Package 'NuCMap'

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Type Package

Title An R package for Nucleosomes Chemical Mapping data analysis.

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Author Liqun Xi, Qingyang Zhang, Kristin Brogaard, Bruce Lindsay, Jonathan Widom, Ji-Ping Wang

Maintainer Ji-Ping Wang<jzwang@northwestern.edu>

Description NuCMap is an R package for analyzing Nucleosome mapping data from the newly developed chemical mapping technology. This package is built upon a locally convoluted Poisson model proposed in Brogaard et al. (2012) and a generalized EM algorithm by Xi et al. (2012). The core of the package was written in Fortran and C++. NuCMap integrates eleven functions including plotCUTS, peakDIST, trainTEMP1, estNCP1, callUNIQUE, callRED, trainTEMP4, estNCP4, plotAATT, estNCPcall, and calOccup to fulfill a complete analysis of chemical mapping data from data visualization, model training and diagnostic, parameter estimation to nucleosome map definition. NuCMap depends on the experiment data package nucmapData, which contains all the illustration data files.

LazyLoad yes

License GPL-2

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R topics documented:

NuCMap-package *An R package for chemical nucleosome mapping data analysis.*

Description

NuCMap is an R package for analyzing Nucleosome positioning signals in Chemical Map. This package is built upon a locally convoluted Poisson model proposed in Xi et al. (2012). The core of the package was written in Fortran and C++. NuCMap integrates eleven functions including plotCUTS, peakDIST, trainTEMP1, estNCP1, callUNIQUE, callRED, trainTEMP4, estNCP4, plotAATT, estNCPcall and calOccup to fulfill a complete analysis of chemical mapping data from data visualization, model training and diagnostics, parameter estimation to nucleosome map definition. NuCMap depends on the experiment data package nucmapData, which contains all the illustration data files.

Details

Package:	NuCMap
Type:	Package
Version:	1.0
Date:	2012-07-27
License:	GPL-2

plotCUTS: R function for visualizing raw cleavage frequency in a specified region on Watson and Crick strands simultaneously.

peakDIST: R function for Crick-Watson cleavage peak-peak distance diagnostic.

trainTEMP1: R function for training one-template model.

estNCP1: R function for estimating NCP score for one-template model using EM algorithm.

callUNIQUE: R function for defining unique nucleosome map based on NCP score/noise ratio.

callRED: R function for defining redundant nucleosome map based on NCP score/noise ratio.

trainTEMP4: R function for training four-template model.

estNCP4: R function for estimating NCP score for four-template mdoel using EM algorithm.

plotAATT: R function for plotting AA/TT/AT/TA frequency against to the distance from nuclesome center.

estNCPcall: R function for estimating NCP score, NCP score/noise ratio and making unique nucleosome center calls.

calOccup: R function for calculating nucleosome occupancy genome-wide.

Author(s)

Liqun Xi, Qingyang Zhang, Kristin Brogaard, Bruce Lindsay, Jonathan Widom, Ji-Ping Wang

Maintainer: Ji-Ping Wang<jzwang@northwestern.edu>

References

Xi, L., Brogaard, K., Zhang, Q., Lindsay, B., Widom, J., Wang, J.-P. (2012), A locally convoluted Poisson cluster model for nucleosome positioning signals in chemical map, Submitted for publication

Brogaard, K., Xi, L., Wang, J.-P. and Widom, J. (2012), A base pair resolution map of nucleosome positions in yeast, Nature 486:496-501

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## plotCUTS
wfile=system.file("extdata", "watson12.txt",package="nucmapData")
cfile=system.file("extdata", "crick12.txt",package="nucmapData")
plotCUTS(seqname="chrI",watsonfile=wfile,crickfile=cfile,startpos=
10000,endpos=12000)

## peakDIST
wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
peakDIST(seqname=c("chrI","chrII"),watsonfile=wfile,crickfile=cfile)

## trainTEMP1
wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
trainTEMP1(seqname=c("chrI","chrII"),watsonfile=wfile,crickfile=cfile)

## estNCP1
chrI=system.file("extdata", "chrI.fa",package="nucmapData")
wfile=system.file("extdata", "watson12.txt",package="nucmapData")
cfile=system.file("extdata", "crick12.txt",package="nucmapData")
estNCP1(seqname="chrI",genfile=chrI,watsonfile=wfile,crickfile=
cfile,temp1="default")

