Package ‘ldaPrototype’

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Title Prototype of Multiple Latent Dirichlet Allocation Runs
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Description Determine a Prototype from a number of runs of Latent Dirichlet Allocation (LDA) measuring its similarities with S-CLOP: A procedure to select the LDA run with highest mean pairwise similarity, which is measured by S-CLOP (Similarity of multiple sets by Clustering with Local Pruning), to all other runs. LDA runs are specified by its assignments leading to estimators for distribution parameters. Repeated runs lead to different results, which we encounter by choosing the most representative LDA run as prototype.

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https://doi.org/10.5281/zenodo.3597978

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**Description**

Determine a Prototype from a number of runs of Latent Dirichlet Allocation (LDA) measuring its similarities with S-CLOP: A procedure to select the LDA run with highest mean pairwise similarity, which is measured by S-CLOP (Similarity of multiple sets by Clustering with Local Pruning), to all other runs. LDA runs are specified by its assignments leading to estimators for distribution parameters. Repeated runs lead to different results, which we encounter by choosing the most representative LDA run as prototype.

For bug reports and feature requests please use the issue tracker: [https://github.com/JonasRieger/ldaPrototype/issues](https://github.com/JonasRieger/ldaPrototype/issues).

**Data**

**reuters** Example Dataset (91 articles from Reuters) for testing.

**Constructor**

**LDA** LDA objects used in this package.

**as.LDARep** LDARep objects.

**as.LDABatch** LDABatch objects.
as.LDABatch

** Getter**

- `getTopics` Getter for LDA objects.
- `getJob` Getter for LDARep and LDABatch objects.
- `getSimilarity` Getter for TopicSimilarity objects.
- `getSCLOP` Getter for PrototypeLDA objects.
- `getPrototype` Determine the Prototype LDA.

**Performing multiple LDAs**

- `LDARep` Performing multiple LDAs locally (using parallelization).
- `LDABatch` Performing multiple LDAs on Batch Systems.

**Calculation Steps (Workflow) to determine the Prototype LDA**

- `mergeTopics` Merge topic matrices from multiple LDAs.
- `jaccardTopics` Calculate topic similarities.
- `dendTopics` Create a dendrogram from topic similarities.
- `SCLOP` Determine various S-CLOP values.
- `pruneSCLOP` Prune TopicDendrogram objects.

**Shortcuts**

- `getPrototype` Shortcut which includes all calculation steps.
- `LDAPrototype` Shortcut which performs multiple LDAs and determines their Prototype.

**Author(s)**

- **Maintainer**: Jonas Rieger <jonas.rieger@tu-dortmund.de> (ORCID)

**See Also**

Useful links:

- [https://github.com/JonasRieger/ldaPrototype](https://github.com/JonasRieger/ldaPrototype)
- [https://doi.org/10.5281/zenodo.3597978](https://doi.org/10.5281/zenodo.3597978)

**Description**

Constructs a LDABatch object for given elements `reg`, `job` and `id`.

**Usage**

```r
as.LDABatch(reg, job, id)
```

```r
is.LDABatch(obj, verbose = FALSE)
```
Arguments

- `reg` ([`Registry`])
  Registry. See `findDone`.

- `job` ([`data.frame` or integer])
  A data.frame or data.table with a column named "job.id" or a vector of integerish job ids. See `reduceResultsList`.

- `id` ([`character(1)`)]
  A name for the registry. If not passed, the folder’s name is extracted from `reg`.

- `obj` ([`R object`])
  Object to test.

- `verbose` ([`logical(1)`])
  Should test information be given in the console?

Details

Given a `Registry` the function returns a `LDABatch` object, which can be handled using the getter functions at `getJob`.

Value

A named list with entries `id` for the registry’s folder name, `jobs` for the submitted jobs' ids and its parameter settings and `reg` for the registry itself.

See Also

Other constructor functions: `LDA()`, `as.LDAREp()`
Other batch functions: `LDABatch()`, `getJob()`, `mergeBatchTopics()`

Examples

```r
batch = LDABatch(docs = reuters_docs, vocab = reuters_vocab, K = 15, chunk.size = 20)
batch

batch2 = as.LDABatch(reg = getRegistry(batch))
batch2
head(getJob(batch2))

batch3 = as.LDABatch()
batch3

### one way of loading an existing registry ###
batchtools::loadRegistry("LDABatch")
batch = as.LDABatch()
```
as.LDAREp 5

as.LDAREp  LDARep Constructor

Description

Constructs a LDARep object for given elements lda, job and id.

Usage

  as.LDAREp(...)  
  
  ## Default S3 method:  
  as.LDAREp(lda, job, id, ...)  
  
  ## S3 method for class 'LDARep'  
  as.LDAREp(x, ...)  
  
  is.LDAREp(obj, verbose = FALSE)

Arguments

...  additional arguments
lda [named list]  
List of LDA objects, named by the corresponding "job.id" (integerish). If list is unnamed, names are set.
job [data.frame or named vector]  
A data.frame or data.table with named columns (at least) "job.id" (integerish), "K", "alpha", "eta" and "num.iterations" or a named vector with entries (at least) "K", "alpha", "eta" and "num.iterations". If not passed, it is interpreted from param of each LDA.
id [character(1)]  
A name for the computation. If not passed, it is set to "LDARep".
x [named list]  
LDABatch or LDARep object.
obj [R object]  
Object to test.
verbose [logical(1)]  
Should test information be given in the console?

