## A.2 SphinxTrain: Executables

### A.2.1 agg_seg

#### Tool Description

Description:
agg_seg sample accumulate feature vectors and used it for quantizing the vector space. This functionality is very useful in S2 training initialization. Not all features vectors are used. They are sampled using option -stride.
There are many other options of this command is currently obsolete. Please type -example yes to get a working argument list.

#### Example

Example:
agg_seg -segdmpdirs segdmpdir -segdmpfn dumpfile -segtype all -ctlfn ctl -cepdir cepdir -cepext .mfc -ceplen 13 -stride 10

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-segdmpdirs** (Default Value : NO DEFAULT VALUE)
  Description: Segment dump directories

- **-segdmpfn** (Default Value : NO DEFAULT VALUE)
  Description: Segment dump file

- **-segidxfn** (Default Value : NO DEFAULT VALUE)
  Description: Segment index into the dump file.

- **-segtype** (Default Value : st)
  Description: Type of segments to dump. all,st,phn

- **-cntfn** (Default Value : NO DEFAULT VALUE)
  Description: Per id count file

- **-ddcodeext** (Default Value : xcode)
  Description: Extension of the VQ 2nd difference cepstrum files

- **-lsnfn** (Default Value : NO DEFAULT VALUE)
  Description: Lexical transcript file (contains all utts in ctl file)

- **-sentdir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of sent (lexical transcript) files

- **-sentext** (Default Value : NO DEFAULT VALUE)
  Description: Extension of sent (lexical transcript) files

- **-ctlfn** (Default Value : NO DEFAULT VALUE)
  Description: The control file name (enumerates utts in corpus)

- **-mllrctlfn** (Default Value : NO DEFAULT VALUE)
  Description: Lists the MLLR transforms for each utterance

- **-mllrdir** (Default Value : NO DEFAULT VALUE)
  Description: Directory for MLLR matrices

- **-nskip** (Default Value : 0)
  Description: The number of utterances to skip in the control file

- **-runlen** (Default Value : -1)
  Description: The number of utterances to process after skipping

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition file containing all the triphones in the corpus. State/transition matrix definitions are ignored.

- **-ts2cbfn** (Default Value : NO DEFAULT VALUE)
  Description: Tied state to codebook mapping file (may be '.semi.' or '.cont.')

- **-cb2mllrfn** (Default Value : NO DEFAULT VALUE)
  Description: codebook to MLLR class mapping file (may be '.1cls.')

- **-dictfn** (Default Value : NO DEFAULT VALUE)
  Description: Lexicon containing all the words in the lexical transcripts.

- **-fdictfn** (Default Value : NO DEFAULT VALUE)
  Description: Lexicon containing all the filler words in the lexical transcripts.

- **-segdir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of the state segmentation files

- **-segext** (Default Value : v8_seg)
  Description: Extension of the state segmentation files

- **-ccodedir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of the VQ cepstrum files

- **-ccodeext** (Default Value : ccode)
  Description: Extension of the VQ cepstrum files

- **-dcodedir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of the VQ difference cepstrum files

- **-dcodeext** (Default Value : d2code)
  Description: Extension of the VQ cepstrum files

- **-pcodedir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of the VQ power files

- **-pcodeext** (Default Value : p3code)
  Description: Extension of the VQ power files

- **-ddcodedir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of the VQ 2nd difference cepstrum files

- **-ddcodeext** (Default Value : xcode)
  Description: Extension of the VQ 2nd difference cepstrum files

- **-cepdir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of the cepstrum files

- **-cepext** (Default Value : mfc)
  Description: Extension of the cepstrum files

- **-ceplen** (Default Value : 13)
  Description: # of coefficients per cepstrum frame

- **-agc** (Default Value : max)
  Description: The type of automatic gain control to do max—emax

- **-cmn** (Default Value : current)
  Description: The do cepstral mean normalization based on current—prior utterance(s)

- **-varnorm** (Default Value : no)
  Description: Normalize utterance by its variance

- **-silcomp** (Default Value : none)
  Description: Do silence compression based on current—prior utterance

- **-feat** (Default Value : NO DEFAULT VALUE)
  Description: Feature set to compute