## callUNIQUE
NCP1=system.file("extdata","NCPscore.ratio_1temp.txt",package="nucmapData")
callUNIQUE(seqname=c("chrI","chrII"),estresults=NCP1)

## callRED
NCP1=system.file("extdata","NCPscore.ratio_1temp.txt",package="nucmapData")
callRED(seqname=c("chrI","chrII"),estresults=NCP1)

## trainTEMP4
wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
chrI=system.file("extdata","chrI.fa",package="nucmapData")
chrII=system.file("extdata","chrII.fa",package="nucmapData")
umap=system.file("extdata","UNIQUEcenters.txt",package="nucmapData")
trainTEMP4(seqname=c("chrI","chrII"),genfile=c(chrI,chrII),watsonfile=
wfile,crickfile=cfile,center=umap)

## estNCP4
chrI=system.file("extdata", "chrI.fa",package="nucmapData")
wfile=system.file("extdata", "watson12.txt",package="nucmapData")
cfile=system.file("extdata", "crick12.txt",package="nucmapData")
```

```
temp4_file=system.file("extdata", "trainTEMP4result.txt",package="nucmapData")
estNCP4(seqname="chrI",genfile=chrI,watsonfile=wfile,crickfile=cfile,temp4=
temp4_file)

## plotAATT
chrI=system.file("extdata", "chrI.fa",package="nucmapData")
chrII=system.file("extdata", "chrII.fa",package="nucmapData")
umap=system.file("extdata", "UNIQUEcenters.txt",package="nucmapData")
plotAATT(seqname=c("chrI","chrII"),genfile=c(chrI,chrII),center=umap)

## estNCPcall
chrI=system.file("extdata","chrI.fa",package="nucmapData")
wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
estNCPcall(seqname="chrI",genfile=chrI,watsonfile=wfile,crickfile=cfile)

## calOccup
NCP4=system.file("extdata","NCPscore.ratio_4temp.txt",package="nucmapData")
chrI=system.file("extdata","chrI.fa",package="nucmapData")
chrII=system.file("extdata","chrII.fa",package="nucmapData")
rmap=system.file("extdata","REDcenters.txt",package="nucmapData")
calOccup(seqname=c("chrI","chrII"),estresults=NCP4,genfile=c(chrI,chrII),
rednufile=rmap)

## End(Not run)
```

`callRED` *R function for defining redundant nucleosome map*

Description

This function defines unique nucleosome map.

Usage

```
callRED(estresults,seqname,threshold)
```

Arguments

`estresults`	one string for the path and name of the output file from function `estNCP1` or `estNCP4`.
`seqname`	the default value is "all", which specifies all chromosomes listed in `estresults`. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in `estresults`.
`threshold`	A cutoff value to define redundant nucleosome map. All the positions where the NCP score/noise ratio exceeds this cutoff are defined as nucleosome centers. The default threshold value is the minimum NCP score/noise ratio from unique nucleosome map used in Brogaard et al. (2012)

Value

callRED defines redundant nucleosome map based on NCP/noise ratio. The output file is named as "REDcenters.txt" and contains three columns:

Position	chromosome coordinate;
NCPscore	estimated NCP score;
Ratio	NCP score/noise ratio.

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

NCP1=system.file("extdata","NCPscore.ratio_1temp.txt",package="nucmapData")
callRED(seqname=c("chrI","chrII"),estresults=NCP1,threshold="default")

## End(Not run)
```

---

callUNIQUE *R function for defining unique nucleosome map*

Description

This function defines unique nucleosome map.

Usage

```
callUNIQUE(estresults,seqname)
```

Arguments

estresults	one string for the path and name of the output file from function estNCP1 or estNCP4.
seqname	the default value is "all", which specifies all chromosomes listed in estresults. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in estresults.

Value

callUNIQUE defines unique nucleosome map based on NCP score/noise ratio. The output file is named as "UNIQUEcenters.txt" and contains three columns:

Position	chromosome coordinate;
NCPscore	estimated NCP score;
Ratio	NCP score/noise ratio.