Details

Given a list of LDA objects the function returns a LDARep object, which can be handled using the getter functions at getJob.
Value

named list with entries id for computation’s name, jobs for the parameter settings and lda for the results themselves.

See Also

Other constructor functions: LDA(), as.LDABatch()
Other replication functions: LDAPrototype(), LDAREp(), getJob(), mergeRepTopics()

Examples

```r
res = LDAREp(docs = reuters_docs, vocab = reuters_vocab, n = 4, K = 7, num.iterations = 20)
lda = getLDA(res)

res2 = as.LDAREp(lda, id = "newName")
res2
gJob(res2)
gJob(res)

batch = LDABatch(docs = reuters_docs, vocab = reuters_vocab, n = 4, id = "TEMP", K = 30)
res3 = as.LDAREp(batch)
res3
gJob(res3)
```

dendTopics  

Topic Dendrogram

Description

Builds a dendrogram for topics based on their pairwise similarities using the cluster algorithm hclust.

Usage

dendTopics(sims, ind, method = "complete")

## S3 method for class 'TopicDendrogram'
plot(x, pruning, pruning.par, ...)

Arguments

sims  

[TopicSimilarity object or lower triangular named matrix] TopicSimilarity object or pairwise jaccard similarities of underlying topics as the sims element from TopicSimilarity objects. The topic names should be formatted as <Run X>.<Topic Y>, so that the name before the first dot identifies the LDA run.
**dendTopics**

ind [integer or character]
An integerish vector for specifying the topics taken into account. Alternatively a character vector can be passed. Then, all topics are taken for which the name contain at least one of the phrases in ind (see grepl). By default all topics are considered.

method [character(1)]
The agglomeration method. See hclust.

x an R object.

pruning [list of dendrograms]
PruningSCLOP object specifying the best possible local pruning state.

pruning.par [list]
List of parameters to mark the pruning. See section "Details" at dendTopics for default parameters. Types for marking the pruning state are "abline", "color" and "both".

... additional arguments.

**Details**

The label’s colors are determined based on their Run belonging using rainbow.hcl by default. Colors can be manipulated using labels_colors. Analogously, the labels themself can be manipulated using labels. For both the function order.dendrogram is useful.

The resulting dendrogram can be plotted. In addition, it is possible to mark a pruning state in the plot, either by color or by separator lines (or both) setting pruning.par. For the default values of pruning.par call the corresponding function on any PruningSCLOP object.

**Value**

dendrogram TopicDendrogram object (and dendrogram object) of all considered topics.

**See Also**

Other plot functions: pruneSCLOP()

Other TopicSimilarity functions: getSimilarity(), jaccardTopics()

Other workflow functions: LDARep(), SCLOP(), getPrototype(), jaccardTopics(), mergeTopics()

**Examples**

res = LDARep(docs = reuters_docs, vocab = reuters_vocab, n = 4, K = 10, num.iterations = 30)
topics = mergeTopics(res, vocab = reuters_vocab)
jacc = jaccardTopics(topics, atLeast = 2)
sim = getSimilarity(jacc)
dend = dendTopics(jacc)
dend2 = dendTopics(sim)

plot(dend)
plot(dendTopics(jacc, ind = c("Rep2", "Rep3"))))
getJob

Getter and Setter for LDARep and LDABatch

Description

Returns the job ids and its parameter set (getJob) or the (registry’s) id (getID) for a LDABatch or LDARep object. getRegistry returns the registry itself for a LDABatch object. getLDA returns the list of LDA objects for a LDABatch or LDARep object. In addition, you can specify one or more LDAs by their id(s).

setFileDir sets the registry’s file directory for a LDABatch object. This is useful if you move the registry’s folder, e.g. if you do your calculations on a batch system, but want to do your evaluation on your desktop computer.

Usage

getJob(x)

getID(x)

getRegistry(x)

getLDA(x, job, reduce, all)

setFileDir(x, file.dir)

Arguments

x [named list] LDABatch or LDARep object.

job [data.frame or integer] A data.frame or data.table with a column named "job.id" or a vector of integerish job ids.

reduce [logical(1)] If the list of LDAs contains only one element, should the list be reduced and the single (unnamed) element be returned? Default is TRUE.
getPrototype

Determine the Prototype LDA

Description

Returns the Prototype LDA of a set of LDAs. This set is given as `LDABatch` object, `LDARep` object, or as list of LDAs. If the matrix of S-CLOP scores `sclop` is passed, no calculation is needed/done.

Usage

```r
generatePrototype(...)  

# S3 method for class 'LDABatch'
generatePrototype(  
  x,  
  vocab,  
  limit.rel,  
  limit.abs,  
  atLeast,  
  progress = TRUE,  
  pm.backend,  
  ncpus,  
  keepTopics = FALSE,  
  keepSims = FALSE,  
  keepLDAs = FALSE,  
  sclop,  
  ...  
)

# S3 method for class 'LDARep'
generatePrototype(  
  x,  
  vocab,  
  limit.rel,  
  limit.abs,  
```

See Also

Other getter functions: `getSCLOP()`, `getSimilarity()`, `getTopics()`
Other replication functions: `LDAPrototype()`, `LDARep()`, `as.LDARep()`, `mergeRepTopics()`
Other batch functions: `LDABatch()`, `as.LDABatch()`, `mergeBatchTopics()`
getPrototype

atLeast, progress = TRUE, pm.backend, ncpus, keepTopics = FALSE, keepSims = FALSE, keepLDAs = FALSE, sclop, ...