- (Default Value : 4s_12c_24d_3p_12d)
  Description: d

- (Default Value : 1s_12c_12d_3p_12d)
  Description: d

- **-cachesz** (Default Value : 200)
  Description: Feature cache size in Mb

- **-stride** (Default Value : 1)
  Description: Take every -stride'th frame when producing dmp

### A.2.2 bldtree

#### Tool Description

Description:
Given a set of questions. Build decision tree for a set of feature of a particular phone. By default, decision tree are not built for filler phones and the phone tagged with SIL. One very confusing parameters of this tool is -stwt, if you are training a n-state HMM, you need to specify n values after this flag.

#### Example

bld_tree -treefn tree -moddeffn mdef -mixwfn mixw -meanfn mean -varfn
var -psetfn questions -stwt 1.0 0.05 0.01 -state 0 -ssplitmin 1 -ssplitmax 7 -ssplitthr 1e-10 -csplitmin 1 -csplitmax 2000 -csplitthr 1e-10 -cntthresh 10

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-treefn** (Default Value : NO DEFAULT VALUE)
  Description: Name of output tree file to produce

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition file of the discrete models

- **-ts2cbfn** (Default Value : .semi.)
  Description: The type of models to build trees on

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: means file for tree building using continuous HMMs

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: variances file for tree building using continuous HMMs

- **-varfloor** (Default Value : 0.00001)
  Description: The minimum variance

- **-cntthresh** (Default Value : 0.00001)
  Description: Ignore all states with counts less than this

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: PDF's for tree building using semicontinuous HMMs

- **-psetfn** (Default Value : NO DEFAULT VALUE)
  Description: phone set definitions for phonetic questions

- **-phone** (Default Value : NO DEFAULT VALUE)
  Description: Build trees over n-phones having this base phone

- **-state** (Default Value : NO DEFAULT VALUE)
  Description: Build tree for this state position. E.g. For a three state HMM, this value can be 0,1 or 2. For a 5 state HMM, this value can be 0,1,2,3 or 4, and so on

- **-mwfloor** (Default Value : 1e-4)
  Description: Mixing weight floor for tree building

- **-stwt** (Default Value : NO DEFAULT VALUE)
  Description: Weights on neighboring states, This flag needs a string of numbers equal to the number of HMM-states

- **-ssplitthr** (Default Value : 8e-4)
  Description: Simple node splitting threshold

- **-ssplitmin** (Default Value : 1)
  Description: Minimum of simple tree splits to do.

- **-ssplitmax** (Default Value : 5)
  Description: The maximum number of bifurcations in the simple tree before it is used to build complex questions.

- **-csplitthr** (Default Value : 8e-4)
  Description: Compound node splitting threshold

- **-csplitmin** (Default Value : 1)
  Description: Minimum # of compound tree splits to do

- **-csplitmax** (Default Value : 100)
  Description: Minimum # of compound tree splits to do

### A.2.3 bw

#### Tool Description

Description:

Strictly speaking, bw only implements the first-part of the Baum-Welch

algorithm. That is it go through forward and backward algortihm and

collect the necessary statistics for parameter estimation.

The advantage of this architecture is that researcher can easily write

programs to do parameter estimation and they have no need to tweak the

huge and usually difficult Baum-Welch algorithm.

In terms of functionality, one important thing you need to know is option

-part and -npart. They can allow you to split the training into N equal parts

Say, if there are M utterances in your control file, then this

will enable you to run the training separately on each (M/N)th

part. This flag may be set to specify which of these parts you want to

currently train on. As an example, if your total number of parts (-npart) is 3,

-part can take one of the values 1,2 or 3.

To control the speed of the training, -abeam (control alpha search)

and -bbeam (control beta search) can be used to control the searching

time. Notice that if the beams are too small, the path may not reach

the end of the search and results in estimation error

Too many lost path may also cause training set likelihood not unable to increase

Several options allow the user to control the behaviour of bw such

that silence or pauses can be taken care. For example. One could use

-sildelfn to specify periods of time which was assume to be silence.

One could also use -sildel and -siltag to specify a silence and allow

them to be optionall deleted.

