### hca

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#### Abstract

hca is research software that does various versions of non-parametric topic models using Gibbs sampling including LDA, HDP-LDA, NP-LDA, all with/without burstiness modelling. Various diagnostics, "document completion" testing and coherence measurements with PMI are also supported. The code runs on multi-core getting about 50% efficiency with 8 cores.

## 1 Synopsis

hca [-?] [-?Arg] DataStem RepStem

## 2 Description

hca reads the collection of files with stem DataStem that form the input set of data. When checkpointing, or at termination, the output is written to files with stem RepStem. On restart with the -r0 option, some of these are also read initially to restore the previous state. A log of the run is reported to stderr if the -e option is used. By default, the log goes to RepStem.log.

The programme is research software, so not all options or combinations of options work correctly. Note that in this release, all the more experimental features have been stripped, so this release contains only moderately well tested components. Note also, this is not intended to be code that others could easily modify. In order to get performance, to provide all the features, and to run multi-core, the code is quite convoluted. Researchers seeking simple code they can experiment and modify themselves should request a cutdown version from the author.

The programme runs a Gibbs sampler for a variety of non-parametric topic models including HDP-LDA. The model selected has three parts:

alpha: this is the prior on topic vector (theta) for each document. LDA has a simple symmetric Dirichlet with parameter alpha and the vector has dimension T (the number of topics).

**beta:** this is the prior on word vector (phi) for each topic. LDA has a simple symmetric Dirichlet with parameter beta and the vector has dimension W (the number of words).

**burst:** this is the burstiness component which has a document specific variant of the word vector for each topic. This is not used by default.

These parts are set using the **-S**, **-A** and **-B** options.

There are various model parameters, notably the discount and concentrations for the different Pitman-Yor processes in the model. These are usually sampled using Adaptive Rejection Sampling. They are also kept bounded using constraints coded into the util/dimdir.h header file. So when a parameter fails to change, check the sampling by increasing verbosity and you may observe the value tries to change but doesn't.

The programme uses generalised second order Stirling numbers with the library extracted from *libstb* version 1.8 released at https://github.com/wbuntine/libstb. This is initialised

with predefined bounds on the tables, and these can be modified with the -N option. This should be used for collections with larger numbers of documents, but its best to run first and on error, increase the bounds.

## 3 Options

Options have a single letter followed by a possible single argument. Options are grouped under the following functions: setting of hyperparameters, controlling sampling of hyperparameters, general control, and testing and reports

### 3.1 Setting up the model and hyperparameters

For these, theta is a vector for each document representing the topic proportions and phi is a vector for each topic representing the word proportions. The task of the system is to estimate these. The vector theta and its various priors and parameters is the Alpha side and the vector phi and its various priors and parameters is the Beta side. All the scalar parameters can be set using the -Svar=value option and thereafter fixed using the -Fvar option or by default sampled using adaptive rejection sampling.

- **-Avalue** Use a symmetric Dirichlet prior on theta using this value for each dimension. The value must be a positive float.
- -Atype A second version of the -A option with a string argument. It defines a distribution on theta and its prior mean (a vector) alpha of type as follows:
  - hdp theta is modelled with a Dirichlet Process with mean alpha and concentrationb, and alpha is modelled with a symmetric Dirichlet with concentration b0.
  - hpdd theta is modelled with a Pitman-Yor Process with mean alpha, discount a and concentration b, and alpha is modelled with a (truncated) GEM with discount a0 and concentration b0. This is the default.
  - pdp theta is modelled with a Pitman-Yor Process with mean alpha, discount a and concentration b, and alpha is uniform. This is not hierarchical because alpha is constant.
- **-B**value Use a symmetric Dirichlet prior with this value for each dimension. The value must be a positive float. Warning: the value stored internally and printed is the total of this over the number of words W.
- -Btype Second form of the -B option. Use a prior beta of type "hdp" "hpdd" or "pdp". Similar to the -A option.
  - hdp phi is modelled with a Dirichlet Process with mean beta and concentration bw and beta is modelled with a Dirichlet with concentration bw0 by default symmetric (a uniform mean) or its mean can be set with the -u option.
  - hpdd phi is modelled with a Pitman-Yor Process with mean beta, discount aw and concentration bw, and beta is modelled with a (truncated) GEM and discount aw0 and concentration bw0. This is the default.
  - pdp phi is modelled with a Pitman-Yor Process with mean beta, discount aw and concentration bw, and beta is by default uniform, or it can be set with the -u option. This is not hierarchical because beta is constant.
- -Svar=value Set variable var to float value, where var can be one of:
  - a discount parameter for the non-parametric distribution on the theta, topic distribution per document.

