Package ‘gprege’

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Title Gaussian Process Ranking and Estimation of Gene Expression time-series
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Suggests spam

Description The gprege package implements the methodology described in
Kalaitzis & Lawrence (2011) "A simple approach to ranking differentially
expressed gene expression time-courses through Gaussian process regression".
The software fits two GPs with the an RBF (+ noise diagonal) kernel on each
profile. One GP kernel is initialised with a short lengthscale hyperparameter,
signal variance as the observed variance and a zero noise variance. It is
optimised via scaled conjugate gradients (netlab). A second GP has fixed
hyperparameters: zero inverse-width, zero signal variance and noise
variance as the observed variance. The log-ratio of marginal likelihoods of
the two hypotheses acts as a score of differential expression for the profile.
Comparison via ROC curves is performed against BATS (Angelini et.al, 2007).
A detailed discussion of the ranking approach and dataset used can be found in
the paper (http://www.biomedcentral.com/1471-2105/12/180).

License AGPL-3
biocViews Microarray, Preprocessing, Bioinformatics,
DifferentialExpression, TimeCourse

URL
BugReports alkalait@gmail.com
NeedsCompilation no

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gprege-package  


gprege - Gaussian Process Ranking and Estimation of Gene Expression.

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Description

This package implements the method of Kalaitzis and Lawrence (2011) for Gaussian process modelling gene expression time-series data. The method can be used to filter quiet genes and quantify differential expression in time-series expression ratios.

Details

Package: gprege
Type: Package
Version: 0.99.0
Date: 2011-07-08
License: A-GPL Version 3

For details of using the package please refer to the Vignette.

Author(s)

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References


See Also
demGpCov2D, demGpSample, demInterpolation, demOptimiseGp, demRegression

Examples

## see demTp63Gp1.R
**compareROC**

Make ROC plots.

**Description**

This rocStats wrapper superimposes ROC curves on a plot to analyse the output performance of a method-A, and optionally compare it with that of a method-B, based on some ground truth labels.

**Usage**

```r
compareROC(output, groundTruthLabels, compareToRanking)
```

**Arguments**

- `output` (vector) The output of ranking scores returned by method-A for each data-point.
- `groundTruthLabels` (vector) A binary vector that contains the ground truth (e.g. which genes are members of the top-100 ground truth list).
- `compareToRanking` A matrix where each column is the output vector of ranking scores returned by another competing method.

**Value**

- `area` A scalar. The area under the ROC curve of method-A.

**See Also**

- `rocStats`

**Examples**

```r
data(FragmentDellaGattaData) # Load demo data.
compareROC(output = rnorm(length(DGatta_labels_byTSNI)) > 0, groundTruthLabels = DGatta_labels_byTSNI)
```

**DellaGattaData**

Fragment dataset of 13 time-point mouse microarray time series of gene expression ratios and and a ranking list of TP63 targets suggested by TSNI.

**Description**

- `exprs_tp63_RMA` 100 gene reporters of 13 time-points mouse Affymetrix microarray gene expression coming from a study on primary mouse keratinocytes with an induced activation of the TRP63 transcription factor (GEO-accession number:GSE10562, see Source section), where a reverse-engineering algorithm was developed (TSNI: time-series network identification) to infer the direct targets of TRP63 (Della Gatta et al. 2008). The data has been processed using rma (affy) and the profiles are centred (zero-mean) across the timepoints.
DGatta_labels_byTSNI, DGatta_labels_byTSNItop100 a ranking list suggested based by TSNI is provided. The inferred direct targets were biologically confirmed by correlation with ChIP-Seq binding regions; therefore the list is used as a noisy ground truth. See Source section.

genesymbols Names of the genes that the transcript IDs (in exprs_tp63_RMA) correspond to.
gpregeOutput Its field ‘rankingScores’ contains log-marginal likelihood ratios, used as ranking scores, for each gene reporter in exprs_tp63_RMA. This is the output from a run of gprege on the full DellaGatta dataset (see demTp63Gp1.R) and stored here for convenience.

