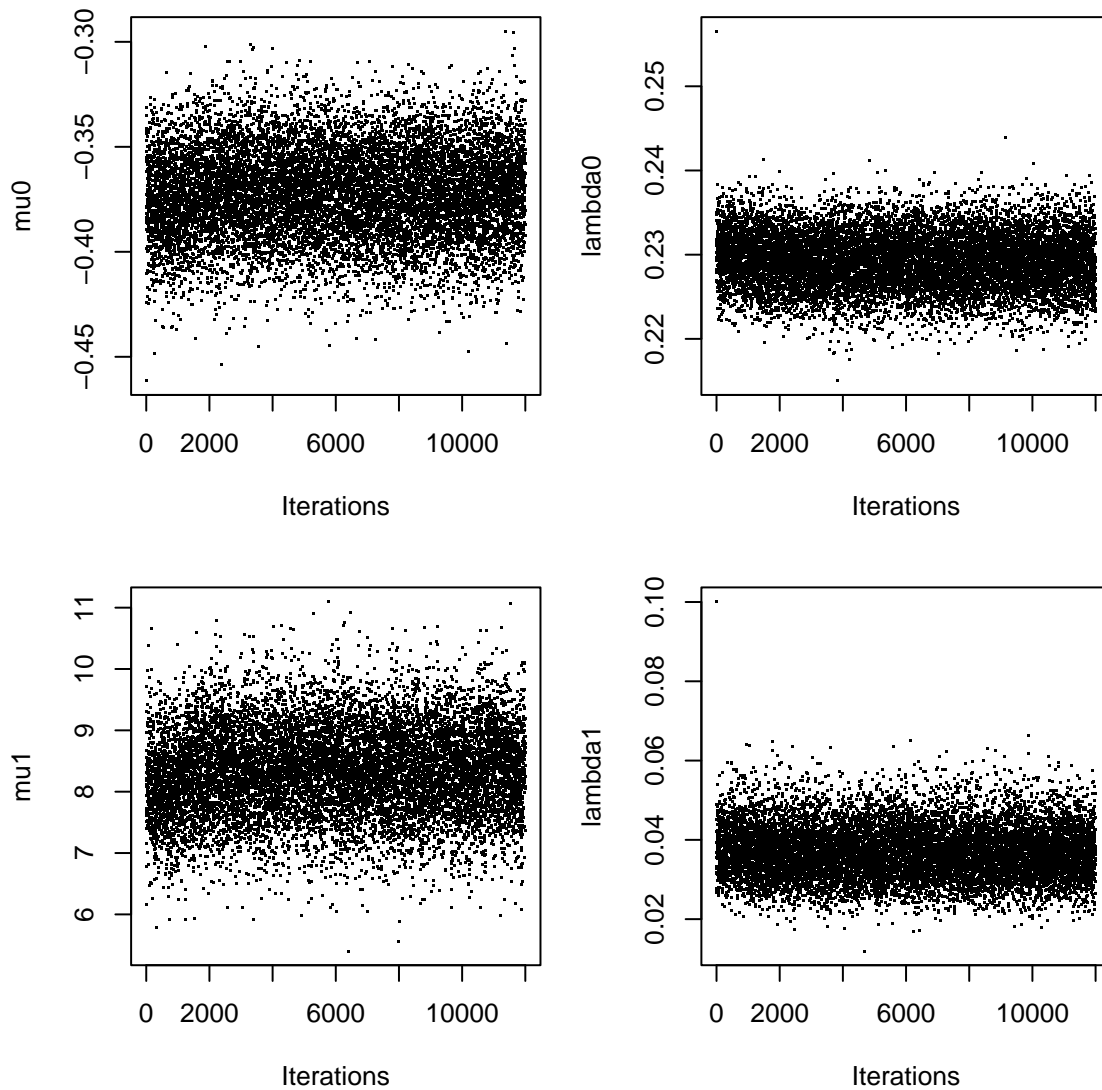
> p53res2 = iChip2(Y=p53Y,burnin=2000,sampling=10000,winsize=2,sdcut=2,beta=2.5)

```