- **b** concentration parameter for the non-parametric distribution on theta, the topic distribution per document.
- a0 discount parameter for the non-parametric distribution on alpha, the prior for theta
- **b0** concentration parameter for the non-parametric distribution on alpha, the prior for theta
- **aw** discount parameter for the non-parametric distribution on phi, word distribution per topic.
- **bw** concentration parameter for the non-parametric distribution on phi, word distribution per topic.
- aw0 discount parameter for the non-parametric distribution on beta, prior for phi.
- **bw0** concentration parameter for the non-parametric distribution on beta, prior for phi.
- ad discount parameter for burstiness.
- **bdk** concentration parameter for burstiness, a constant initially but subsequent sampling will allow a different value per topic.
- -ufile the value for the beta vector is given by the text file. It should contain W floats, W being the number of words.

### 3.2 Controlling sampling of hyperparameters

- -Dcycles, start Start sampling alpha of the symmetric Dirichlet for alpha after start cycles and then repeat every cycles cycles.
- -Ecycles, start Start sampling beta of the symmetric Dirichlet for beta after start cycles and then repeat every cycles cycles.
- **-F**var Fix the variable var where it takes the value **alpha**, **beta** or one of the arguments to the **-S** option.
- -Gvar,cycles,start Sample the variable var where it takes the value alpha, beta or one of the arguments to the -S option. The start and cycles integers are used as for the -D option.

#### 3.3 General control

- -ccycles Do a checkpoint every this many cycles. This saves the output statistics and the parameter file adequate to do a restart with  $-r\theta$  option.
- -Ccycles Stop after this many cycles. Default is 100.
- -ddots For really big batches of data, print a "." every dots documents within a single cycle.
- -e Reroute logging to the stderr.
- -fformat Read input data from data formatted according to the type format. Data is expected to come from an input file with name DataStem.Suff where Suff is an appropriate suffix. These are given with Input Files below. Allowed formats are: ldac, witdit, docword, bag and lst.
- **-K**topics Set T the maximum number of topics. Default is 10.
- -Mmaxtime Quit early when total training time exceeds this many seconds.
- -NmaxN,maxT Set maximum for the Stirling number tables to count maxN and table count maxT. Default is 10000,1000. On collections with more than 20k documents, can require more.

-qthreads If compiled with threading, enables this many threads. Default is 1.

-roffset Restart. Currently must use offset equal to "0" for a normal restart.

-rphi Second version of the -r option using the string "phi" as the argument. Restart but now fix the word by topic matrix to the previous value saved at RepStem.phi, and the beta side is held constant and not sampled. Can significantly speed up testing or querying sometimes.

**-sseed** Initialise the random number seed.

-v Up verbosity by one increment. Starts at zero and currently understands 0-3.

-x Enable use of exclude topics with -Q.

### 3.4 Testing and reports

-h*Hold,arg* Do document completion testing on the test set. There are three styles of document completion implemented given by the Hold parameter.

doc every arg-th word is held out in estimating the latent variables (like theta) for the document and used instead for testing of perplexity. That is, words at document positions arg-1, 2\*arg-1, etc.

dict every arg-th word in the dictionary is held out in estimating and used for testing. So if a word has dictionary index arg-1, 2\*arg-1, etc., it is held out.

fract then the fract proportion at the tail of the document is held out. The initial proportion is used in estimating.

-lDiag, cycles, start Do a run-time estimation of the diagnostic Diag starting after the start cycle and then taking the estimate every cycles cycle. Diagnostics are:

Estimate topic sparsity in the theta matrix for the words given in DataStem.smap. Results placed in RepStem.smap. The report gives "topic/weight" for topics including the word.

**prog** How often to do the standard diagnostic reports (default is every 5-th cycle).

phi Estimate the word probability vector for each topic. Stored in the RepStem.phi file.

**testprob** Estimate the topic probability vector for each test document. Stored in the RepStem.testprob file.

theta Estimate the topic probability vector for each training document. Stored in the RepStem.theta file.

Note that for <code>Diag="testprob"</code> or "theta", an additional argument after <code>start</code> giving the lowerbound on probabilities. Lower ones are dropped.

**-L**Diag,cycles,start Do a diagnostic estimate Diag after all Gibbs sampling is complete. Sampling of the estimate starts after the start cycle and goes for a total of cycles cycles (including the starting ones). Diagnostics are:

class Estimate class probabilities with "true" classes given in DataStem.class and then produce confusion matrix for the test data. Output to files DataStem.cnfs and DataStem.pcnfs.

like Estimate likelihood/perplexity on the test set using the standard (biased) document likelihood, or document completion if the -h option is used. Can also be instigated during run-time with the -P option.