Finally, one can use the viterbi training mode of the code. Notice though, the code is not always tested by CMU's researcher

I also included the following paragraph from Rita's web page. I largely adapted from

here and I think it is a pretty good wrap-up of the convergence issues "bw is an iterative

re-estimation process, so you have to run many passes of the

Baum-Welch re-estimation over your training data. Each of these

passes, or iterations, results in a slightly better set of models for

the CI phones. However, since the objective function maximized in each

of theses passes is the likelihood, too many iterations would

ultimately result in models which fit very closely to the training

data. you might not want this to happen for many reasons. Typically,

5-8 iterations of Baum-Welch are sufficient for getting good estimates

of the CI models. You can automatically determine the number of

iterations that you need by looking at the total likelihood of the

training data at the end of the first iteration and deciding on a

"convergence ratio" of likelihoods. This is simply the ratio of the

total likelihood in the current iteration to that of the previous

iteration. As the models get more and more fitted to the training data

in each iteration, the training data likelihoods typically increase

monotonically. The convergence ratio is therefore a small positive

number. The convergence ratio becomes smaller and smaller as the

iterations progress, since each time the current models are a little

less different from the previous ones. Convergence ratios are data and

task specific, but typical values at which you may stop the Baum-Welch

iterations for your CI training may range from 0.1-0.001. When the

models are variance-normalized, the convergence ratios are much

smaller."

**Example**

Example:

Command used to train continuous HMM

(Beware, this only illustrates how to use this command, for detail on how to tune it, please consult the manual. )

bw

-moddeffn mdef -ts2cbfn .cont.

-mixwfn mixw -tmatfn tmatn -meanfn mean -varfn var

-dictfn dict -fdictfn fillerdict

-ctlfn control_files

-part 1 -npart 1

-cepdir feature_dir -cepext mfc

-lsnfn transcription

-accumdir accumdir

-abeam 1e-200 -bbeam 1e-200

-meanreest yes -varreest yes

-tmatreest yes -feat 1s_12c_12d_3p_12dd

-ceplen 13

If yo want to do parallel training for N machines. Run N trainers with

-part 1 -npart N

-part 2 -npart N

.

.

-part N -npart N

**Command-line Argument Description**

*Usage: [options]*

- (Default Value : NO DEFAULT VALUE)
  Description: [Switch] [Default] [Description]

- (Default Value : NO DEFAULT VALUE)
  Description: -help no Shows the usage of the tool

- (Default Value : NO DEFAULT VALUE)
  Description: -example no Shows example of how to use the tool

- (Default Value : NO DEFAULT VALUE)
  Description: -moddeffn The model definition file for the model inventory to train

- (Default Value : NO DEFAULT VALUE)
  Description: -tmatfn The transition matrix parameter file name

- (Default Value : NO DEFAULT VALUE)
  Description: -mixwfn The mixture weight parameter file name

- (Default Value : NO DEFAULT VALUE)
  Description: -meanfn The mean parameter file name

- (Default Value : NO DEFAULT VALUE)
  Description: -varfn The var parameter file name

- (Default Value : NO DEFAULT VALUE)
  Description: -mwfloor 0.00001 Mixing weight smoothing floor

- (Default Value : NO DEFAULT VALUE)
  Description: -tpfloor 0.0001 Transition probability smoothing floor

- (Default Value : NO DEFAULT VALUE)
  Description: -varfloor 0.00001 The minimum variance

- (Default Value : NO DEFAULT VALUE)
  Description: -topn 4 Compute output probabilities based this number of top scoring densities.

