Package ‘handwriter’

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Maintainer Stephanie Reinders <srein@iastate.edu>
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Author Iowa State University of Science and Technology on behalf of its Center for Statistics and Applications in Forensic Evidence [aut, cph, fnd],
Nick Berry [aut],
Stephanie Reinders [aut, cre],
James Taylor [aut],
Felix Baez-Santiago [ctb],
Jon González [ctb]
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### about_variable

**Description**

about_variable() returns information about the model variable.

**Usage**

```r
about_variable(variable, model)
```

**Arguments**

- `variable`: A variable in the fitted model output by `fit_model()`
- `model`: A fitted model created by `fit_model()`

**Value**

Text that explains the variable

**Examples**

```r
about_variable(
  variable = "mu[1,2]",
  model = example_model
)
```

### AddLetterImages

**Description**

Pulls out letterlist as its own object, and adds the image matrix as well

**Usage**

```r
AddLetterImages(letterList, dims)
```

**Arguments**

- `letterList`: Letter list from `processHandwriting` function
- `dims`: Dimensions of the original document

**Value**

letterList with a new matrix `image` value for each sublist.
Examples

twoSent_document = list()
twoSent_document$image = twoSent
twoSent_document$thin = thinImage(twoSent_document$image)
twoSent_processList = processHandwriting(twoSent_document$thin, dim(twoSent_document$image))

dims = dim(twoSent_document$image)
withLetterImages = AddLetterImages(twoSent_processList$letterList, dims)

Description

addToFeatures

Usage

addToFeatures(FeatureSet, LetterList, vectorDims)

Arguments

FeatureSet The current list of features that have been calculated
LetterList List of all letters and their information
vectorDims Vectors with image Dims

Value

A list consisting of current features calculated in FeatureSet as well as measures of compactness, loop count, and loop dimensions

analyze_questioned_documents

Analyze Questioned Documents

Description

analyze_questioned_documents() estimates the posterior probability of writership for the questioned documents using Markov Chain Monte Carlo (MCMC) draws from a hierarchical model created with fit_model().
analyze_questioned_documents

Usage

analyze_questioned_documents(
  main_dir,
  questioned_docs,
  model,
  num_cores,
  writer_indices,
  doc_indices
)

Arguments

main_dir A directory that contains a cluster template created by `make_clustering_template()`
questioned_docs A directory containing questioned documents
model A fitted model created by `fit_model()`
num_cores An integer number of cores to use for parallel processing with the doParallel package.
writer_indices A vector of start and stop characters for writer IDs in file names
doc_indices A vector of start and stop characters for document names in file names

Value

A list of likelihoods, votes, and posterior probabilities of writership for each questioned document.

Examples

```r
## Not run:
main_dir <- "/path/to/main_dir"
questioned_docs <- "/path/to/questioned_images"
analysis <- analyze_questioned_documents(
  main_dir = main_dir,
  questioned_docs = questioned_docs,
  model = model,
  num_cores = 2,
  writer_indices = c(2, 5),
  doc_indices = c(7, 18)
)
analysis$posterior_probabilities
## End(Not run)
```
**calculate_accuracy**  

*Calculate Accuracy*

**Description**

Fit a model with `fit_model()` and calculate posterior probabilities of writership with `analyze_questioned_documents()` of a set of test documents where the ground truth is known. Then use `calculate_accuracy()` to measure the accuracy of the fitted model on the test documents. Accuracy is calculated as the average posterior probability assigned to the true writer.

**Usage**

```r
calculate_accuracy(analysis)
```

**Arguments**

- `analysis`  
  Writership analysis output by `analyze_questioned_documents`

**Value**

The model’s accuracy on the test set as a number

**Examples**

```r
# calculate the accuracy for example analysis performed on test documents and a model with 1 chain
calculate_accuracy(example_analysis)
```

```r
## Not run:
main_dir <- "/path/to/main_dir"
test_images_dir <- "/path/to/test_images"
analysis <- analyze_questioned_documents(
  main_dir = main_dir,
  questioned_docs = test_images_dir,
  model = model,
  num_cores = 2,
  writer_indices = c(2, 5),
  doc_indices = c(7, 18)
)
calculate_accuracy(analysis)
```

## End(Not run)
**cleanBinaryImage**

**Description**

Removes alpha channel from png image.

**Usage**

`cleanBinaryImage(img)`

**Arguments**

- **img**: A matrix of 1s and 0s.