-oscore Scoring rule to pick top words for printing. Methods are 'count', 'idf', 'cost' and 'phi'. Default is 'idf'.

- **-O** Report log likelihood, not log perplexity. Both are done in base 2.
- Report topic coherency in the log file, and save results in the parameter file. This requires a DataStem.pmi or DataStem.pmi.gz file exist in the right format. This can be created with the mkmat.pl and cooc2pmi.pl scripts in the scripts directory of the release. The format is a simple sparse matrix form with lines of the form "N M PMI" for word indices (offset by 0) N and M and PMI value. WARNING: the file DataStem.pmi needs to be specifically built for the dataset as the word indices must align.
- **-Psecs** Calculate test perplexity (using document completion) every interval in **secs** seconds. If Gibbs cycles are long, will report only after the cycle finishes.
- -Qnres, file submit list queries given in the file, and return nres results for each. Must use the -rphi option with a pre-estimated phi matrix (for efficiency).
- -tsize Specify size of training set. It takes the first size entries in the data set. Default is all the set minus the test data.
- -Tfilestem Specify a separate test set. Assumes the same suffix as for DataStem. When using this, be sure to fix the training set size with -tsize if you do not want to train on the full data set.
- **-T**size Specify size of test set. It takes the **size** entries immediately following the training set. Default is zero. This option can be confused with the above, so do not use filestems that are just integers.
- -V load the dictionary from the DataStem.tokens file for use in reporting. It has one token per line. Must have at least level two verbosity or this is ignored.
- -X Instigate report on naive Bayes classification using the topic model and classes given in DataStem.class file. The report is a confusion matrix to file RepStem.tbyc built on the training data.

# 4 Input Files

The following files provide details about the dataset. The filenames are constructed by adding a suffix to the data stem. The data (document+word) format itself can be one of four different formats and is specified with the **-f** option.

DataStem.class Class index for each document, one per line. Optional file used with some reports instigated by -X or -L class options.

DataStem.dit+DataStem.wit Simple document index and word index files, both indices offset by 1, one index per line. Words in the collection are listed by document. The DataStem.dit file gives the document index, and the corresponding line in DataStem.wit gives the dictionary index.

DataStem.docword This format appears in some UCI data sets at <a href="http://archive.ics.uci.edu/ml/datasets/Bag+of+Words">http://archive.ics.uci.edu/ml/datasets/Bag+of+Words</a>. Word indices offset by 1.

DataStem.ldac Standard LdaC format. Word indices to the dictionary are offset by 0.

DataStem.smap A list of word indices (offset by 0) about which one wants a sparsity report generated. The report is instigated by the -lsp option.

DataStem.tokens tokens/words in the dictionary, one per line. Optional file used with  $-\mathbf{V}$  option. DataStem.txtbag default bag or list format for linkBags(1) command of text-bags. Word indices offset by 0.

The various output files such as RepStem.par (Parameter and dimension output file) are also read on restart with the  $-\mathbf{r}\theta$  option.

## 5 Output Files

The following files are output when the system checkpoints or at the end of the run. These are built by adding a suffix to the report stem, RepStem. The first set of files are:

RepStem.beta If a constant beta vector is specified using the -u option, this saves the value, for possible use in a restart.

RepStem.cnfs+RepStem.pcnfs Best prediction and probability vector confusion matrices built on the test data with the -Lclass command.

RepStem.log Log file created if -e option not used.

RepStem.par Parameter and dimensions file in simple "var = value" format. These are detailed in the next section.

RepStem.phi The Phi matrix written as a binary file: first W (dictionary size), T (topics), C (sample size) are written as 32 bit integers and then the full Phi matrix as native floats with W as the minor index. Only generated with appropriate use of the -lphi option.

RepStem.smap Optional sparsity report on the word indices listed in DataStem.smap. The report is instigated by the -lsp option.

RepStem.tbyc Optional confusion matrix printed when the -X option is used.

RepStem.top A simple text report giving the top word indices for each topic. If a hierarchical model in use, then the "-1" topic is for the base distribution of words. Word indices are offset from 0.

RepStem.theta Estimated topic probabilities for each training document written in a simple sparse form. The class index ("-1" or "+1" for binary classes, otherwise just the index) is also added if it exists. Topic indices are offset by 0. Only generated with appropriate use of the -ltheta option.