- (Default Value : NO DEFAULT VALUE)
  Description: -dictfn The content word dictionary

- (Default Value : NO DEFAULT VALUE)
  Description: -fdictfn The filler word dictionary (e.g. SIL, SILb, ++COUGH++)

- (Default Value : NO DEFAULT VALUE)
  Description: -ctlfn The training corpus control file

- (Default Value : NO DEFAULT VALUE)
  Description: -nskip The number of utterances to skip at the beginning of a control file

- (Default Value : NO DEFAULT VALUE)
  Description: -runlen -1 The number of utterances to process in the (skipped) control file

- (Default Value : NO DEFAULT VALUE)
  Description: -part Identifies the corpus part number (range 1..NPART)

- (Default Value : NO DEFAULT VALUE)
  Description: -npart Partition the corpus into this many equal sized subsets

- (Default Value : NO DEFAULT VALUE)
  Description: -cepext mfc The cepstrum file extension

- (Default Value : NO DEFAULT VALUE)
  Description: -cepdir The cepstrum data root directory

- (Default Value : NO DEFAULT VALUE)
  Description: -segext v8_seg State segmentation file extension

- (Default Value : NO DEFAULT VALUE)
  Description: -segdir State segmentation file root directory

- (Default Value : NO DEFAULT VALUE)
  Description: -sentdir The sentence transcript file directory

- (Default Value : NO DEFAULT VALUE)
  Description: -sentext sent The sentence transcript file extension

- (Default Value : NO DEFAULT VALUE)
  Description: -lsnfn The corpus word transcript file

- (Default Value : NO DEFAULT VALUE)
  Description: -accumdir A path where accumulated counts are to be written.

- (Default Value : NO DEFAULT VALUE)
  Description: -ceplen 13 The length of the input feature (e.g. MFCC) vectors

- (Default Value : NO DEFAULT VALUE)
  Description: -agc max The type of automatic gain control to do max—emax

- (Default Value : NO DEFAULT VALUE)
  Description: -cmn current The do cepstral mean normalization based on current—prior utterance(s)

- (Default Value : NO DEFAULT VALUE)
  Description: -varnorm no Variance Normalize?

- (Default Value : NO DEFAULT VALUE)
  Description: -silcomp none Do silence compression based on current—prior utterance

- (Default Value : NO DEFAULT VALUE)
  Description: m. -sildel no Allow optional silence deletion in the Baum-Welch algorithm or the Viterbi algorithm.

- (Default Value : NO DEFAULT VALUE)
  Description: -siltag SIL Specify the tag of silence, by default it is <sil>.

- (Default Value : NO DEFAULT VALUE)
  Description: -abeam 1e-100 Evaluate alpha values subject to this beam

- (Default Value : NO DEFAULT VALUE)
  Description: -bbeam 1e-100 Evaluate beta values (update

reestimation sums) subject to this beam

- (Default Value : NO DEFAULT VALUE)
  Description: -varreest yes Reestimate variances

- (Default Value : NO DEFAULT VALUE)
  Description: -meanreest yes Reestimate means

- (Default Value : NO DEFAULT VALUE)
  Description: -mixwreest yes Reestimate mixing weights

- (Default Value : NO DEFAULT VALUE)
  Description: -tmatreest yes Reestimate transition probability matrices

- (Default Value : NO DEFAULT VALUE)
  Description: -spkrxfrm A speaker transform to use for SAT modelling

- (Default Value : NO DEFAULT VALUE)
  Description: -mllrmult no Reestimate multiplicative term of MLLR adatpation of means

- (Default Value : NO DEFAULT VALUE)
  Description: -mllradd no Reestimate shift term of MLLR adaptation of means

- (Default Value : NO DEFAULT VALUE)
  Description: -ts2cbfn Tied-state-to-codebook mapping file name

- (Default Value : NO DEFAULT VALUE)
  Description: -feat This argument selects the derived feature computation to use.

- (Default Value : NO DEFAULT VALUE)
  Description: -timing yes Controls whether profiling information is displayed

- (Default Value : NO DEFAULT VALUE)
  Description: -viterbi no Controls whether Viterbi training is done

- (Default Value : NO DEFAULT VALUE)
  Description: -2passvar no Reestimate variances based on prior means

- (Default Value : NO DEFAULT VALUE)
  Description: -sildelfn File which specifies frames of background 'silence' to delete

- (Default Value : NO DEFAULT VALUE)
  Description: -cb2mllrfn Codebook-to-MLLR-class mapping file name

- (Default Value : NO DEFAULT VALUE)
  Description: ted-spthresh 0.0 State posterior probability floor for reestimation. States below this are not counted

- (Default Value : NO DEFAULT VALUE)
  Description: -maxuttlen 0 Maximum # of frames for an utt ( 0 => no fixed limit )

- (Default Value : NO DEFAULT VALUE)
  Description: -ckptintv Checkpoint the reestimation sums every -chkptintv utts

### A.2.4 cp_parm

#### Tool Description

Description:

Copy parameters such as means and variances from one model to another model.