**Value**

A png image with the alpha channel removed

---

**csafe**

**Cursive written word:** csafe

**Description**

Cursive written word: csafe

**Usage**

`csafe`

**Format**

Binary image matrix. 111 rows and 410 columns.

**Examples**

```r
csafe_document <- list()
csafe_document$image <- csafe
plotImage(csafe_document)
csafe_document$thin <- thinImage(csafe_document$image)
plotImageThinned(csafe_document)

processHandwriting(csafe_document$thin, dim(csafe_document$image))
```
**drop_burnin**  
*Drop Burn-In*

**Description**  
drop_burnin() removes the burn-in from the Markov Chain Monte Carlo (MCMC) draws.

**Usage**  
```r  
drop_burnin(model, burn_in)  
```

**Arguments**  
- ```model``` A list of MCMC draws from a model fit with `fit_model()`.
- ```burn_in``` An integer number of starting iterations to drop from each MCMC chain.

**Value**  
A list of data frames of MCMC draws with burn-in dropped.

**Examples**  
```r  
model <- drop_burnin(model = example_model, burn_in = 25)  
plot_trace(variable = "mu[1,2]", model = example_model)  
```

---

**example_analysis**  
*Example of writership analysis*

**Description**  
Example of writership analysis.

**Usage**  
```r  
example_analysis  
```

**Format**  
The results of `analyze_questioned_documents()` stored in a named list with 5 items:

- **graph_measurements** A data frame of that shows the writer, document name, cluster assignment, slope, principle component rotation angle, and wrapped principle component rotation angle for each training graph in each questioned documents.
- **cluster_fill_counts** A data frame of the cluster fill counts for each questioned document.
likelihoods  A list of data frames where each data frame contains the likelihoods for a questioned
document for each MCMC iteration.

votes       A list of vote tallies for each questioned document.

posterior_probabilities  A list of posterior probabilities of writership for each questioned document
and each known writer in the closed set used to train the hierarchical model.

Examples

plot_cluster_fill_counts(formatted_data = example_analysis)
plot_posterior_probabilities(analysis = example_analysis)

example_cluster_template

Example cluster template

Description

An example cluster template created with make_clustering_template(). The cluster template
was created from handwriting samples "w0016_s01_pLND_r01.png", "w0080_s01_pLND_r01.png",
"w0124_s01_pLND_r01.png", "w0138_s01_pLND_r01.png", and "w0299_s01_pLND_r01.png"
from the CSAFE Handwriting Database. The template has K=5 clusters.

Usage

example_cluster_template

Format

A list containing a single cluster template created by make_clustering_template(). The cluster
template was created by sorting a random sample of 1000 graphs from 10 training
documents into 10 clusters with a K-means algorithm. The cluster template is a named list with 16 items:

seed  An integer for the random number generator.

cluster  A vector of cluster assignments for each graph used to create the cluster template.

centers  A list of graphs used as the starting cluster centers for the K-means algorithm.

K  The number of clusters to build (10) with the K-means algorithm.

n  The number of training graphs to use (1000) in the K-means algorithm.

docnames  A vector that lists the training document from which each graph originated.

writers  A vector that lists the writer of each graph.

iters  The maximum number of iterations for the K-means algorithm (3).

changes  A vector of the number of graphs that changed clusters on each iteration of the K-means
algorithm.

outlierCutoff  A vector of the outlier cutoff values calculated on each iteration of the K-means
algorithm.
stop_reason The reason the K-means algorithm terminated.

wcd A matrix of the within cluster distances on each iteration of the K-means algorithm. More specifically, the distance between each graph and the center of the cluster to which it was assigned on each iteration.

wcss A vector of the within-cluster sum of squares on each iteration of the K-means algorithm.

Examples

# view cluster fill counts for template training documents
template_data <- format_template_data(example_cluster_template)
plot_cluster_fill_counts(template_data, facet = TRUE)

Description

Example of a hierarchical model

Usage

dexample_model

Format

A hierarchical model created by fit_model with a single chain of 100 MCMC iterations. It is a named list of 4 objects:

graph_measurements A data frame of model training data that shows the writer, document name, cluster assignment, slope, principle component rotation angle, and wrapped principle component rotation angle for each training graph.

cluster_fill_counts A data frame of the cluster fill counts for each model training document.

rjags_data The model training information from graph_measurements and cluster_fill_counts formatted for RJAGS.

tfitted_model A model fit using the rjags_data and the RJAGS and coda packages. It is an MCMC list that contains a single MCMC object.