## Default S3 method:
getPrototype(
  lda, vocab, id, limit.rel, limit.abs, atLeast, progress = TRUE, pm.backend, ncpus, keepTopics = FALSE, keepSims = FALSE, keepLDAs = FALSE, sclop, ...
)

Arguments

... additional arguments

x [named list] LDABatch or LDARep object.

vocab [character] Vocabularies taken into consideration for merging topic matrices. Not considered, if sclop is passed. Default is the vocabulary of the first LDA.

limit.rel [0,1] See jaccardTopics. Default is 1/500. Not considered for calculation, if sclop is passed. But should be passed determining the correct value for the resulting object.

limit.abs [integer(1)] See jaccardTopics. Default is 10. Not considered for calculation, if sclop is passed. But should be passed determining the correct value for the resulting object.

atLeast [integer(1)] See jaccardTopics. Default is 0. Not considered for calculation, if sclop is
getPrototype passed. But should be passed determining the correct value for the resulting object.

progress [logical(1)]
Should a nice progress bar be shown for the steps of mergeTopics and jaccardTopics? Turning it off, could lead to significantly faster calculation. Default ist TRUE. Not considered, if sclop is passed.

pm.backend [character(1)]
One of "multicore", "socket" or "mpi". If pm.backend is set, parallelStart is called before computation is started and parallelStop is called after. Not considered, if sclop is passed.

ncpus [integer(1)]
Number of (physical) CPUs to use. If pm.backend is passed, default is determined by availableCores. Not considered, if sclop is passed.

keepTopics [logical(1)]
Should the merged topic matrix from mergeTopics be kept? Not considered, if sclop is passed.

keepSims [logical(1)]
Should the calculated topic similarities matrix from jaccardTopics be kept? Not considered, if sclop is passed.

keepLDAs [logical(1)]
Should the considered LDAs be kept?

sclop [symmetrical named matrix]
(optional) All pairwise S-CLOP scores of the given LDA runs determined by SCLOP.pairwise. Matching of names is not implemented yet, so order matters.

lda [named list]
List of LDA objects, named by the corresponding "job.id".

id [character(1)]
A name for the computation. If not passed, it is set to "LDARep". Not considered for LDABatch or LDARep objects.

Details

While LDAPrototype marks the overall shortcut for performing multiple LDA runs and choosing the Prototype of them, getPrototype just hooks up at determining the Prototype. The generation of multiple LDAs has to be done before use of this function. The function is flexible enough to use it at at least two steps/parts of the analysis: After generating the LDAs (no matter whether as LDABatch or LDARep object) or after determing the pairwise SCLOP values.

To save memory a lot of interim calculations are discarded by default.

If you use parallel computation, no progress bar is shown.

For details see the details sections of the workflow functions.

Value
	named list with entries
getPrototype

1da  List of \texttt{LDA} objects of the determined Prototype LDA and - if \texttt{keepLDAs is TRUE} - all considered LDAs.

protoid [character(1)] Name (ID) of the determined Prototype LDA.

id [character(1)] See above.

param [named list] with parameter specifications for \texttt{limit.rel [0,1]}, \texttt{limit.abs [integer(1)]} and \texttt{atLeast [integer(1)]} See above for explanation.

topics [named matrix] with the count of vocabularies (row wise) in topics (column wise).

sims [lower triangular named matrix] with all pairwise jaccard similarities of the given topics.

wordslimit [integer] with counts of words determined as relevant based on \texttt{limit.rel} and \texttt{limit.abs}.

wordsconsidered [integer] with counts of considered words for similarity calculation. Could differ from \texttt{wordslimit}, if \texttt{atLeast} is greater than zero.

sclop [symmetrical named matrix] with all pairwise S-CLOP scores of the given LDA runs.

\textbf{See Also}

Other shortcut functions: \texttt{LDAPrototype()} 

Other PrototypeLDA functions: \texttt{LDAPrototype()}, \texttt{getSCLOP()}

Other workflow functions: \texttt{LDARep()}, \texttt{SCLOP()}, \texttt{dendTopics()}, \texttt{jaccardTopics()}, \texttt{mergeTopics()}

\textbf{Examples}

res = LDARep(docs = reuters_docs, vocab = reuters_vocab,
  n = 4, K = 10, num.iterations = 30)
topics = mergeTopics(res, vocab = reuters_vocab)
jacc = jaccardTopics(topics, atLeast = 2)
dend = dendTopics(jacc)
sclop = SCLOP.pairwise(jacc)

getPrototype(lda = getLDA(res), sclop = sclop)

proto = getPrototype(res, vocab = reuters_vocab, keepSims = TRUE,
  limit.abs = 20, atLeast = 10)
proto
getPrototype(proto) # = getLDA(proto)
getConsideredWords(proto)
# > 10 if there is more than one word which is the 10-th often word (ties)
getRelevantWords(proto)
getSCLOP(proto)
**getSCLOP**  
*Getter for PrototypeLDA*

**Description**

Returns the corresponding element of a *PrototypeLDA* object.

**Usage**

```r
getSCLOP(x)

## S3 method for class 'PrototypeLDA'
getSimilarity(x)

## S3 method for class 'PrototypeLDA'
getRelevantWords(x)

## S3 method for class 'PrototypeLDA'
getConsideredWords(x)

getMergedTopics(x)

getPrototypeID(x)

## S3 method for class 'PrototypeLDA'
getLDA(x, job, reduce = TRUE, all = FALSE)

## S3 method for class 'PrototypeLDA'
getID(x)

## S3 method for class 'PrototypeLDA'
getParam(x)
```

**Arguments**

- **x**  
  [named list]
  *PrototypeLDA* object.