You need to specify a "copy operation file" which each operation looks like

this

dest_idx1 src_idx1

dest_idx2 src_idx2

dest_idx3 src_idx3

.

.

.

For example, the first line will instruct cp_param copy src model index 1 to

destionation model index 1.

This tool is still under heavy development at 20040807

#### Example

Example:

This example copy mean from a single file from the source file to 5 mean vector in

th destination file.

First you need to prepare a file like this

0 0

1 0

2 0

3 0

4 0

Lets call it cp_op

cp_parm -cpopsfn cp_op

-igaufn globalmean

-ncbout 5

-ogaufn out.means

-feat [Your feature type]

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-cpopsfn** (Default Value : NO DEFAULT VALUE)
  Description: Copy operation file name

- **-imixwfn** (Default Value : NO DEFAULT VALUE)
  Description: Input mixing weight file

- **-omixwfn** (Default Value : NO DEFAULT VALUE)
  Description: Output mixing weight file

- **-nmixwout** (Default Value : NO DEFAULT VALUE)
  Description: # of mixing weight arrays in the output file

- **-itmatfn** (Default Value : NO DEFAULT VALUE)
  Description: Input transition matrix file

- **-otmatfn** (Default Value : NO DEFAULT VALUE)
  Description: Output transition matrix file

- **-ntmatout** (Default Value : NO DEFAULT VALUE)
  Description: # of transition matrices in the output file

- **-igaufn** (Default Value : NO DEFAULT VALUE)
  Description: Input Gaussian density parameter file

- **-ogaufn** (Default Value : NO DEFAULT VALUE)
  Description: Output Gaussian density parameter file

- **-ncbout** (Default Value : NO DEFAULT VALUE)
  Description: # of codebooks in the output file

- **-feat** (Default Value : c[1..L-1]d[1..L-1]c[0]d[0]dd[0]dd[1..L-1])
  Description: Feature set to use

### A.2.5 delint

#### Tool Description

Description: (copied from Rita's web page.)

Deleted interpolation is the final step in creating semi-continuous models. The output of deleted interpolation are semi-continuous models

in sphinx-3 format. These have to be further converted to sphinx-2 format, if you want to use the SPHINX-II decoder.

Deleted interpolation is an iterative process to interpolate between CD and CI mixture-weights to reduce the effects of overfitting. The data are divided into two sets, and the data from one set are used to estimate the optimal interpolation factor between CI and CD models trained from the other set. Then the two data sets are switched and this procedure is repeated using the last estimated interpolation factor as an initialization for the current step. The switching is continued until the interpolation factor converges.

To do this, we need *two* balanced data sets. Instead of the actual data, however, we use the Bauim-Welch buffers, since the related math

is convenient. we therefore need an *even* number of buffers that can

be grouped into two sets. DI cannot be performed if you train using only one buffer. At least in the final iteration of the training, you must perform the training in (at least) two parts. You could also do this serially as one final iteration of training AFTER BW has converegd, on a non-lsf setup.

Note here that the norm executable used at the end of every Baum-Welch

iteration also computes models from the buffers, but it does not require an even number of buffers. BW returns numerator terms and denominator terms for the final estimation, and norm performs the actual division. The number of buffers is not important, but you would

need to run norm at the end of EVERY iteration of BW, even if you did the training in only one part. When you have multiple parts norm sums

up the numerator terms from the various buffers, and the denominator

terms, and then does the division.

### Example

delint -accumdirs accumdir -moddeffn mdef -mixwfn mixw -cilambda 0.9 -feat c/1..L-1/,d/1..L-1/,c/0/d/0/dd/0/,dd/1..L-1/ -ceplen 13 -maxiter 4000

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: The model definition file name

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The mixture weight parameter file name

- **-accumdirs** (Default Value : NO DEFAULT VALUE)
  Description: A path where accumulated counts are to be read.