Examples

# convert to a data frame and view all variable names
df <- as.data.frame(coda::as.mcmc(example_model$fitted_model))
colnames(df)

# view a trace plot
plot_trace(variable = "mu[1,1]", model = example_model)
# drop the first 25 MCMC iterations for burn-in
model <- drop_burnin(model = example_model, burn_in = 25)

## Not run:
# analyze questioned documents
main_dir <- /path/to/main_dir
questioned_docs <- /path/to/questioned_documents_directory
analysis <- analyze_questioned_documents(
  main_dir = main_dir,
  questioned_docs = questioned_docs
  model = example_model
  num_cores = 2
)

analysis$posterior_probabilities

## End(Not run)

---

**extractGraphs**

---

**Extract Graphs**

### Description

'\texttt{r lifecycle::badge("superseded")}'

### Usage

```
extractGraphs(source_folder = getwd(), save_folder = getwd())
```

### Arguments

- `source_folder`  
  path to folder containing .png images
- `save_folder`  
  path to folder where graphs are saved to

### Details

Development on `extractGraphs()` is complete. We recommend using `process_batch_dir()` instead.

Extracts graphs from .png images and saves each by their respective writer.

### Value

saves graphs in an rds file
Examples

```r
## Not run:
sof = "path to folder containing .png images"
saf = "path to folder where graphs will be saved to"
extractGraphs(sof, saf)

## End(Not run)
```

---

**fit_model**

*Fit Model*

**Description**

`fit_model()` fits a Bayesian hierarchical model to the model training data in `model_docs` and draws samples from the model as Markov Chain Monte Carlo (MCMC) estimates.

**Usage**

```r
fit_model(
  main_dir,    # A directory that contains a cluster template created by make_clustering_template()
  model_docs,  # A directory containing model training documents
  num_iters,   # An integer number of iterations of MCMC.
  num_chains = 1,  # An integer number of chains to use.
  num_cores,   # An integer number of cores to use for parallel processing clustering assignments. The model fitting is not done in parallel.
  writer_indices,  # A vector of the start and stop character of the writer ID in the model training file names. E.g., if the file names are writer0195_doc1, writer0210_doc1, writer0033_doc1 then writer_indices is `c(7,10)`.
  doc_indices,
  a = 2,
  b = 0.25,
  c = 2,
  d = 2,
  e = 0.5
)
```

**Arguments**

- `main_dir`  
- `model_docs`  
- `num_iters`  
- `num_chains`  
- `num_cores`  
- `writer_indices`  
- `doc_indices`  
- `a`  
- `b`  
- `c`  
- `d`  
- `e`
fit_model

doc_indices A vector of the start and stop character of the "document name" in the model training file names. This is used to distinguish between two documents written by the same writer. E.g., if the file names are writer0195_doc1, writer0195_doc2, writer0033_doc1, writer0033_doc2 then doc_indices are 'c(12,15)'.

a The shape parameter for the Gamma distribution in the hierarchical model
b The rate parameter for the Gamma distribution in the hierarchical model
c The first shape parameter for the Beta distribution in the hierarchical model
d The second shape parameter for the Beta distribution in the hierarchical model
e The scale parameter for the hyper prior for mu in the hierarchical model

Value

A list of training data used to fit the model and the fitted model

Examples

## Not run:
main_dir <- "/path/to/main_dir"
model_docs <- "path/to/model_training_docs"
questioned_docs <- "path/to/questioned_docs"

model <- fit_model(
  main_dir = main_dir,
  model_docs = model_docs,
  num_iters = 100,
  num_chains = 1,
  num_cores = 2,
  writer_indices = c(2, 5),
  doc_indices = c(7, 18)
)

model <- drop_burnin(model = model, burn_in = 25)

analysis <- analyze_questioned_documents(
  main_dir = main_dir,
  questioned_docs = questioned_docs,
  model = model,
  num_cores = 2
)

analysis$posterior_probabilities

## End(Not run)
get_clusters_batch

format_template_data  Format Template Data

Description

format_template_data() formats the template data for use with plot_cluster_fill_counts().
The output is a list that contains a data frame called cluster_fill_counts.