- **job**  
  [data.frame or integer]
  A data.frame or data.table with a column named "job.id" or a vector of integerish job ids. Default is the (integerish) ID of the Prototype LDA.

- **reduce**  
  [logical(1)]
  If the list of LDAs contains only one element, should the list be reduced and the single (unnamed) element be returned? Default is TRUE. Not considered, if all is TRUE.

- **all**  
  [logical(1)]
  Shortcut for job: Should all stored LDAs be returned?
See Also

Other getter functions: `getJob()`, `getSimilarity()`, `getTopics()
Other PrototypeLDA functions: `LDAPrototype()`, `getPrototype()`

---

**getSimilarity**  
**Getter for TopicSimilarity**

**Description**

Returns the corresponding element of a `TopicSimilarity` object.

**Usage**

```r
getSimilarity(x)
getRelevantWords(x)
getConsideredWords(x)
```

```r
## S3 method for class 'TopicSimilarity'
getParam(x)
```

**Arguments**

`x`  
[named list]  
`TopicSimilarity` object.

**See Also**

Other getter functions: `getJob()`, `getSCLOP()`, `getTopics()`
Other TopicSimilarity functions: `dendTopics()`, `jaccardTopics()`

---

**getTopics**  
**Getter for LDA**

**Description**

Returns the corresponding element of a `LDA` object. `getEstimators` computes the estimators for phi and theta.
Usage

getTopics(x)

getAssignments(x)

getDocument_sums(x)

getDocument_expects(x)

getLog.likelihoods(x)

getParam(x)

getK(x)

getAlpha(x)

g ETA(x)

ggetNum.iterations(x)

gEstimators(x)

Arguments

x [named list]
LDA object.

Details

The estimators for phi and theta in

\[
\begin{align*}
\mathbf{w}_n^{(m)} \mid T_n^{(m)}, \phi_k & \sim \text{Discrete}(\phi_k), \\
\phi_k & \sim \text{Dirichlet}(\eta), \\
T_n^{(m)} \mid \theta_m & \sim \text{Discrete}(\theta_m), \\
\theta_m & \sim \text{Dirichlet}(\alpha)
\end{align*}
\]

are calculated referring to Griffiths and Steyvers (2004) by

\[
\hat{\phi}_{k,v} = \frac{n_k^{(v)} + \eta}{n_k + V\eta},
\]

\[
\hat{\theta}_{m,k} = \frac{n_k^{(m)} + \alpha}{N^{(m)} + K\alpha}
\]

with \( V \) is the vocabulary size, \( K \) is the number of modeled topics; \( n_k^{(v)} \) is the count of assignments of the \( v \)-th word to the \( k \)-th topic. Analogously, \( n_k^{(m)} \) is the count of assignments of the \( m \)-th text to the \( k \)-th topic. \( N^{(m)} \) is the total number of assigned tokens in text \( m \) and \( n_k \) the total number of assigned tokens to topic \( k \).
jaccardTopics

References


See Also

Other getter functions: getJob(), getSCLOP(), getSimilarity()
Other LDA functions: LDABatch(), LDARep(), LDA()

Description

Calculates the similarity of all pairwise topic combinations using a modified Jaccard Coefficient.

Usage

jaccardTopics(
  topics,
  limit.rel,
  limit.abs,
  atLeast,
  progress = TRUE,
  pm.backend,
  ncpus
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>topics</td>
<td>[named matrix] The counts of vocabularies/words (row wise) in topics (column wise).</td>
</tr>
<tr>
<td>limit.rel</td>
<td>[0,1] A relative lower bound limit for which words are taken into account. Those words are taken as relevant for a topic that have a count higher than limit.rel multiplied by the total count of the given topic. Default is 1/500.</td>
</tr>
<tr>
<td>limit.abs</td>
<td>[integer(1)] An absolute lower bound limit for which words are taken into account. All words are taken as relevant for a topic that have a count higher than limit.abs. Default is 10.</td>
</tr>
<tr>
<td>atLeast</td>
<td>[integer(1)] An absolute count of how many words are at least considered as relevant for a topic. Default is 0.</td>
</tr>
</tbody>
</table>
progress [logical(1)]
Should a nice progress bar be shown? Turning it off, could lead to significantly faster calculation. Default is TRUE. If pm.backend is set, parallelization is done and no progress bar will be shown.

pm.backend [character(1)]
One of "multicore", "socket" or "mpi". If pm.backend is set, parallelStart is called before computation is started and parallelStop is called after.

ncpus [integer(1)]
Number of (physical) CPUs to use. If pm.backend is passed, default is determined by availableCores.