RepStem.testprob Like the -ltheta option but for the test documents. Only generated with appropriate use of the -ltestprob option.

The second set of files gives the actual runtime statistics. Output matrices are in a simple readable sparse vector format the same as the DataStem.docword format.

RepStem.ndt Document by topic counts.

RepStem.nwt Word by topic counts.

RepStem.tdt Document by topic table counts if the Alpha side of the model is non-parametric.

RepStem.twt Word by topic table counts if the Beta side of the model is non-parametric.

RepStem.zt With no burstiness, gives topic index (offset by 0), one per line. With burstiness, gives one "z,r" per line where "z" is the topic index (offset by 0) and "r" is the burst table indicator, which is 1 if the word contributes to standard LDA statistics, and 0 if burstiness modelling says the word is a burst so does not contribute to LDA statistics.

These files along with RepStem.par are input on a restart using  $-r\theta$ .

#### 6 The Parameter File

The parameter file has the following dimensions:

N – number of words in the full collection, summed over all documents.

NT – number of words in the training set, summed over all training documents.

W – number of words in the dictionary.

D – number of documents in total.

TRAIN – number of documents to train on, is always the the first ones in the file.

TEST – number of documents to test on, is always the the last ones in the file.

T – maximum number of topics.

ITER – number of major cycles made last.

In addition, the float parameters allowed to be specified with the **-F** and **-G** options are also given. Finally, the type of model for alpha as specified by the **-A** option is coded in the PYalpha variable. It is 0 if the mode is a symmetric Dirichlet, the LDA default. It is 1 for hdp, 2 for hpdd and 3 for pdp. Likewise for the PYbeta variable and the **-B** option.

## 7 Examples

### 7.1 Basic running

These examples work as is on late model Linux, Macs and Windows. However, you need to replace the executable, hca, by the system dependent one, from the install directory where the data/directory is. For instance, on Windows that might be hca/hca.exe.

Run basic HDP-LDA with parameter fitting on the full dataset and no testing, sending logging to stderr.

```
hca -v -e -K20 -B0.001 -C100 data/ch c1
```

The command line means:

"-v": use level one verbosity;

"-e": send the log file to stderr, not to "c1.log";

"-**K20**": use 20 topics (the truncation level);

"-B0.001": use a symmetric Dirichlet prior on word probability vectors (i.e., topics) with this value;

"-C100": run for 100 cycles;

"data.ch": stem for data file;

"c1": stem for results file.

The parameters as they are sampled will be printed on a line beginning wth "Par:". At the end, the top 20 words will be printed and the final training perplexity printed. This is based on the posterior probability, not word probability estimates.

If you have the multicore version compiled, and you have an 8-core CPU, then run with 8 threads:

```
hca -v -e -K20 -B0.001 -C100 -q8 data/ch c1
```

"-q8": use 8 threads for Gibbs sampling.

This just repeats the above but should be faster!

### 7.2 Restart and print words for the topics

Restart from checkpoint after the previous run but run no cycles. Input the tokens from data/ch.tokens, and print top 10 words for each topic.

The command line means:

"-v -v": use level two verbosity;

"-r0": restart from document 0, i.e., on all documents;

"-V": input the tokens from "data/ch.tokens," and print top 10 words for each topic. Note must have at least level two verbosity;

"-C0": do not run any cycles, just do reporting.

This will have lines like:

Topic 15 (p=5.88%, ws=71.8%, ds=69.4%) words =, museum, salonika, byzantine

which means the topic is observed in 5.88% of word occurrences, word sparsity for the topic is 71.8% (71.8% of the words have zero data for this topic), and document sparsity for the topic is 69.4% (69.4% of the documents have zero data for this topic).

### 7.3 Produce sparsity mappings and document topic probabilities

Restart again and build a topic probability vector for each document, as well as sparsity mappings for the words in data/ch.smap file. This you need to create/edit ahead of time. This must run a number of cycles because the estimates are done during the Gibbs sampling.

"-lsp2,1": sample for sparsity every 2nd cycle starting at the 1st.

"-ltheta,2,1,0.001": sample probabilities per document (theta) every 2nd cycle starting at the 1st. Only report probabilities above 0.001.

"-C20": sampling done for 20 cycles.

Now view the sparsity report at c1.smap and the topic probabilities at c1.theta, and the values saved in the parameter file c1.par. Again, add the -q8 option to run this faster, with 8 threads (if you have 8 cores).