Usage

format_template_data(template)

Arguments

template A single cluster template created by make_clustering_template()

Value

List that contains the cluster fill counts

Examples

template_data <- format_template_data(template = example_cluster_template)
plot_cluster_fill_counts(formatted_data = template_data, facet = TRUE)

get_clusters_batch

Description

get_clusters_batch

Usage

get_clusters_batch(
    template,
    input_dir,
    output_dir,
    writer_indices,
    doc_indices,
    num_cores = 1
)
get_cluster_fill_counts

Arguments
- template: A cluster template created with `make_clustering_template`.
- input_dir: A directory containing graphs created with `process_batch_dir`.
- output_dir: Output directory for cluster assignments.
- writer_indices: Vector of start and end indices for the writer id in the graph file names.
- doc_indices: Vector of start and end indices for the document id in the graph file names.
- num_cores: Integer number of cores to use for parallel processing.

Value
A list of cluster assignments.

Examples
```r
## Not run:
# template <- readRDS('path/to/template.rds')
get_clusters_batch(template=template, input_dir='path/to/dir',
                   output_dir='path/to/dir',
                   writer_indices=c(2,5), doc_indices=c(7,18), num_cores=1)
get_clusters_batch(template=template, input_dir='path/to/dir',
                   output_dir='path/to/dir',
                   writer_indices=c(1,4), doc_indices=c(5,10), num_cores=5)
## End(Not run)
```

get_cluster_fill_counts

Description
`get_cluster_fill_counts()` creates a data frame that shows the number of graphs in each cluster for each input document.

Usage
`get_cluster_fill_counts(df)`

Arguments
df: A data frame with columns `writer`, `doc`, and `cluster`. Each row corresponding to a graph and lists the writer of that graph, the document from which the graph was obtained, and the cluster to which the graph is assigned.

Value
A dataframe of cluster fill counts for each document in the input data frame.
get_credible_intervals

Get Credible Intervals

Description

In a model created with `fit_model()` the pi parameters are the estimate of the true cluster fill count for a particular writer and cluster. The function `get_credible_intervals()` calculates the credible intervals of the pi parameters for each writer in the model.

Usage

```r
get_credible_intervals(model, interval_min = 0.025, interval_max = 0.975)
```

Arguments

- `model`: A model output by `fit_model()`
- `interval_min`: The lower bound for the credible interval. The number must be between 0 and 1.
- `interval_max`: The upper bound for the credible interval. The number must be greater than `interval_min` and must be less than 1.

Value

A list of data frames. Each data frame lists the credible intervals for a single writer.

Examples

```r
get_credible_intervals(model=example_model)
get_credible_intervals(model=example_model, interval_min=0.05, interval_max=0.95)
```
get_posterior_probabilities

Get Posterior Probabilities

Description
Get the posterior probabilities for questioned document analyzed with `analyze_questioned_documents()`.

Usage
```r
get_posterior_probabilities(analysis, questioned_doc)
```

Arguments
- **analysis**: The output of `analyze_questioned_documents()`. If more than one questioned document was analyzed with this function, then the data frame `analysis$posterior_probabilities` lists the posterior probabilities for all questioned documents. `get_posterior_probabilities()` creates a data frame of the posterior probabilities for a single questioned document and sorts the known writers from the most likely to least likely to have written the questioned document.
- **questioned_doc**: The filename of the questioned document

Value
A data frame of posterior probabilities for the questioned document

Examples
```r
get_posterior_probabilities(
    analysis = example_analysis,
    questioned_doc = "w0030_s03_pWOZ_r01"
)
```

london

Cursive written word: London

Description
Cursive written word: London

Usage
```r
london
```
Format

Binary image matrix. 148 rows and 481 columns.

Examples

```r
london_document <- list()
london_document$image <- london
plotImage(london_document)
london_document$thin <- thinImage(london_document$image)
plotImageThinned(london_document)
london_processList <- processHandwriting(london_document$thin, dim(london_document$image))
```

make_clustering_template

*Make Clustering Template*

Description

`make_clustering_template()` applies a K-means clustering algorithm to the input handwriting samples pre-processed with `process_batch_dir()` and saved in the input folder `main_dir > data > template_graphs`. The K-means algorithm sorts the graphs in the input handwriting samples into groups, or *clusters*, of similar graphs.