```

> par(mfrow=c(2,2), mar=c(4.1, 4.1, 2.0, 1.0))
> plot(p53res2$mu0, pch=".", xlab="Iterations", ylab="mu0")
> plot(p53res2$lambda0, pch=".", xlab="Iterations", ylab="lambda0")
> plot(p53res2$mu1, pch=".", xlab="Iterations", ylab="mu1")
> plot(p53res2$lambda1, pch=".", xlab="Iterations", ylab="lambda1")

```



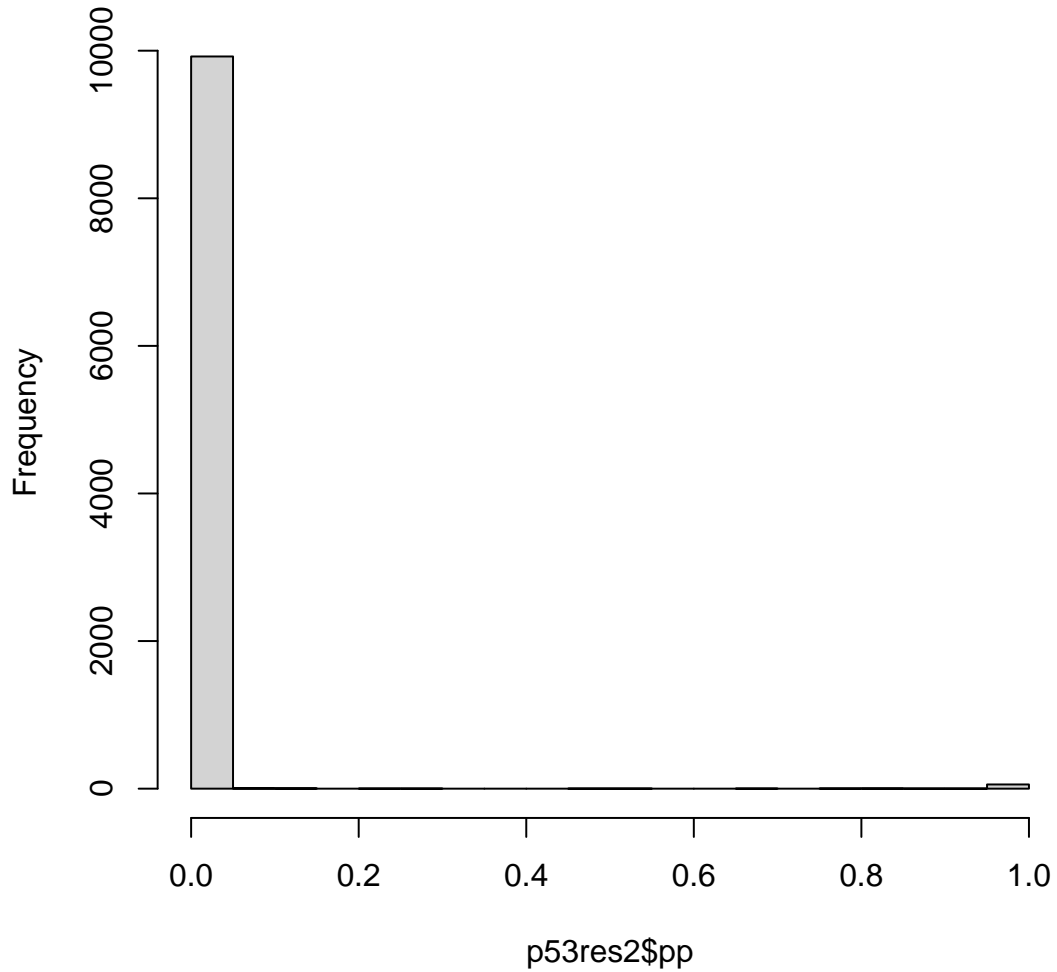
The histogram of the posterior probabilities should be dichotomized, either 0 or 1. For transcription factor binding site studies, the histogram should be dominated by 0.