Read lines in the sparsity report, c1.smap, as follows:

```
--(12): 5/2.6 14/1.3 19/219.0 perp=1.149816
```

Token with index 12 occurs in topics 5, 14 and 19. It has 2.6 counts (its a sample average so counts can be a fraction) in topic 5 and 219.0 in topic 19. The log-2 entropy of the topic distribution based on these counts is 1.149816.

Read lines in the topic probabilities report, c1.theta, as follows:

```
15: 16:0.006699 17:0.088948 19:0.902410
```

Document 15 has 0.006699 for topic 15 and 0.902410 for topic 17. The three topics only add to 0.998057 because some smaller topics must have been dropped.

#### 7.4 Run with testing

Run basic LDA with training and parameter fitting on a subset and testing on the final 100 documents. The training subset is the full dataset minus the test data. Logging now to c1.log. Checkpoint every 20 cycles (note, we usually only do this for cycles taking over 10 minutes each).

hca -v -K20 -C100 -c20 -T100 data/ch c1

Again run multi-core with -q8 if needed.

"-c20": do a checkpoint with any reporting every 20 cycles.

"-T100": use the last 100 documents for testing, so the first (datasetsize-100) are used for training. The documents must be ordered so the test data is at the end. Alternatively, a file stem can be given if test data is in a separate file, so loaded from there.

View the end of the log file to get the test perplexity, which is printed after "log\_2(test perpML)". Now restart but use document completion (every 4th word) to get perplexity, with no more Gibbs cycles. Without -h the default is to use a standard likelihood calculation so will be biased.

hca -v -e -r0 -C0 -hdoc,4 -T100 data/ch c1

"-hdoc,4": hold out every 4-th word in the document.

"-T100": the test set size must be repeated, since it is not reloaded with the restart.

View the end of the log file to get the test perplexity, which is printed after "log\_2(test perpHold)". Note it is also recorded in the parameter file.

Restart and record the PMI and the classification details on test data.

hca -v -v -V -r0 -C0 -Llike,0,0 -X -p -T100 data/ch c1

"-Llike,0,0": prevent it doing test likelihood calculations, which are potentially slow on larger data sets.

"-X": load up class data from data/ch.clas file to enable classification on test data.

"-p": initiate PMI calculation.

The PMI data has a value printed for each topic as well as a final average. It bases its calculations on the matrix data/ch.pmi.gz created explicitly for this test set. For other datasets, you will need to download prepared PMI matrices from the project homepage. The PMI output in the log file is:

```
PMI :: 0:2.051 1:3.172 2:5.170 3:0.353 ...
PMI = 1.257
```

The first line gives the PMI per topic. The second line gives the mean PMI.

#### 7.5 Burstiness

The burstiness version significantly improves everything. Our best bet, currently, is to run with optimisation of the hyperparameters:

```
hca -v -v -e -K20 -C100 -Sbdk=100 -Sad=0.5 data/ch c1
```

"-Sbdk=100": burstiness document concentration is different for every topic. This initialises all of them to 100. Default has no burstiness.

"-Sad=0.5": burstiness document discount set to 0.5, same for all topics. Default is zero.

The initial discount for the bursty topics is 0.5. The concentration we set quite high initially, and these will be sampled separately with each topic in batches, so bdk is a vector in the parameter file. The hyperparameter sampling slows it down quite a bit but seems to make a significant difference. Unused topics sometimes get a very low concentration. Alternatively, fix the burstiness discount with  $-\mathbf{F}ad$  and continue sampling burstiness concentration only, which is quite a lot faster.

### 8 Errors

There is some error reporting on failure.

If the software quits during a run on larger data with an error message like:

```
S_V(N,M,A) tagged 'XXX' hit bounds (BN,BM)
```

for integers N,M and label XXX then you need to increase the bounds BN,BM. If only the BM bound is violated, then set BN to its default (10000) and increase BM to, say 5000 (your choice) with the option -N10000,5000. The BN bound should only be violated when the Beta side table is affected, in which case the label will be XXX="SB, topicXword PYP". Now increase BN to, say 30000 (your choice) with the option -N30000,1000, leaving BM as it was.

For other errors, please report to the maintainer. Best bet is to recompile with "MYDEBUG=g" set in the Makefile and possibly run under a memory checker to get details of the reason for the crash.

### 9 See Also

The command linkBags(1) is available from text-bags at https://github.com/wbuntine/text-bags and was previously released at http://mloss.org. The extended library libstb, parts of which are included, is available individually from http://mloss.org also at https://github.com/wbuntine/libstb

### 10 Version

This programme is version 0.5 of June 4, 2014. This incorporates parts of the library *libstb* version 1.8 also of June 4, 2014.

# 11 License and Copyright

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