Usage

```r
make_clustering_template(
  main_dir,
  template_docs,
  writer_indices,
  centers_seed,
  K = 40,
  num_dist_cores = 1,
  max_iters = 25
)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>main_dir</td>
<td>Main directory that will store template files</td>
</tr>
<tr>
<td>template_docs</td>
<td>A directory containing template training images</td>
</tr>
<tr>
<td>writer_indices</td>
<td>A vector of the starting and ending location of the writer ID in the file name.</td>
</tr>
<tr>
<td>centers_seed</td>
<td>Integer seed for the random number generator when selecting starting cluster centers.</td>
</tr>
<tr>
<td>K</td>
<td>Integer number of clusters</td>
</tr>
<tr>
<td>num_dist_cores</td>
<td>Integer number of cores to use for the distance calculations in the K-means algorithm. Each iteration of the K-means algorithm calculates the distance between each input graph and each cluster center.</td>
</tr>
<tr>
<td>max_iters</td>
<td>Maximum number of iterations to allow the K-means algorithm to run</td>
</tr>
</tbody>
</table>
**Value**

List containing the cluster template

**Examples**

```r
## Not run:
main_dir <- "path/to/folder"
template_docs <- "path/to/template_training_docs"
template_list <- make_clustering_template(
  main_dir = main_dir,
  template_docs = template_docs,
  writer_indices = c(2, 5),
  K = 10,
  num_dist_cores = 2,
  max_iters = 25,
  centers_seed = 100,
)
## End(Not run)
```

---

**message**  

*Full page image of the handwritten London letter.*

**Description**

Full page image of the handwritten London letter.

**Usage**

```r
message
```

**Format**

Binary image matrix. 1262 rows and 1162 columns.

**Examples**

```r
message_document <- list()
message_document$image <- message
plotImage(message_document)

## Not run:
message_document <- list()
message_document$image <- message
plotImage(message_document)
message_document$thin <- thinImage(message_document$image)
plotImageThinned(message_document)
message_processList <- processHandwriting(message_document$thin, dim(message_document$image))
```
nature1  

*Full page image of the 4th sample (nature) of handwriting from the first writer.*

**Description**

Full page image of the 4th sample (nature) of handwriting from the first writer.

**Usage**

```
nature1
```

**Format**

Binary image matrix. 811 rows and 1590 columns.

**Examples**

```
nature1_document <- list()
nature1_document$image <- nature1
plotImage(nature1_document)

## Not run:
nature1_document <- list()
nature1_document$image <- nature1
plotImage(nature1_document)
nature1_document$thin <- thinImage(nature1_document$image)
plotImageThinned(nature1_document)
nature1_processList <- processHandwriting(nature1_document$thin, dim(nature1_document$image))

## End(Not run)
```

---

**plotImage**  

*Plot Image*

**Description**

This function plots a basic black and white image.

**Usage**

```
plotImage(doc)
```
plotImageThinned

Arguments

doc A document processed with \texttt{processDocument()} or a binary matrix (all entries are 0 or 1)

Value

ggplot plot

Examples

\begin{verbatim}
csafe_document <- list()
csafe_document$image <- csafe
plotImage(csafe_document)

## Not run:
document <- processDocument('path/to/image.png')
plotImage(document)

## End(Not run)
\end{verbatim}

plotImageThinned \hspace{1cm} \textit{Plot Thinned Image}

Description

This function returns a plot with the full image plotted in light gray and the thinned skeleton printed in black on top.

Usage

\texttt{plotImageThinned(doc)}

Arguments

doc A document processed with \texttt{processHandwriting()}

Value

ggplot plot of thinned image

Examples

\begin{verbatim}
csafe_document <- list()
csafe_document$image <- csafe
csafe_document$thin <- thinImage(csafe_document$image)
plotImageThinned(csafe_document)
\end{verbatim}
plotLetter

Description

This function returns a plot of a single graph extracted from a document. It uses the letterList parameter from the `processHandwriting()` or `processDocument()` function and accepts a single value as whichLetter. Dims requires the dimensions of the entire document, since this isn’t contained in `processHandwriting()` or `processDocument()`.

Usage

```r
plotLetter(
  doc,
  whichLetter,
  showPaths = TRUE,
  showCentroid = TRUE,
  showSlope = TRUE,
  showNodes = TRUE
)
```

Arguments

- `doc`: A document processed with `processHandwriting()` or `processDocument()`
- `whichLetter`: Single value in `1:length(letterList)` denoting which letter to plot.
- `showPaths`: Whether the calculated paths on the letter should be shown with numbers.
- `showCentroid`: Whether the centroid should be shown.
- `showSlope`: Whether the slope should be shown.
- `showNodes`: Whether the nodes should be shown.

Value

Plot of single letter.

Examples

```r
twoSent_document = list()
twoSent_document$image = twoSent
twoSent_document$thin = thinImage(twoSent_document$image)
twoSent_document$process = processHandwriting(twoSent_document$thin, dim(twoSent_document$image))
plotLetter(twoSent_document, 1)
plotLetter(twoSent_document, 4, showPaths = FALSE)
```
**plotLine**

*Plot Line*

**Description**

This function returns a plot of a single line extracted from a document. It uses the letterList parameter from the processHandwriting function and accepts a single value as whichLetter. Dims requires the dimensions of the entire document, since this isn’t contained in processHandwriting.

**Usage**