```

> hist(p53res2$pp)

```

Histogram of p53res2\$pp



```
> enrichreg(pos=p53[,1:2],enrich=p53lmt,pp=p53res2$pp,cutoff=0.9,  
+           method="ppcut",maxgap=500)
```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	22	28211540	28211540	2991	2991	28211540	0.96	0.96	1
2	22	28269526	28270158	3705	3724	28269751	1.00	1.00	20
3	22	28345939	28346341	4831	4842	28346226	1.00	1.00	12
4	22	28380484	28380676	5440	5446	28380676	1.00	1.00	7
5	22	28775272	28775790	9878	9895	28775550	1.00	1.00	18

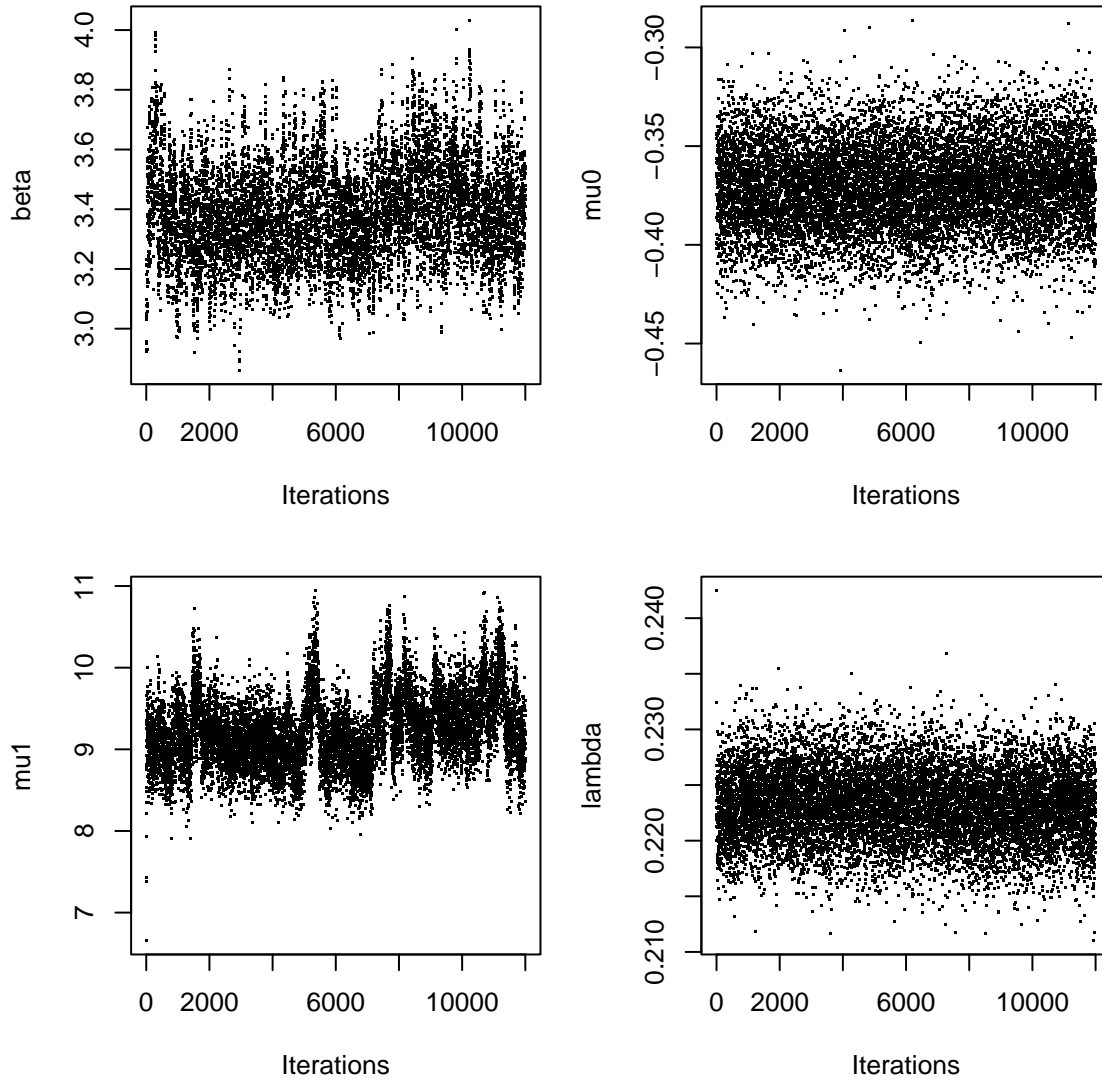
```
> enrichreg(pos=p53[,1:2],enrich=p53lmt,pp=p53res2$pp,cutoff=0.01,  
+           method="fdrcut",maxgap=500)
```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	22	28211540	28211540	2991	2991	28211540	0.96	0.96	1
2	22	28269497	28270158	3704	3724	28269751	0.99	1.00	21
3	22	28345939	28346341	4831	4842	28346226	1.00	1.00	12
4	22	28380484	28380725	5440	5447	28380676	0.98	1.00	8
5	22	28775272	28775790	9878	9895	28775550	1.00	1.00	18

Model the p53 data using the first-order Ising model.