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

NCP1=system.file("extdata","NCPscore.ratio_1temp.txt",package="nucmapData")
callUNIQUE(seqname=c("chrI","chrII"),estresults=NCP1)

## End(Not run)
```

---

calOccup *R function for calculating nucleosome occupancy genome-wide*

Description

This function calculates nucleosome occupancy genome-wide.

Usage

```
calOccup(estresults,genfile,rednufile,seqname)
```

Arguments

estresults	one string for the path and name of the output file from function estNCP1 or estNCP4.
genfile	one or multiple strings, each for the path and name of a DNA sequence file in FASTA format. The sequence files can be located in any directory. It must contain only one sequence. By FASTA format, we require each line to be of the same length (the last line can be shorter; the first line should be '>sequenceName'). The length of each line should be no longer than 400 bp.
rednufile	one string for the path and name of the file (output file from callRED) where a redundant nucleosome map is saved.
seqname	the default value is "all", which specifies all chromosomes listed in estresults. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in estresults.

Value

calOccup calculates nucleosome occupancy on the genome. The output file is named as "NuOccupancy.txt" and contains two columns:

Position	chromosome coordinate;
Occupancy	nucleosome occupancy score.

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

NCP4=system.file("extdata","NCPscore.ratio_4temp.txt",package="nucmapData")
chrI=system.file("extdata","chrI.fa",package="nucmapData")
chrII=system.file("extdata","chrII.fa",package="nucmapData")
rmap=system.file("extdata","REDcenters.txt",package="nucmapData")
calOccup(estresults=NCP4,genfile=c(chrI,chrII),rednufile=rmap,seqname=
c("chrI","chrII"))

## End(Not run)
```

`estNCP1` *R function for estimating NCP score and NCP score/noise ratio using one-template model*

Description

This function invokes Fortran codes to estimate NCP score and NCP score/noise ratio using one-template model.

Usage

```
estNCP1(seqname,genfile,watsonfile,crickfile,temp1)
```

Arguments

`seqname`	the default value is "all", which specifies all chromosomes listed in Watson and Crick cleavage files. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in Watson and Crick cleavage files.
`genfile`	one or multiple strings, each for the path and name of DNA sequence files in FASTA format. This sequence file can be located in any directory. It must contain only one sequence. By FASTA format, we require each line to be of the same length (the last line can be shorter; the first line should be '>sequenceName'). The length of each line should be no longer than 400 bp.
`watsonfile`	one string for the path and name of Watson cleavage file. The file may contain two or more chormosomes. The first columm is chromosome name, the second column is the chromosome coordinate, the third column is the cleavage frequency.
`crickfile`	see requirement for `watsonfile`.
`temp1`	one string for the path and name of the output file of `trainTEMP1`. The default choice (by setting temp1="default") is the template trained based on the yeast chemical mapping data from Brogaard et al. (2012) and Xi et al. (2012).

Value

estNCP1 outputs the estimation results under the current working directory. The output file is named as "NCPscore.ratio_1temp.txt", 1temp stands for one-template model. It contains five columns:

chr.	chromosome name;
Position	chromosome coordinate;
NCPscore	estimated NCP score;
Ratio	NCP/noise ratio;
cNCPscore	NCP score after correction for strand asymmetry of cleavages. It is used for nucleosome occupancy calculation (see function calOccup).

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

chrI=system.file("extdata", "chrI.fa",package="nucmapData")
wfile=system.file("extdata", "watson12.txt",package="nucmapData")
cfile=system.file("extdata", "crick12.txt",package="nucmapData")
estNCP1(seqname="chrI",genfile=chrI,watsonfile=wfile,crickfile=cfile)

## End(Not run)
```

---

estNCP4 *R function for estimating NCP score and NCP score/noise ratio using four-template model*

Description

This function invokes Fortran codes to estimate NCP score and NCP score/noise ratio using four-template model.

Usage

```
estNCP4(seqname,genfile,watsonfile,crickfile,temp4)
```

Arguments

seqname	the default value is "all", which specifies all chromosomes listed in Watson and Crick cleavage files. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in Watson and Crick cleavage files.
genfile	one or multiple strings, each for the path and name of a DNA sequence file in FASTA format. This sequence file can be located in any directory. It must contain only one sequence. By FASTA format, we require each line to be of the same length (the last line can be shorter; the first line should be '>sequenceName'). The length of each line should be not longer than 400 bp.

watsonfile	one string for the path and name of Watson cleavage file. The file may contain two or more chormosomes. The first columm is chromosome name, the second column is the chromosome coordinate, the third column is the cleavage frequency.
crickfile	see requirement for watsonfile.
temp4	one string for the path and name of the output file of trainTEMP4. The default choice (by setting temp4="default") is the template trained based on the yeast chemical mapping data from Brogaard et al. (2012) and Xi et al. (2012).

Value

estNCP4 outputs the estimation results under the current working directory. The output file is named as "NCPscore.ratio_4temp.txt", 4temp stands for four-template model. It contains five columns:

chr.	chromosome name;
Position	chromosome coordinate;
NCPscore	estimated NCP score;
Ratio	NCP/noise ratio;
cNCPscore	NCP score after correction for strand asymmetry of cleavages. It is used for nucleosome occupancy calculation (see function calOccup).

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

chrI=system.file("extdata", "chrI.fa",package="nucmapData")
wfile=system.file("extdata", "watson12.txt",package="nucmapData")
cfile=system.file("extdata", "crick12.txt",package="nucmapData")
temp4_file=system.file("extdata", "trainTEMP4result.txt",package="nucmapData")
estNCP4(seqname="chrI",genfile=chrI,watsonfile=wfile,crickfile=cfile,temp4
=temp4_file)

## End(Not run)
```