Details

The modified Jaccard Coefficient $J_m$ is calculated by

$$J_m(z_i, z_j | c) = \frac{\sum_{v=1}^{V} \left\{ \frac{n_i^{(v)} > c_i \land n_j^{(v)} > c_j}{n_i^{(v)} \land n_j^{(v)}} \right\} \left( \frac{n_i^{(v)} n_j^{(v)}}{n_i^{(v)} \lor n_j^{(v)}} \right) \right\} \sum_{v=1}^{V} \left\{ \frac{n_i^{(v)} > c_i \lor n_j^{(v)} > c_j}{n_i^{(v)} \lor n_j^{(v)}} \right\} \left( \frac{n_i^{(v)} n_j^{(v)}}{n_i^{(v)} \land n_j^{(v)}} \right)$$

with $V$ is the vocabulary size, and $n_k^{(v)}$ is the count of assignments of the $v$-th word to the $k$-th topic. The threshold vector $c$ is determined by the maximum threshold of the user given lower bounds limit.rel and limit.abs. In addition, at least atLeast words per topic are considered for calculation. According to this, if there are less than atLeast words considered as relevant after applying limit.rel and limit.abs the atLeast most common words per topic are taken to determine topic similarities.

The procedure of determining relevant words is executed for each topic individually. The values wordslimit and wordsconsidered describes the number of relevant words per topic.

Value

named list with entries

sims [lower triangular named matrix] with all pairwise jaccard similarities of the given topics.

wordslimit [integer] with counts of words determined as relevant based on limit.rel and limit.abs.

wordsconsidered [integer] with counts of considered words for similarity calculation. Could differ from wordslimit, if atLeast is greater than zero.

param [named list] with parameter specifications for limit.rel [0,1], limit.abs [integer(1)] and atLeast [integer(1)] See above for explanation.

See Also

Other TopicSimilarity functions: dendTopics(), getSimilarity()

Other workflow functions: LDARep(), SCLOP(), dendTopics(), getPrototype(), mergeTopics()
Examples

```r
res = LDARep(docs = reuters_docs, vocab = reuters_vocab, n = 4, K = 10, num.iterations = 30)
topics = mergeTopics(res, vocab = reuters_vocab)
jacc = jaccardTopics(topics, atLeast = 2)
jacc

n1 = getConsideredWords(jacc)
n2 = getRelevantWords(jacc)
(n1 - n2)[n1 - n2 != 0]

sim = getSimilarity(jacc)
dim(sim)
```

---

**LDA**

**LDA Object**

Description

Constructor for LDA objects used in this package.

Usage

```r
LDA(
  x,
  param,
  assignments,
  topics,
  document_sums,
  document_expects,
  log.likelihoods
)
```

```r
as.LDA(
  x,
  param,
  assignments,
  topics,
  document_sums,
  document_expects,
  log.likelihoods
)
```

```r
is.LDA(obj, verbose = FALSE)
```
Arguments

- **x**  
  [named list]  
  Output from `lda.collapsed.gibbs.sampler`. Alternatively each element can be passed for individual results. Individually set elements overwrite elements from `x`.

- **param**  
  [named list]  
  Parameters of the function call `lda.collapsed.gibbs.sampler`. List always should contain names "K", "alpha", "eta" and "num.iterations".

- **assignments**  
  Individual element for LDA object.

- **topics**  
  Individual element for LDA object.

- **document_sums**  
  Individual element for LDA object.

- **document_expects**  
  Individual element for LDA object.

- **log.likelihoods**  
  Individual element for LDA object.

- **obj**  
  [R object]  
  Object to test.

- **verbose**  
  [logical(1)]  
  Should test information be given in the console?

Details

The functions LDA and as.LDA do exactly the same. If you call LDA on an object x which already is of the structure of an LDA object (in particular a LDA object itself), the additional arguments `param, assignments,...` may be used to override the specific elements.

Value

named list LDA object.

See Also

Other constructor functions: `as.LDABatch()`, `as.LDARep()`

Other LDA functions: `LDABatch()`, `LDARep()`, `getTopics()`

Examples

```r
res = LDARep(docs = reuters_docs, vocab = reuters_vocab, n = 1, K = 10)
lda = getLDA(res)
LDA(lda)  # does not change anything
LDA(lda, assignments = NULL)  # creates a new LDA object without the assignments element
LDA(param = getParam(lda), topics = getTopics(lda))
```
LDABatch

Description
Performs multiple runs of Latent Dirichlet Allocation on a batch system using the \texttt{batchtools-package}.

Usage
LDABatch(
  docs,
  vocab,
  n = 100,
  seeds,
  id = "LDABatch",
  load = FALSE,
  chunk.size = 1,
  resources,
  ...
)

Arguments
- \texttt{docs} \texttt{[list]}
  Documents as received from \texttt{LDAprep}.
- \texttt{vocab} \texttt{[character]}
  Vocabularies passed to \texttt{lda.collapsed.gibbs.sampler}.
- \texttt{n} \texttt{[integer(1)]}
  Number of Replications.
- \texttt{seeds} \texttt{[integer(n)]}
  Random Seeds for each Replication.
- \texttt{id} \texttt{[character(1)]}
  Name for the registry's folder.
- \texttt{load} \texttt{[logical(1)]}
  If a folder with name \texttt{id} exists: should the existing registry be loaded?
- \texttt{chunk.size} \texttt{[integer(1)]}
  Requested chunk size for each single chunk. See \texttt{chunk}.
- \texttt{resources} \texttt{[named list]}
  Computational resources for the jobs to submit. See \texttt{submitJobs}.
- ... additional arguments passed to \texttt{lda.collapsed.gibbs.sampler}. Arguments will be coerced to a vector of length \texttt{n}.
Details

The function generates multiple LDA runs with the possibility of using a batch system. The integration is done by the `batchtools-package`. After all jobs of the corresponding registry are terminated, the whole registry can be ported to your local computer for further analysis.

The function returns a `LDABatch` object. You can receive results and all other elements of this object with getter functions (see `getJob`).