```
> p53res1 =iChip1(enrich=p53lmt,burnin=2000,sampling=10000,sdcut=2,beta0=3,
+   minbeta=0,maxbeta=10,normsd=0.1,verbose=FALSE)

> par(mfrow=c(2,2), mar=c(4.1, 4.1, 2.0, 1.0))
> plot(p53res1$beta, pch=".", xlab="Iterations", ylab="beta")
> plot(p53res1$mu0, pch=".", xlab="Iterations", ylab="mu0")
> plot(p53res1$mu1, pch=".", xlab="Iterations", ylab="mu1")
> plot(p53res1$lambda, pch=".", xlab="Iterations", ylab="lambda")
```



```
> enrichreg(pos=p53[,1:2],enrich=p53lmt,pp=p53res1$pp,cutoff=0.9,
+           method="ppcut",maxgap=500)
```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	22	28211540	28211540	2991	2991	28211540	1.00	1	1
2	22	28269526	28270058	3705	3721	28269751	0.97	1	17
3	22	28345939	28346341	4831	4842	28346226	1.00	1	12
4	22	28380574	28380676	5443	5446	28380676	1.00	1	4
5	22	28775272	28775790	9878	9895	28775550	0.99	1	18

```
> enrichreg(pos=p53[,1:2],enrich=p53lmt,pp=p53res1$pp,cutoff=0.01,
+           method="fdrcut",maxgap=500)
```

	chr	gstart	gend	rstart	rend	peakpos	meanpp	maxpp	nprobe
1	22	28211540	28211540	2991	2991	28211540	1.00	1	1
2	22	28269526	28270058	3705	3721	28269751	0.97	1	17
3	22	28345939	28346341	4831	4842	28346226	1.00	1	12
4	22	28380546	28380676	5442	5446	28380676	0.97	1	5
5	22	28775272	28775790	9878	9895	28775550	0.99	1	18

5 Tips

What happens when there is no enriched region? Suppose the data are just random noises.

```
> randomY = cbind(p53[,1],rnorm(10000,0,1))
> randomres2 = iChip2(Y=randomY,burnin=1000,sampling=5000,winsize=2,
+   sdcut=2,beta=2.5,verbose=FALSE)
```

```
Warning: all probes are in the same state at the last MCMC iteration.
NO enriched region is found!
```

```
> table(randomres2$pp)
```

```
1
10000
```

In this case, all the probes are only in one state. Since there is no enriched probe, the mean and variance become $-\infty$ or ∞ . In the MCMC simulations, we relabel the outputs according to the constraint $\mu_0 < \mu_1$, where μ_0 and μ_1 are the population means for the non-enriched and enriched probes, respectively (For details, see Mo and Liang, 2010a). That is, when $\mu_0 > \mu_1$, μ_0 will be treated as the population mean of the enriched probes. As a result, no matter $\mu_1 = \infty$ or $\mu_1 = -\infty$, the posterior probabilities of the probes are all 1s or close to 1. Therefore, when this happens, it means there is no enriched region.

In addition, for the studies of transcription factor binding sites, if the posterior probabilities are not dichotomized and dominated by 0, the Ising model is not in the super-paramagnetic phase. Only the super-paramagnetic phase reflects the binding events on the chromosomes. Therefore, the user should increase the value of beta to let the phase transition occur so that the Ising model reach the super-paramagnetic phase.

The probes' states reported by iChip1 are also in the same state if there is no enriched region.