```r
plotLine(letterList, whichLine, dims)
```

**Arguments**

- `letterList` Letter list from processHandwriting function
- `whichLine` Single value denoting which line to plot - checked if too big inside function.
- `dims` Dimensions of the original document

**Value**

ggplot plot of single line

**Examples**

```r
twoSent_document = list()
twoSent_document$image = twoSent
twoSent_document$thin = thinImage(twoSent_document$image)
twoSent_processList = processHandwriting(twoSent_document$thin, dim(twoSent_document$image))

dims = dim(twoSent_document$image)
plotLine(twoSent_processList$letterList, 1, dims)
```

**plotNodes**

*Plot Nodes*

**Description**

This function returns a plot with the full image plotted in light gray and the skeleton printed in black, with red triangles over the vertices. Also called from plotPath, which is a more useful function, in general.

**Usage**

```r
plotNodes(doc, plot_break_pts = FALSE, nodeSize = 3, nodeColor = "red")
```
Arguments

- **doc**: A document processed with `processHandwriting()`. 
- **plot_break_pts**: Logical value as to whether to plot nodes or break points. `plot_break_pts=FALSE` plots nodes and `plot_break_pts=TRUE` plots break points. 
- **nodeSize**: Size of triangles printed. 3 by default. Move down to 2 or 1 for small text images. 
- **nodeColor**: Which color the nodes should be.

Value

Plot of full and thinned image with vertices overlaid.

Examples

```r
csafe_document <- list()
csafe_document$image <- csafe
csafe_document$thin <- thinImage(csafe_document$image)
csafe_document$process <- processHandwriting(csafe_document$thin, dim(csafe_document$image))
plotNodes(csafe_document)
plotNodes(csafe_document, nodeSize=6, nodeColor="black")
```

---

**plot_cluster_fill_counts**

*Plot Cluster Fill Counts*

Description

Plot the cluster fill counts for each document in `formatted_data`.

Usage

```r
plot_cluster_fill_counts(formatted_data, facet = FALSE)
```

Arguments

- **formatted_data**: Data created by `format_template_data()`, `fit_model()`, or `analyze_questioned_documents()`.
- **facet**: TRUE uses `facet_wrap` to create a subplot for each writer. FALSE plots the data on a single plot.

Value

ggplot plot of cluster fill counts
plot_cluster_fill_rates

Examples

# Plot cluster fill counts for template training documents
template_data <- format_template_data(example_cluster_template)
plot_cluster_fill_counts(formatted_data = template_data, facet = TRUE)

# Plot cluster fill counts for model training documents
plot_cluster_fill_counts(formatted_data = example_model, facet = TRUE)

# Plot cluster fill counts for questioned documents
plot_cluster_fill_counts(formatted_data = example_analysis, facet = FALSE)

plot_cluster_fill_rates

Plot Cluster Fill Rates

Description

Plot the cluster fill rates for each document in formatted_data.

Usage

plot_cluster_fill_rates(formatted_data, facet = FALSE)

Arguments

formatted_data Data created by format_template_data(), fit_model(), or analyze_questioned_documents()
facet TRUE uses facet_wrap to create a subplot for each writer. FALSE plots the data on a single plot.

Value

ggplot plot of cluster fill rates

Examples

# Plot cluster fill rates for template training documents
template_data <- format_template_data(example_cluster_template)
plot_cluster_fill_rates(formatted_data = template_data, facet = TRUE)

# Plot cluster fill rates for model training documents
plot_cluster_fill_rates(formatted_data = example_model, facet = TRUE)

# Plot cluster fill rates for questioned documents
plot_cluster_fill_rates(formatted_data = example_analysis, facet = FALSE)
plot_credible_intervals

Plot Credible Intervals

Description

Plot credible intervals for the model’s pi parameters that estimate the true writer cluster fill counts.

Usage

plot_credible_intervals(
  model,
  interval_min = 0.025,
  interval_max = 0.975,
  facet = FALSE
)

Arguments

model A model created by fit_model()
interval_min The lower bound of the credible interval. It must be greater than zero and less than 1.
interval_max The upper bound of the credible interval. It must be greater than the interval minimum and less than 1.
facet TRUE uses facet_wrap to create a subplot for each writer. FALSE plots the data on a single plot.

Value

ggplot plot credible intervals

Examples

plot_credible_intervals(model = example_model)
plot_credible_intervals(model = example_model, facet = TRUE)
plot_posterior_probabilities

Plot Posterior Probabilities

Description

Creates a tile plot of posterior probabilities of writership for each questioned document and each known writer analyzed with `analyze_questioned_documents()`.

Usage