Value

Named list with entries `id` for the registry’s folder name, `jobs` for the submitted jobs’ ids and its parameter settings and `reg` for the registry itself.

See Also

Other batch functions: `as.LDABatch()`, `getJob()`, `mergeBatchTopics()`
Other LDA functions: `LDARep()`, `LDA()`, `getTopics()`

Examples

```r
batch = LDABatch(docs = reuters_docs, vocab = reuters_vocab, n = 4, K = 15)
batch
getRegistry(batch)
getJob(batch)
getLDA(batch, 2)

batch2 = LDABatch(docs = reuters_docs, vocab = reuters_vocab, K = 15, chunk.size = 20)
batch2
head(getJob(batch2))
```
id = "LDARep",
pm.backend,
ncpus,
limit.rel,
limit.abs,
atLeast,
progress = TRUE,
keepTopics = FALSE,
keepSims = FALSE,
keepLDAs = FALSE,
...
)

Arguments

docs [list]
Documents as received from LDAprep.
vocabLDA [character]
Vocabularies passed to lda.collapsed.gibbs.sampler.
vocabMerge [character]
Vocabularies taken into consideration for merging topic matrices.
n [integer(1)]
Number of Replications.
seeds [integer(n)]
Random Seeds for each Replication.
id [character(1)]
Name for the computation.

pm.backend [character(1)]
One of "multicore", "socket" or "mpi". If pm.backend is set, parallelStart is called before computation is started and parallelStop is called after.
ncpus [integer(1)]
Number of (physical) CPUs to use. If pm.backend is passes, default is determined by availableCores.

limit.rel [0,1]
See jaccardTopics. Default is 1/500.

limit.abs [integer(1)]
See jaccardTopics. Default is 10.

atLeast [integer(1)]
See jaccardTopics. Default is 0.

progress [logical(1)]
Should a nice progress bar be shown for the steps of mergeTopics and jaccardTopics? Turning it off, could lead to significantly faster calculation. Default ist TRUE.

keepTopics [logical(1)]
Should the merged topic matrix from mergeTopics be kept?
keepSims [logical(1)]
Should the calculated topic similarities matrix from jaccardTopics be kept?

keepLDAs [logical(1)]
Should the considered LDAs be kept?

... additional arguments passed to \texttt{lda.collapsed.gibbs.sampler}. Arguments will be coerced to a vector of length n.

**Details**

While \texttt{LDAPPrototype} marks the overall shortcut for performing multiple LDA runs and choosing the Prototype of them, \texttt{getPrototype} just hooks up at determining the Prototype. The generation of multiple LDAs has to be done before use of \texttt{getPrototype}.

To save memory a lot of interim calculations are discarded by default.

If you use parallel computation, no progress bar is shown.

For details see the details sections of the workflow functions at \texttt{getPrototype}.

**Value**

\texttt{named list} with entries

- \texttt{lda} List of \texttt{LDA} objects of the determined Prototype LDA and - if \texttt{keepLDAs} is \texttt{TRUE} - all considered LDAs.
- \texttt{protoid} [character(1)] Name (ID) of the determined Prototype LDA.
- \texttt{id} [character(1)] See above.
- \texttt{param} \texttt{named list} with parameter specifications for limit.rel [0,1], limit.abs [integer(1)] and atLeast [integer(1)] See above for explanation.
- \texttt{topics} \texttt{named matrix} with the count of vocabularies (row wise) in topics (column wise).
- \texttt{sims} \texttt{lower triangular named matrix} with all pairwise jaccard similarities of the given topics.
- \texttt{wordslimit} [integer] with counts of words determined as relevant based on limit.rel and limit.abs.
- \texttt{wordsconsidered} [integer] with counts of considered words for similarity calculation. Could differ from wordslimit, if atLeast is greater than zero.
- \texttt{sclop} \texttt{symmetrical named matrix} with all pairwise S-CLOP scores of the given LDA runs.

**See Also**

Other shortcut functions: \texttt{getPrototype()}

Other PrototypeLDA functions: \texttt{getPrototype()}, \texttt{getSCLOP()}

Other replication functions: \texttt{LDARep()}, \texttt{as.LDARep()}, \texttt{getJob()}, \texttt{mergeRepTopics()}

Examples

```r
res = LDAPrototype(docs = reuters_docs, vocabLDA = reuters_vocab,
                   n = 4, K = 10, num.iterations = 30)
res
getPrototype(res) # = getLDA(res)
getSCLOP(res)

res = LDAPrototype(docs = reuters_docs, vocabLDA = reuters_vocab,
                   n = 4, K = 10, num.iterations = 30, keepLDAs = TRUE)
res
getLDA(res, all = TRUE)
getPrototypeID(res)
getParam(res)
```

LDARep | LDA Replications

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Performs multiple runs of Latent Dirichlet Allocation.</td>
</tr>
</tbody>
</table>

Usage

```r
LDARep(docs, vocab, n = 100, seeds, id = "LDARep", pm.backend, ncpus, ...)
```