---

estNCPcall *R function for estimating NCP score, NCP/noise ratio and making unique nucleosome center calls using four-template model.*

Description

This function produces NCP score estimation and unique nucleosome set based on the NCP/noise ratio using four-template model.

Usage

```
estNCPcall(seqname,genfile,watsonfile,crickfile)
```

Arguments

seqname	the default value is "all", which means all chromosomes listed in Watson and Crick cleavage files. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in Watson and Crick cleavage files.
genfile	one or multiple strings, each for the path and name of a DNA sequence file in FASTA format. This sequence file can be located in any directory. It must contain only one sequence. By FASTA format, we require each line to be of the same length (the last line can be shorter; the first line should be '>sequenceName'). The length of each line should be not longer than 400 bp.
watsonfile	one string for the path and name of Watson cleavage file. The file can contain information of multiple chormosomes. For the Watson cleavage file, the first columm is chromosome's name, the second columm is chromosome coordinate, the third column is the cleavage frequency.
crickfile	see requirement for watsonfile.

Value

estNCPcall outputs estimated NCP score, NCP/noise ratio and unique nucleosome centers under current working directory. Please refer to estNCP1, estNCP4 and callUNIQUE about the output file names and format.

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

chrI=system.file("extdata","chrI.fa",package="nucmapData")
wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
estNCPcall(seqname="chrI",genfile=chrI,watsonfile=wfile,crickfile=cfile)

## End(Not run)
```

---

peakDIST *R function for Crick-Watson cleavage peak-peak distance diagnostic.*

Description

This function produces frequency plot for cross-strand cleavage peak-peak distance.

Usage

```
peakDIST(seqname,watsonfile,crickfile)
```

Arguments

seqname	the default value is "all", which speficies all chromosomes listed in Watson and Crick cleavage files. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in Watson and Crick cleavage files.
watsonfile	one string for the path and name of Watson cleavage file. The file may contain two or more chormosomes. The first columm is chromosome name, the second column is the chromosome coordinate, the third column is the cleavage frequency.
crickfile	see requirement for watsonfile.

Value

peakDIST outputs frequency plot for cross-strand cleavage peak-peak distance.

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
peakDIST(seqname=c("chrI","chrII"),watsonfile=wfile,crickfile=cfile)

## End(Not run)
```

---

plotAATT *R function for plotting AA/TT/TA/AT frequency against to the distance from the nucleosome center*

Description

This function plots AA/TT/TA/AT frequency against to the distance from the nucleosome center.

Usage

```
plotAATT(seqname,genfile,center)
```

Arguments

genfile	one or multiple strings, each string is for the path and name of a DNA sequence file in FASTA format. This sequence file can be located in any directory. It must contain only one sequence. By FASTA format, we require each line to be of the same length (the last line can be shorter; the first line should be '>sequenceName'). The length of each line should be no longer than 400 bp.
center	one string for the path and name of the file where a unique or redundant nucleosome map is saved.
seqname	the default value is "all", which specifies all chromosomes listed in center. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in center.

Value

plotAATT plots AA/TT/TA/AT frequency against to the distance from the nucleosome center.