Usage

data(FragmentDellaGattaData)

Source

GEO: http://www.ncbi.nlm.nih.gov/geo/, TSNI ranking: genome.cshlp.org/content/suppl/2008/05/05/gr.073601.107.DC1/DellaGatta_SupTable1.xls

References


demTp63Gp1 gprege on TP63 expression time-series.

Description

Demo script of Gaussian Process Regression and Estimation of Gene Expression on TP63 time-series data (see gprege.m). See Kalaitzis & Lawrence (2011) for a detailed discussion of the ranking algorithm and dataset used.

Usage

demTp63Gp1(fulldataset=FALSE)

Arguments

fulldataset (Logical) TRUE downloads and uses the full dataset.

See Also

gprege

Examples

demTp63Gp1(fulldataset=FALSE)
BATS rankings (Angelini, 2007) Case 1: Delta error prior Case 2: Inverse Gamma error prior Case 3: Double Exponential error prior

Description

DGdat_p63_case1_GL  Case 1: Delta error prior
DGdat_p63_case2_GL  Case 2: Inverse Gamma error prior
DGdat_p63_case3_GL  Case 3: Double Exponential error prior

Usage

data(DGdat_p63)

Source

GEO: http://www.ncbi.nlm.nih.gov/geo/, TSNI ranking: genome.cshlp.org/content/suppl/2008/05/05/gr.073601.107.DC1/DellaGatta_SupTable1.xls

References


exhaustivePlot  Plot of the LML function by exhaustive search.

Description

Exhaustively searches the hyperparameter space by a grid, whose resolution is passed as an argument, and plots the LML function for every point in the space.

Usage

exhaustivePlot(y, x, xstar, options, maxwidth, res, nlevels)

Arguments

y  the target (output) data.
x  the input data matrix.
xstar  the points to predict function values.
options  options structure as defined by gpOptions.m.
maxwidth  maximum lengthscale to search for.
res  The search resolution. Number of points to plot for in the search range.
nlevels  Number of contour levels.


\section*{Value}
\begin{itemize}
  \item \textbf{area} \hspace{1cm} \text{Area under the ROC curve of method-A.}
\end{itemize}

\section*{See Also}
- \texttt{rocStats}

\section*{Examples}

\begin{verbatim}
noiseLevel <- 0.2
noiseVar <- noiseLevel^2
options <- gpOptions()
options$kern$comp <- list('rbf', 'white')
## Create data set
l <- 9; x <- matrix(seq(0,240,by=20), ncol=1)
trueKern <- kernCreate(x, 'rbf')
trueKern$inverseWidth <- 1/(20^2) ## Characteristic inverse-width.
K <- kernCompute(trueKern, x) + diag(dim(x)[1]) * noiseVar
## Sample some true function values.
y <- gaussSamp(Sigma=K, numSamps=1)
xTest <- as.matrix(seq(0, 240, length=200))
graphics.off(); dev.new(); plot.new(); dev.new(); plot.new()
exhaustivePlot(y, x, xTest, options=options, maxwidth=100, res=50, nlevels=75)
\end{verbatim}

\begin{itemize}
  \item \texttt{gprege} \hspace{1cm} \textit{Gaussian process ranking and estimation of gene expression time-series}
\end{itemize}

\section*{Description}
Fits two GPs with the an RBF (+ noise diagonal) kernel on each profile. One GP kernel is initialised with a short lengthscale hyperparameter, signal variance as the observed variance and a zero noise variance. It is optimised via scaled conjugate gradients (netlab). The other GP has fixed hyperparameters with a zero inverse-width, zero signal variance and noise variance as the observed variance. The log-ratio of marginal likelihoods of the two hypotheses acts as a score of differential expression for the profile. Comparison via ROC curves is performed against BATS (Angelini et.al, 2007). See Kalaitzis & Lawrence (2011) for a detailed discussion of the ranking algorithm and dataset used.