Arguments

<table>
<thead>
<tr>
<th>docs</th>
<th>[list]</th>
<th>Documents as received from <code>LDAprep</code>.</th>
</tr>
</thead>
<tbody>
<tr>
<td>vocab</td>
<td>[character]</td>
<td>Vocabularies passed to <code>lda.collapsed.gibbs.sampler</code>.</td>
</tr>
<tr>
<td>n</td>
<td>[integer(1)]</td>
<td>Number of Replications.</td>
</tr>
<tr>
<td>seeds</td>
<td>[integer(n)]</td>
<td>Random Seeds for each Replication.</td>
</tr>
<tr>
<td>id</td>
<td>[character(1)]</td>
<td>Name for the computation.</td>
</tr>
<tr>
<td>pm.backend</td>
<td>[character(1)]</td>
<td>One of &quot;multicore&quot;, &quot;socket&quot; or &quot;mpi&quot;. If <code>pm.backend</code> is set, <code>parallelStart</code> is called before computation is started and <code>parallelStop</code> is called after.</td>
</tr>
<tr>
<td>ncpus</td>
<td>[integer(1)]</td>
<td>Number of (physical) CPUs to use. If <code>pm.backend</code> is passes, default is determined by <code>availableCores</code>.</td>
</tr>
</tbody>
</table>

additional arguments passed to `lda.collapsed.gibbs.sampler`. Arguments will be coerced to a vector of length `n`. |
mergeBatchTopics

Details

The function generates multiple LDA runs with the possibility of using parallelization. The integration is done by the parallelMap-package.

The function returns a LDARep object. You can receive results and all other elements of this object with getter functions (see getJob).

Value

named list with entries id for computation’s name, jobs for the parameter settings and lda for the results itself.

See Also

Other replication functions: LDAPrototype(), as.LDARep(), getJob(), mergeRepTopics()
Other LDA functions: LDABatch(), LDA(), getTopics()
Other workflow functions: SCLOP(), dendTopics(), getPrototype(), jaccardTopics(), mergeTopics()

Examples

res = LDARep(docs = reuters_docs, vocab = reuters_vocab, n = 4, seeds = 1:4,
       id = "myComputation", K = 7:10, alpha = 1, eta = 0.01, num.iterations = 20)
res
getJob(res)
getID(res)
getLDA(res, 4)

LDARep(docs = reuters_docs, vocab = reuters_vocab,
       K = 10, num.iterations = 100, pm.backend = "socket")

mergeBatchTopics

Merge LDA Topic Matrices

Description

Collects LDA results from a given registry and merges their topic matrices for a given set of vocabularies.

Usage

mergeBatchTopics(...)

## S3 method for class 'LDABatch'
mergeBatchTopics(x, vocab, progress = TRUE, ...)

## Default S3 method:
mergeBatchTopics(vocab, reg, job, id, progress = TRUE, ...)
mergeRepTopics

Arguments

... additional arguments
x [named list]
LDABatch object. Alternatively job, reg and id can be passed or their defaults are taken.
vocab [character]
Vocabularies taken into consideration for merging topic matrices. Default is the vocabulary of the first LDA.
progress [logical(1)]
Should a nice progress bar be shown? Turning it off, could lead to significantly faster calculation. Default ist TRUE.
reg [Registry]
Registry. See reduceResultsList.
job [data.frame or integer]
A data.frame or data.table with a column named "job.id" or a vector of integerish job ids. See reduceResultsList.
id [character(1)]
A name for the registry. If not passed, the folder’s name is extracted from reg.

Details

For details and examples see mergeTopics.

Value

named matrix with the count of vocabularies (row wise) in topics (column wise).

See Also

Other merge functions: mergeRepTopics(), mergeTopics()
Other batch functions: LDABatch(), as.LDABatch(), getJob()

mergeRepTopics  Merge LDA Topic Matrices

Description

Collects LDA results from a list of replicated runs and merges their topic matrices for a given set of vocabularies.
mergeRepTopics

Usage

mergeRepTopics(...)

## S3 method for class 'LDARep'
mergeRepTopics(x, vocab, progress = TRUE, ...)

## Default S3 method:
mergeRepTopics(lda, vocab, id, progress = TRUE, ...)

Arguments

... additional arguments

x [named list]
   LDARep object. Alternatively lda and id can be passed.

vocab [character]
   Vocabularies taken into consideration for merging topic matrices. Default is the vocabulary of the first LDA.

progress [logical(1)]
   Should a nice progress bar be shown? Turning it off, could lead to significantly faster calculation. Default ist TRUE.

lda [named list]
   List of LDA objects, named by the corresponding "job.id".

id [character(1)]
   Name for the computation. Default is "LDARep".

Details

For details and examples see mergeTopics.

Value

named matrix with the count of vocabularies (row wise) in topics (column wise).

See Also

Other merge functions: mergeBatchTopics(), mergeTopics()

Other replication functions: LDAPrototype(), LDARep(), as.LDARep(), getJob()
mergeTopics

Merge LDA Topic Matrices

Description

Generic function, which collects LDA results and merges their topic matrices for a given set of vocabularies.

Usage

mergeTopics(x, vocab, progress = TRUE)

Arguments

x  
[named list]
LDARep or LDABatch object.

vocab  
[character]
Vocabularies taken into consideration for merging topic matrices.

progress  
[logical(1)]
Should a nice progress bar be shown? Turning it off, could lead to significantly faster calculation. Default ist TRUE.

Details

This function uses the function mergeRepTopics or mergeBatchTopics. The topic matrices are transponed and cbinded, so that the resulting matrix contains the counts of vocabularies/words (row wise) in topics (column wise).

Value

named matrix with the count of vocabularies (row wise) in topics (column wise).