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

chrI=system.file("extdata", "chrI.fa",package="nucmapData")
chrII=system.file("extdata", "chrII.fa",package="nucmapData")
umap=system.file("extdata", "UNIQUEcenters.txt",package="nucmapData")
plotAATT(genfile=c(chrI,chrII),center=umap,seqname=c("chrI","chrII"))

## End(Not run)
```

---

plotCUTS *R function for visualizing the cleavage frequency on Watson and Crick strands*

Description

This function produces cleavage frequency plot in any specified region on Watson and Crick strands simultaneously.

Usage

```
plotCUTS(seqname,watsonfile,crickfile,startpos,endpos)
```

Arguments

seqname	the specified chromosome's name, e.g. "chrI". This sequence name should be consistant with the chromosome's name in Watson and Crick cleavage files.
watsonfile	one string for the path and name of Watson cleavage file. The file may contain two or more chormosomes. The first columm is chromosome name, the second column is the chromosome coordinate, the third column is the cleavage frequency.
crickfile	see the requirement for watsonfile.
startpos	an integer standing for the starting position of the genome region.
endpos	an integer standing for the ending position of the genome region.

Value

plotCUTS produces cleavage frequency plot in a specified region on both Watson and Crick strands simultaneously.

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

wfile=system.file("extdata", "watson12.txt",package="nucmapData")
cfile=system.file("extdata", "crick12.txt",package="nucmapData")
plotCUTS(seqname="chrI",watsonfile=wfile,crickfile=cfile,startpos=
10000,endpos=12000)

## End(Not run)
```

`trainTEMP1` *R function for training one-template model*

Description

This function trains cleavage template for one-template model.

Usage

```
trainTEMP1(seqname,watsonfile,crickfile)
```

Arguments

`seqname`	the default value is "all", which specifies all chromosomes listed in Watson and Crick cleavage files. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in Watson and Crick cleavage files.
`watsonfile`	one string for the path and name of Watson cleavage file. The file may contain two or more chormosomes. The first columm is chromosome name, the second column is the chromosome coordinate, the third column is the cleavage frequency.
`crickfile`	see requirement for `watsonfile`.

Value

`trainTEMP1` outputs cleavage trained template for one-template model under the current working directory. The output file contains a 1 by 8 matrix, standing for average cleavage frequency on the clustered positions including (-2, -1, 0, 1, 4, 5, 6, 7) around nucleosome center. The file is named as "trainTEMP1result.txt".

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.
```

```
wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
trainTEMP1(seqname=c("chrI","chrII"),watsonfile=wfile,crickfile=cfile)

## End(Not run)
```

`trainTEMP4` *R function for training four-template model*

Description

This function trains cleavage template for four-template model.

Usage

```
trainTEMP4(seqname,genfile,watsonfile,crickfile,center)
```

Arguments

`seqname`	the default value is "all", which specifies all chromosomes listed in Watson and Crick cleavage files. One can also specify one or more individual chromosomes, e.g. "chrI" or c("chrI", "chrII"). The sequence name format must be same as in Watson and Crick cleavage files.
`genfile`	one or multiple strings, each string is for the path and name of a DNA sequence file in FASTA format. This sequence file can be located in any directory. It must contain only one sequence. By FASTA format, we require each line to be of the same length (the last line can be shorter; the first line should be '>sequence-Name'). The length of each line should be no longer than 400 bp.
`watsonfile`	one string for the path and name of Watson cleavage file. The file may contain two or more chormosomes. The first columm is chromosome name, the second column is the chromosome coordinate, the third column is the cleavage frequency.
`crickfile`	see requirement for `watsonfile`.
`center`	one string for the path and name of the file (output file from `callUNIQUE`) where a unique nucleosome map is saved.

Value

`trainTEMP4` outputs trained template for four-template model under the current working directory. The file contains a 4 by 8 matrix, standing for average cleavage frequency on the clustered positions including (-2, -1, 0, 1, 4, 5, 6, 7) around nucleosome centers for four templates(+A(-3)+T(+3), (+A(-3)-T(+3), (-A(-3)+T(+3) and (-A(-3)-T(+3), where a +/- in front of the A/T nucleotide stands for presence/absence of the letter at -3/+3 postion respectively relative to the nucleosome center). The file is named as "trainTEMP4result.txt".

Examples

```
## Not run:
library(NuCMap)
library(nucmapData)
## the user should replace "system.file("extdata",~,package="nucmapData")"
## by the actual path and file name.

wfile=system.file("extdata","watson12.txt",package="nucmapData")
cfile=system.file("extdata","crick12.txt",package="nucmapData")
chrI=system.file("extdata","chrI.fa",package="nucmapData")
chrII=system.file("extdata","chrII.fa",package="nucmapData")
umap=system.file("extdata","UNIQUEcenters.txt",package="nucmapData")
trainTEMP4(seqname=c("chrI","chrII"),genfile=c(chrI,chrII),watsonfile=wfile,crickfile=
cfile,center=umap)

## End(Not run)
```

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