

"scripts used in Raj et al 2015 to run PIQ"

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January 1, 2015

Contents

To run PIQ, we followed instructions from the authors of PIQ (see [here](#), [here](#), and [here](#)). We have bam file for each replicate in

```
~anilraj/histmod/cache/PIQdata/
```

and selected motifs sites for each TF as bed file in

```
~anilraj/histmod/cache/PIQ/<tfid>_Gm12878_sites.bed
```

First, we created directories:

```
cd /mnt/lustre/home/shim/pbm_dnase_profile/analysis/piq/  
mkdir motifsites  
mkdir readfiles  
mkdir tmp  
mkdir res_pooled  
mkdir res_Rep1  
mkdir res_Rep2
```

We prepare R binary file from bam file, for each replicate:

```
/data/tools/R-3.1.1/bin/Rscript bam2rdata.r common.r /mnt/lustre/home/shim/pbm_  
dnase_profile/analysis/piq/readfiles/Rep1.RData ~anilraj/histmod/cache/  
PIQdata/Gm12878_Rep1.sort.bam  
/data/tools/R-3.1.1/bin/Rscript bam2rdata.r common.r /mnt/lustre/home/shim/pbm_  
dnase_profile/analysis/piq/readfiles/Rep2.RData ~anilraj/histmod/cache/  
PIQdata/Gm12878_Rep2.sort.bam
```

and after pooling two replicates:

```
/data/tools/R-3.1.1/bin/Rscript bam2rdata.r common.r /mnt/lustre/home/shim/pbm_
dnase_profile/analysis/piq/readfiles/pooled.RData ~anilraj/histmod/cache/
PIQdata/Gm12878_pooled.sort.bam
```

and to run two replicates

```
/data/tools/R-3.1.1/bin/Rscript bam2rdata.r common.r /mnt/lustre/home/shim/pbm_
dnase_profile
/analysis/piq/readfiles/multi.RData ~anilraj/histmod/cache/PIQdata/Gm12878_Rep1
.sort.bam ~anilraj/histmod/cache/PIQdata/Gm12878_Rep2.sort.bam
```

We prepare motif sites input file for each TF ('\${tfid}' indicates TF name):

```
/data/tools/R-3.1.1/bin/Rscript bed2pwm.r common.r ~anilraj/histmod/cache/PIQ/S
${tfid}_Gm12878_sites.bed S ${tfid} /mnt/lustre/home/shim/pbm_dnase_profile
/analysis/piq/motifsites/
```

and run PIQ for each TF, for each replicate:

```
/data/tools/R-3.1.1/bin/Rscript pertf.r common.r /mnt/lustre/home/shim/pbm_
dnase_profile/analysis/piq/motifsites/ /mnt/lustre/home/shim/pbm_dnase_
profile/analysis/piq/tmp/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/
piq/res_Rep1/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/piq/
readfiles/Rep1.RData ${tfid}

/data/tools/R-3.1.1/bin/Rscript pertf.r common.r /mnt/lustre/home/shim/pbm_
dnase_profile/analysis/piq/motifsites/ /mnt/lustre/home/shim/pbm_dnase_
profile/analysis/piq/tmp/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/
piq/res_Rep2/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/piq/
readfiles/Rep2.RData ${tfid}
```

and after pooling two replicates:

```
/data/tools/R-3.1.1/bin/Rscript pertf.r common.r /mnt/lustre/home/shim/pbm_
dnase_profile/analysis/piq/motifsites/ /mnt/lustre/home/shim/pbm_dnase_
profile/analysis/piq/tmp/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/
piq/res_pooled/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/piq/
readfiles/pooled.RData ${tfid}
```

and run two replicates

```
/data/tools/R-3.1.1/bin/Rscript pertf.r common.r /mnt/lustre/home/shim/pbm_
dnase_profile/analysis/piq/motifsites/ /mnt/lustre/home/shim/pbm_dnase_
profile/analysis/piq/tmp/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/
piq/res_multi/ /mnt/lustre/home/shim/pbm_dnase_profile/analysis/piq/
readfiles/multi.RData ${tfid}
```