See Also

Other merge functions: mergeBatchTopics(), mergeRepTopics()
Other workflow functions: LDARep(), SCLOP(), dendTopics(), getPrototype(), jaccardTopics()

Examples

res = LDARep(docs = reuters_docs, vocab = reuters_vocab, n = 4, K = 10, num.iterations = 30)
topics = mergeTopics(res, vocab = reuters_vocab)
dim(topics)
length(reuters_vocab)

res = LDABatch(docs = reuters_docs, vocab = reuters_vocab, n = 4, K = 10, num.iterations = 30)
topics = mergeTopics(res, vocab = reuters_vocab)
dim(topics)
The function `SCLOP` calculates the S-CLOP value for the best possible local pruning state of a dendrogram from `dendTopics`. The function `pruneSCLOP` supplies the corresponding pruning state itself.

**Usage**

```r
pruneSCLOP(dend)
```

## S3 method for class 'PruningSCLOP'

```r
plot(x, dend, pruning.par, ...)
```

`pruning.par(pruning)`

**Arguments**

- **dend** [dendrogram]
  - TopicDendrogram (and dendrogram) object of all considered topics as the output from `dendTopics`.
- **x** an R object.
- **pruning.par** [list]
  - List of parameters to mark the pruning. See section "Details" at `dendTopics` for default parameters. Types for marking the pruning state are "abline", "color" and "both".
- **...** additional arguments.
- **pruning** [list of dendrograms]
  - PruningSCLOP object specifying the best possible local pruning state.

**Details**

For details of computing the S-CLOP values see `SCLOP`.

For details and examples of plotting the pruning state see `dendTopics`.

**Value**

list of dendrograms PruningSCLOP object specifying the best possible local pruning state.

**See Also**

- Other plot functions: `dendTopics()`
- Other SCLOP functions: `SCLOP()`
**SCLOP**

---

**reuters**

*A Snippet of the Reuters Dataset*

---

**Description**

Example Dataset from Reuters consisting of 91 articles. It can be used to familiarize with the bunch of functions offered by this package.

**Usage**

```r
data(reuters_docs)

data(reuters_vocab)
```

**Format**

- `reuters_docs` is a list of documents of length 91 prepared by `LDAPrep`.
- `reuters_vocab` is a character vector of length 2141.

**Source**


**References**


---

**SCLOP**

*Similarity/Stability of multiple sets of Objects using Clustering with Local Pruning*

---

**Description**

The function `SCLOP` calculates the S-CLOP value for the best possible local pruning state of a dendrogram from `dendTopics`. The function `pruneSCLOP` supplies the corresponding pruning state itself.

To get all pairwise S-CLOP scores of two LDA runs, the function `SCLOP.pairwise` can be used. It returns a matrix of the pairwise S-CLOP scores.

All three functions use the function `disparitySum` to calculate the least possible sum of disparities (on the best possible local pruning state) on a given dendrogram.
Usage

SCLOP(dend)

disparitySum(dend)

SCLOP.pairwise(sims)

Arguments

dend  
[dendrogram] 
Output from dendTopics.

sims  
[TopicSimilarity object or lower triangular named matrix] 
TopicSimilarity object or pairwise jaccard similarities of underlying topics as the sims element from TopicSimilarity objects. The topic names should be formatted as <Run X>,<Topic Y>, so that the name before the first dot identifies the LDA run.

Details

For one specific cluster $g$ and $R$ LDA Runs the disparity is calculated by

$$U(g) := \frac{1}{R} \sum_{r=1}^{R} |t_r^{(g)} - 1| \cdot \sum_{r=1}^{R} t_r^{(g)},$$

while $t^{(g)} = (t_1^{(g)},...,t_R^{(g)})^T$ contains the number of topics that belong to the different LDA runs and that occur in cluster $g$.

The function disparitySum returns the least possible sum of disparities $U_{\Sigma}(G^*)$ for the best possible pruning state $G^*$ with $U_{\Sigma}(G) = \sum_{g \in G} U(g) \rightarrow \min$. The highest possible value for $U_{\Sigma}(G^*)$ is limited by

$$U_{\Sigma,\max} := \sum_{g \in \tilde{G}} U(g) = N \cdot R - \frac{1}{R},$$

with $\tilde{G}$ denotes the corresponding worst case pruning state. This worst case scenario is useful for normalizing the SCLOP scores.

The function SCLOP then calculates the value

$$S-CLOP(G^*) := 1 - \frac{1}{U_{\Sigma,\max}} \cdot \sum_{g \in G^*} U(g) \in [0,1],$$

where $\sum_{g \in G^*} U(g) = U_{\Sigma}(G^*)$.

Value

SCLOP [0,1] value specifying the S-CLOP for the best possible local pruning state of the given dendrogram.

disparitySum [numeric(1)] value specifying the least possible sum of disparities on the given dendrogram.

SCLOP.pairwise [symmetrical named matrix] with all pairwise S-CLOP scores of the given LDA runs.
See Also

Other SCLOP functions: pruneSCLOP()
Other workflow functions: LDARep(), dendTopics(), getPrototype(), jaccardTopics(), mergeTopics()

Examples

res = LDARep(docs = reuters_docs, vocab = reuters_vocab, n = 4, K = 10, num.iterations = 30)
topics = mergeTopics(res, vocab = reuters_vocab)
jacc = jaccardTopics(topics, atLeast = 2)
dend = dendTopics(jacc)

SCLOP(dend)
disparitySum(dend)

SCLOP.pairwise(jacc)
SCLOP.pairwise(getSimilarity(jacc))
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