```r
plot_posterior_probabilities(analysis)
```

Arguments

- `analysis` A named list of analysis results from `analyze_questioned_documents()`.

Value

A tile plot of posterior probabilities of writership.

Examples

```r
plot_posterior_probabilities(analysis = example_analysis)
```

plot_trace

Plot Trace

Description

Create a trace plot for all chains for a single variable of a fitted model created by `fit_model()`. If the model contains more than one chain, the chains will be combined by pasting them together.

Usage

```r
plot_trace(variable, model)
```

Arguments

- `variable` The name of a variable in the model
- `model` A model created by `fit_model()`

Value

A trace plot
Examples

plot_trace(model = example_model, variable = "pi[1,1"]
plot_trace(model = example_model, variable = "mu[2,3"]

processDocument  

Process Document

Description

Load a handwriting sample from a PNG image. Then binarize, thin, and split the handwriting into graphs.

Usage

processDocument(path)

Arguments

path  
File path for handwriting document. The document must be in PNG file format.

Value

The processed document as a list

Examples

image_path <- system.file("extdata", "phrase_example.png", package = "handwriter")
doc <- processDocument(image_path)
plotImage(doc)
plotImageThinned(doc)
plotNodes(doc)

processHandwriting  

Process Handwriting by Component

Description

The main driver of handwriting processing. Takes in an image of thinned handwriting created with thinImage() and splits the handwriting into shapes called graphs. Instead of processing the entire document at once, the thinned writing is separated into connected components and each component is split into graphs.

Usage

processHandwriting(img, dims)
Arguments

`img`  Thinned binary image created with `thinImage()`.

`dims`  Dimensions of thinned binary image.

Value

A list of the processed images.

Examples

```r
twoSent_document <- list()
twoSent_document$image <- twoSent
twoSent_document$thin <- thinImage(twoSent_document$image)
twoSent_processList <- processHandwriting(twoSent_document$thin, dim(twoSent_document$image))
```

---

**process_batch_dir  **

**Process Batch Directory**

**Description**

Process a list of handwriting samples saved as PNG images in a directory: (1) Load the image and convert it to black and white with `readPNGBinary()` (2) Thin the handwriting to one pixel in width with `thinImage()` (3) Run `processHandwriting()` to split the handwriting into parts called `edges` and place `nodes` at the ends of edges. Then combine edges into component shapes called `graphs`. (4) Save the processed document in an RDS file. (5) Optional. Return a list of the processed documents.

**Usage**

```r
process_batch_dir(input_dir, output_dir = ".", skip_docs_on_retry = TRUE)
```

**Arguments**

- `input_dir`  Input directory that contains images
- `output_dir`  A directory to save the processed images
- `skip_docs_on_retry`  Logical whether to skip documents in `input_dir` that caused errors on a previous run. The errors and document names are stored in `output_dir > problems.txt`. If this is the first run, `process_batch_list` will attempt to process all documents in `input_dir`.

**Value**

A list of processed documents.
process_batch_list

Process Batch List

Description

Process a list of handwriting samples saved as PNG images: (1) Load the image and convert it to black and white with `readPNGBinary()` (2) Thin the handwriting to one pixel in width with `thinImage()` (3) Run `processHandwriting()` to split the handwriting into parts called `edges` and place `nodes` at the ends of edges. Then combine edges into component shapes called `graphs`. (4) Save the processed document in an RDS file. (5) Optional. Return a list of the processed documents.

Usage

```
process_batch_list(images, output_dir, skip_docs_on_retry = TRUE)
```

Arguments

- `images` A vector of image file paths
- `output_dir` A directory to save the processed images
- `skip_docs_on_retry` Logical whether to skip documents in the images argument that caused errors on a previous run. The errors and document names are stored in `output_dir > problems.txt`. If this is the first run, `process_batch_list` will attempt to process all documents in the images argument.

Value

A list of processed documents

Examples

```
## Not run:
images <- c('path/to/image1.png', 'path/to/image2.png', 'path/to/image3.png')
process_batch_list(images, "path/to/output_dir", FALSE)
docs <- process_batch_list(images, "path/to/output_dir", TRUE)