- **-cilambda** (Default Value : 0.9)
  Description: Weight of CI distributions with respect to uniform distribution

- **-maxiter** (Default Value : 100)
  Description: max # of iterations if no lambda convergence

- **-feat** (Default Value : 4s_12c_24d_3p_1)
  Description: 2dd feature stream definition

- **-ceplen** (Default Value : 13)
  Description: Input feature vector length (e.g. MFCC)

### A.2.6 dict2tri

#### Tool Description

Description:
find the triphone list from the dictionary

#### Example

Example :
dict2tri -dictfn dict -basephnfn phonelist -btwtri yes

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-dictfn** (Default Value : NO DEFAULT VALUE)
  Description: Dictionary file name

- **-basephnfn** (Default Value : NO DEFAULT VALUE)
  Description: Base phone list file name

- **-btwtri** (Default Value : yes)
  Description: Compute between-word triphone set

### A.2.7 inc_comp

#### Tool Description

Description:

Increase the number of mixture of a continuous HMM. Notice that option

-ninc actually means the finally number of mixture one wants to

obtain. Usually, it is the power of two. You are also recommended to

split the number of mixture from 1 -> 2 -> 4 -> 8 -> and so on.

#### Example

Example :

inc_comp

-ninc 16

-dcountfn mixture_weights

-inmixwfn mixture_weights

-outmixwfn out_mixture_weights

-inmeanfn means

-outmeanfn out_means

-invarfn variance

-outvarfn out_variance

-ceplen 13

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-ninc** (Default Value : 1)
  Description: The # of densities to split

- **-inmixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The weight file for all N den/mix

- **-outmixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The output mixing weight file name w/ N+NINC density weights/mixture

- **-inmeanfn** (Default Value : NO DEFAULT VALUE)
  Description: The source mean file w/ N means

- **-outmeanfn** (Default Value : NO DEFAULT VALUE)
  Description: The new mean file w/ N+NINC means

- **-invarfn** (Default Value : NO DEFAULT VALUE)
  Description: The source variance file w/ N means

- **-outvarfn** (Default Value : NO DEFAULT VALUE)
  Description: The new variance file w/ N+NINC means

- **-dcountfn** (Default Value : NO DEFAULT VALUE)
  Description: The density counts for the N source den/mix

- **-ceplen** (Default Value : 13)
  Description: The length of the input feature (e.g. MFCC) vectors

- **-feat** (Default Value : NO DEFAULT VALUE)
  Description: Defines the acoustic feature set.

### A.2.8 init_gau

#### Tool Description

Description: (Copy from Rita's web manual) To initialize the means and variances, global values of

these parameters are first estimated and then copied into appropriate positions in the parameter files. The global mean is computed using all the vectors you have in your feature files. This is usually a very large number, so the job is divided into many parts. At this stage you tell the Sphinx how many parts you want it to divide this operation into (depending on the computing facilities you have) and the Sphinx "accumulates" or gathers up the vectors for each part separately and writes it into an intermediate buffer on your machine. The executable init_gau is used for this purpose.

#### Example

Example:

init_gau -accumdir accumdir -ctlfn controlfn -part 1 -npart 1 -cepdir cepdir -feat 1s_12c_12d_3p_12dd -ceplen 13

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition file for the single density HMM's to initialize

- **-ts2cbfn** (Default Value : NO DEFAULT VALUE)
  Description: Tied-state-to-codebook mapping file

- **-accumdir** (Default Value : NO DEFAULT VALUE)
  Description: Where to write mean/var counts

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: Mean file for variance initialization

- **-ctlfn** (Default Value : NO DEFAULT VALUE)
  Description: Control file of the training corpus

- **-nskip** (Default Value : NO DEFAULT VALUE)
  Description: # of lines to skip in the control file

- **-runlen** (Default Value : NO DEFAULT VALUE)
  Description: # of lines to process in the control file (after any skip)

- **-part** (Default Value : NO DEFAULT VALUE)
  Description: Identifies the corpus part number (range 1..NPART)

- **-npart** (Default Value : NO DEFAULT VALUE)
  Description: Partition the corpus into this many equal sized subsets

- **-lsnfn** (Default Value : NO DEFAULT VALUE)
  Description: All word transcripts for the training corpus

(consistent order w/ -ctlfn!)