```
> randomres1 = iChip1(enrich=randomY[,2],burnin=1000,sampling=5000,sdcut=2,
+   beta0=3,minbeta=0,maxbeta=10,normsd=0.1,verbose=FALSE)
```

```
Warning: all probes are in the same state at the last MCMC iteration.
NO enriched region is found!
```

```
> table(randomres1$pp)
```

0
10000

Although the above two examples only show the analysis for the data on a single chromosome, one can use `iChip2` and `iChip1` functions to analyze data with multiple chromosomes. Although a probe may not be physically close to its adjacent probes (e.g., the last probe of a chromosome and the first probe of the next chromosome, and the probes in the same chromosome that are adjacent but separated by a long genomic distance), in practice, it should be acceptable to consider the interactions between these adjacent and boundary probes. There are two reasons for this. First, the number of these probes is quite small, compared to all the probes in the tiling arrays. Second, these boundary probes have a very high probability of being non-enriched, thus it should be reasonable to consider the interactions between them. If we let these boundary and adjacent probes interact with each other, it has little effect on the results, but significantly simplify the algorithms for modeling ChIP-chip data. In addition, it should be noted that when the data are very noisy, the posterior mean of beta will be relatively small (e.g., around 1) when the `iChip1` method is used, and the posterior probabilities are not dichotomized and dominated by 0. In this case, the user should increase the value of parameter `minbeta` or use the **`iChip2`** method for modeling.

6 Parallel Computaton

If the total number of probes is relatively small (e.g., a half million), one may analyze the data in a single run. If the total number of probes are large (e.g., several millions), one may perform parallel computation. For example, one can model the data chromosome by chromosome and run many jobs simultaneously. The following is an example of parallel computation using the `snowfall` package (<http://cran.r-project.org/web/packages/snowfall/>).

```
library(snow)
library(snowfall)
dataList = list(oct4t=oct4lmt,p53t=p53lmt)
sfInit(parallel=TRUE,cpus=2,type="SOCK")
res=sfLapply(dataList,iChip1,burnin = 2000, sampling = 10000, sdcut = 2,
beta0 = 3,minbeta = 0, maxbeta = 10, normsd = 0.1, verbose = FALSE)
```

In addition, Mo (2012) has applied Ising models to analysis of ChIP-seq data, and provided an R script named 'iSeq.R' that can be used as a command line program in Unix/Linux environment. If the user is interested in it, the user may modify the script to automate ChIP-chip data analysis. The R script `iSeq.R` is available at <https://sites.google.com/site/quincymobio/teaching-materials>.

7 Citing iChip

If you use `iChip2` function, please cite Mo and Liang (2010a). If you use `iChip1` function, please cite Mo and Liang (2010b).

```

> sessionInfo()

R version 4.3.0 RC (2023-04-13 r84269 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2022 x64 (build 20348)

Matrix products: default

locale:
 [1] LC_COLLATE=C
 [2] LC_CTYPE=English_United States.utf8
 [3] LC_MONETARY=English_United States.utf8
 [4] LC_NUMERIC=C
 [5] LC_TIME=English_United States.utf8

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods    base

other attached packages:
[1] iChip_1.54.0

loaded via a namespace (and not attached):
[1] compiler_4.3.0 limma_3.56.0  tools_4.3.0

```

References

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- Mo, Q. (2012). A fully Bayesian hidden Ising model for ChIP-seq data analysis. *Biostatistics* **13(1)**, 113-28.
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