## End(Not run)
```
**Description**

This function reads in and binarizes a PNG image.

**Usage**

```r
readPNGBinary(
  path,
  cutoffAdjust = 0,
  clean = TRUE,
  crop = TRUE,
  inversion = FALSE
)
```

**Arguments**

- `path`: File path for image.
- `cutoffAdjust`: Multiplicative adjustment to the K-means estimated binarization cutoff.
- `clean`: Whether to fill in white pixels with 7 or 8 neighbors. This will help a lot when thinning – keeps from getting little white bubbles in text.
- `crop`: Logical value dictating whether or not to crop the white out around the image. TRUE by default.
- `inversion`: Logical value dictating whether or not to flip each pixel of binarized image. Flipping happens after binarization. FALSE by default.

**Value**

Returns image from path. 0 represents black, and 1 represents white by default.

**Examples**

```r
image_path <- system.file("extdata", "phrase_example.png", package = "handwriter")
csafe_document <- list()
csafe_document$image = readPNGBinary(image_path)
plotImage(csafe_document)
```
read_and_process  

**Read and Process**  

**Description**  

[Superseded]  
Development on `read_and_process()` is complete. We recommend using `processDocument()`.  
`read_and_process(image_name, "document")` is equivalent to `processDocument(image_name)`.  

**Usage**  

`read_and_process(image_name, transform_output)`  

**Arguments**  

- `image_name`: The file path to an image  
- `transform_output`: The type of transformation to perform on the output  

**Value**  

A list of the processed image components  

**Examples**  

```r  
# use handwriting example from handwriter package  
image_path <- system.file("extdata", "phrase_example.png", package = "handwriter")  
doc <- read_and_process(image_path, "document")  
```

---

**rgb2grayscale**  

**Description**  

Changes RGB image to grayscale  

**Usage**  

`rgb2grayscale(img)`  

**Arguments**  

- `img`: A 3D array with slices R, G, and B  

**Value**  

`img` as a 3D array as grayscale
rgba2rgb

Description
Removes alpha channel from png image.

Usage
rgba2rgb(img)

Arguments
img A 3-d array with slices R, G, B, and alpha.

Value
img as a 3D array with alpha channel removed

SaveAllLetterPlots

Description
This function returns a plot of a single graph extracted from a document. It uses the letterList parameter from the processHandwriting() or processDocument() function and accepts a single value as whichLetter. Dims requires the dimensions of the entire document, since this isn’t contained in processHandwriting() or processDocument(). Requires the magick package.

Usage
SaveAllLetterPlots(letterList, filePaths, dims, bgTransparent = TRUE)

Arguments
letterList Letter list from processHandwriting() or processDocument() function
filePaths Folder path to save images to
dims Dimensions of original document
bgTransparent Logical determines if the image is transparent

Value
No return value.
See Also

image_transparent
image_write
image_read

Examples

twoSent_document = list()
twoSent_document$image = twoSent
twoSent_document$thin = thinImage(twoSent_document$image)
twoSent_processList = processHandwriting(twoSent_document$thin, dim(twoSent_document$image))

dims = dim(twoSent_document$image)
## Not run:
withLetterImages = AddLetterImages(twoSent_processList$letterList, "path/to/save", dims)
## End(Not run)

Description

This function returns a vector of locations for black pixels in the thinned image. Thinning done using Zhang - Suen algorithm.

Usage

thinImage(img)

Arguments

img A binary matrix of the text that is to be thinned.

Value

A thinned, one pixel wide, image.
**twoSent**

Two sentence printed example handwriting

**Description**

Two sentence printed example handwriting

**Usage**

twoSent

**Format**

Binary image matrix. 396 rows and 1947 columns

**Examples**

```r
twoSent_document <- list()
twoSent_document$image <- twoSent
plotImage(twoSent_document)

## Not run:
twoSent_document <- list()
twoSent_document$image <- twoSent
plotImage(twoSent_document)
twoSent_document$thin <- thinImage(twoSent_document$image)
plotImageThinned(twoSent_document)
twoSent_processList <- processHandwriting(twoSent_document$thin, dim(twoSent_document$image))

## End(Not run)
```

**whichToFill**

whichToFill

**Description**

Finds pixels in the plot that shouldn’t be white and makes them black. Quick and helpful cleaning for before the thinning algorithm runs.

**Usage**

whichToFill(img)

**Arguments**

- **img** A binary matrix.
Value

A cleaned up image.
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