- **-dictfn** (Default Value : NO DEFAULT VALUE)
Description: Dictionary for the content words

- **-fdictfn** (Default Value : NO DEFAULT VALUE)
Description: Dictionary for the filler words

- **-segdir** (Default Value : NO DEFAULT VALUE)
Description: Root directory of the training corpus state segmentation files.

- **-segext** (Default Value : v8_seg)
Description: Extension of the training corpus state segmentation files.

- **-scaleseg** (Default Value : no)
Description: Scale existing segmentation to fit new parameter stream length.

- **-cepdir** (Default Value : NO DEFAULT VALUE)
Description: Root directory of the training corpus cepstrum files.

- **-cepext** (Default Value : mfc)
Description: Extension of the training corpus cepstrum files.

- **-silcomp** (Default Value : none)
Description: Controls silence compression.

- **-cmn** (Default Value : current)
Description: Controls cepstral mean normalization.

- **-varnorm** (Default Value : no)
Description: Controls variance normalization.

- **-agc** (Default Value : max)
Description: Controls automatic gain control.

- **-feat** (Default Value : NO DEFAULT VALUE)
Description: Controls which feature extraction algorithm is used.

- **-ceplen** (Default Value : 13)
  Description: # of components in cepstrum vector

### A.2.9 init_mixw

#### Tool Description

Description:

Initialization of mixture weight

#### Example

Example:

init_mixw -src_moddeffn src_moddeffn -src_ts2cbfn .semi. -src_mixwfn

src_mixwfn -src_meanfn src_meanfn -src_varfn src_varfn -src_tmatfn

src_tmatfn -dest_moddeffn dest_moddeffn -dest_ts2cbfn

.semi. -dest_mixwfn dest_mixwfn -dest_me anfn dest_meanfn -dest_varfn

dest_varfn -dest_tmatfn dest_tmatfn -feat

c/1..L-1/,d/1..L-1/,c/0/d/0/dd/0/,dd/1..L-1/ -ceplen 13

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-src_moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: The source model definition file name

- **-src_ts2cbfn** (Default Value : NO DEFAULT VALUE)
  Description: The source state definition file name

- **-src_mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The source mixing weight file name

- **-src_meanfn** (Default Value : NO DEFAULT VALUE)
  Description: The source mean file name

- **-src_varfn** (Default Value : NO DEFAULT VALUE)
  Description: The source variance file name

- **-src_tmatfn** (Default Value : NO DEFAULT VALUE)
  Description: The source transition matrix file name

- **-dest_moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: The destination model definition file name

- **-dest_ts2cbfn** (Default Value : NO DEFAULT VALUE)
  Description: The destination state definition file name

- **-dest_mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The destination mixing weight file name

- **-dest_meanfn** (Default Value : NO DEFAULT VALUE)
  Description: The destination mean file name

- **-dest_varfn** (Default Value : NO DEFAULT VALUE)
  Description: The destination variance file name

- **-dest_tmatfn** (Default Value : NO DEFAULT VALUE)
  Description: The destination transition matrix file name

- **-feat** (Default Value : 1s_12c_12d_3p_1)
  Description: 2dd Derived feature computation to use

- **-ceplen** (Default Value : 13)
  Description: Size of the input feature vector length

### A.2.10 kmeans_init

#### Tool Description

Description:
Using the segment dump file generated by external software such as agg_seg to initilaize the model. It performs k-mean clustering to create the initial means and variances for s2 hmms. This is an important process of initialization of s2 training.