\section*{Usage}
\begin{verbatim}
gprege(data, inputs, gpregeOptions)
\end{verbatim}

\section*{Arguments}
\begin{itemize}
  \item \texttt{data} \hspace{1cm} The matrix of gene expression profiles; one profile per row.
  \item \texttt{inputs} \hspace{1cm} Inputs (timepoints) to the GP.
  \item \texttt{gpregeOptions} \hspace{1cm} Options list for gprege with fields
    \begin{itemize}
      \item \texttt{explore} Logical. TRUE operates in a user interactive mode. Used for examining individual gene expression profiles.
      \item \texttt{labels} A binary vector. TRUE specifies whether the corresponding profile comes from a differentially expressed gene (usually from a ground truth).
    \end{itemize}
\end{itemize}
indexRange  A numeric vector. Range of indices of profiles on which the function should operate. Useful for selective exploration of specific profiles, e.g. only genes marked as differentially expressed in a ground truth list.

interpolatedT  A numeric vector. New timepoints to interpolate for each profile, based on the estimated function values.

iters  A scalar. The number of iterations for scaled-conjugate gradients (SCG) optimisation.

display  Logical. Display gradient and LML information on each SCG iteration.

inihypers  The matrix of hyperparameter configurations as its rows. Each row has the following format: [inverse-lengthscale percent-signal-variance percent-noise-variance] The first row corresponds to a (practically constant) function with a very large lengthscale. Such a function will account for 0 percent of the observed variance in the expression profile (hence 0 for signal) and explain it as noise (hence 1 for noise). Subsequent rows (initialisations for SCG optimisation) correspond to functions of various lengthscales that explain all the observed variance as signal. A reasonable lengthscale would be roughly in line with the time-point sampling intervals.

exhaustPlotRes  A scalar. The search resolution. Used for interactive mode (explore == 1).

exhaustPlotLevels  A scalar. Number of contour levels in the exhaustive plot. Used for interactive mode (explore == 1).

exhaustPlotMaxWidth  A scalar. the maximum lengthscale to search for. Used for interactive mode (explore == 1).

Value  
gpregeOutput  Output list with fields:

signalvar  A numeric vector of the vertical lengthscales of the optimised RBF kernel; one for each profile.

noisevar  A numeric vector. Similar to signalvar, but for the noise hyperparameter.

width  A numeric vector. Similar to signalvar and noisevar, but for the horizontal lengthscales of the RBF.

LMLs  A numeric vector of log-marginal likelihoods of the GP; one for each profile.

interpolatedData  A matrix of the extended dataset with interpolated values as the augmenting columns.

rankingScores  A numeric vector of the ranking scores, based on the log-ratio of marginal likelihoods.

See Also  
gpOptions, gpCreate, gpExpandParam, gpOptimise, gpExtractParam, gpLogLikelihood, gpPosterior

Examples  

## see demTp63Gp1.R
data(FragmentDellaGattaData) ## Load demo data.
## Setup other gprege options.
gpregeOptions = list(indexRange=(1:2), explore=TRUE, exhaustPlotRes=30, exhaustPlotLevels=10,
## Matrix of different hyperparameter configurations as rows:
## \[\text{inverse-lengthscale} \quad \text{percent-signal-variance} \quad \text{percent-noise-variance}\].

```r
gpregeOptions$inithypers <- matrix( c(1/1000,1e-3,0.999,1/20,0.999,1e-3), ncol=3, byrow=TRUE)
gpregeOutput <- gprege(data=exprs_tp63_RMA, inputs=matrix(seq(0,240,by=20), ncol=1), gpregeOptions=gpregeOptions)
```

---

**Description**

Computes the points on an ROC curve by varying a threshold on the sorted outputs of the method in question.

**Usage**

```r
rocStats(outputs, groundTruthLabels, decreasing = TRUE)
```

**Arguments**

- **outputs**
  A numeric vector with the outputs of the evaluated method (e.g. likelihoods from `gprege`).

- **groundTruthLabels**
  A binary vector that contains the ground truth (e.g. which genes belong in the top-100 ground truth list).

- **decreasing**
  Logical. TRUE sorts outputs by decreasing order.

**Value**

- **stats**
  A list of numeric variables with the necessary statistics to compute an ROC curve, a precision-recall curve, etc.

**Examples**

```r
## see compareROC.R
data(FragmentDellaGattaData) ## Load demo data.
rocStats(gpregeOutput$rankingScores, DGatta_labels_byTSNItop100, decreasing=TRUE)
```
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