#### Example

Example :

kmeans_init -gthobj single -stride 1 -ntrial 1 -minratio 0.001

-ndensity 256 -meanfn $outhmm/means - varfn$outhmm/variances -reest no

-segdmpdirs $segdmpdir - segdmpfn$dumpfile -ceplen 13

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-segdir** (Default Value : NO DEFAULT VALUE)
  Description: Directory containing the state segmentations

- **-segext** (Default Value : v8_seg)
  Description: Extention of state segmentation files

- **-omoddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition of output models

- **-dmoddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition used for observation dump

- **-ts2cbfn** (Default Value : NO DEFAULT VALUE)
  Description: Tied-state-to-codebook mapping file

- **-lsnfn** (Default Value : NO DEFAULT VALUE)
  Description: LSN file name (word transcripts)

- **-dictfn** (Default Value : NO DEFAULT VALUE)
  Description: Dictionary file name

- **-fdictfn** (Default Value : NO DEFAULT VALUE)
  Description: Filler word dictionary file name

- **-cbcntfn** (Default Value : NO DEFAULT VALUE)
  Description: File containing # of times a codebook ID appears in the corpus

- **-maxcbobs** (Default Value : NO DEFAULT VALUE)
  Description: Cluster at most this many observations per codebook

- **-maxtotobs** (Default Value : NO DEFAULT VALUE)
  Description: Cluster at most approximately this many observations over all codebooks

- **-featsel** (Default Value : NO DEFAULT VALUE)
  Description: The feature stream ( 0, 1, ...) to select

- **-ctlfn** (Default Value : NO DEFAULT VALUE)
  Description: The training corpus control file

- **-cepext** (Default Value : mfc)
  Description: The cepstrum file extension

- **-cepdir** (Default Value : NO DEFAULT VALUE)
  Description: The cepstrum data root directory

- **-ceplen** (Default Value : 13)
  Description: The length of the input feature (e.g. MFCC) vectors

- **-agc** (Default Value : max)
  Description: The type of automatic gain control to do max—emax

- **-cmn** (Default Value : current)
  Description: The do cepstral mean normalization based on current—prior utterance(s)

- **-varnorm** (Default Value : no)
  Description: Normalize utterance by its variance

- **-silcomp** (Default Value : none)
  Description: Do silence compression based on current—prior utterance

- **-feat** (Default Value : 1s_12c_12d_3p_1)
  Description: 2dd This argument selects the derived feature computation to use.

- **-segdmpdirs** (Default Value : NO DEFAULT VALUE)
  Description: segment dmp directories

- **-segdmpfn** (Default Value : NO DEFAULT VALUE)
  Description: segment dmp file

- **-segidxfn** (Default Value : NO DEFAULT VALUE)
  Description: segment dmp index file

- **-fpcachesz** (Default Value : 3000)
  Description: # of file descriptors to cache for observation dmp files

- **-obscachesz** (Default Value : 92)
  Description: # of Mbytes cache to use for observations

- **-ndensity** (Default Value : NO DEFAULT VALUE)
  Description: # of densities to initialize per tied state per feature

- **-ntrial** (Default Value : 5)
  Description: random initialized K-means: # of trials of k-means w/ random initialization from within corpus

- **-minratio** (Default Value : 0.01)
  Description: K-means: minimum convergence ratio, (p_squerr - squerr) / p_squerr

- **-maxiter** (Default Value : 100)
  Description: K-means: maximum # of iterations of updating to apply

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: Output file for mixing weights

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: Output file for means

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: Output file for variances

- **-method** (Default Value : rkm)
  Description: Initialization method. Options: rkm — fnkm

- **-reest** (Default Value : yes)
  Description: Reestimate states according to usual definitions

assuming vit seg.

- **-niter** (Default Value : 20)
  Description: # of iterations of reestimation to perform per state

- **-gthobj** (Default Value : state)
  Description: Gather what kind of obj state, phn, frame

- **-stride** (Default Value : 32)
  Description: Gather every -stride'th frame

- **-runlen** (Default Value : NO DEFAULT VALUE)
  Description: # of utts to process from ctl file

- **-tsoff** (Default Value : 0)
  Description: Begin tied state reestimation with this tied state

- **-tscnt** (Default Value : NO DEFAULT VALUE)
  Description: Reestimate this many tied states (if available)

- **-tsrngfn** (Default Value : NO DEFAULT VALUE)
  Description: The range of tied states reestimated expressed as offset,count

- **-vartiethr** (Default Value : 0)
  Description: Tie variances if # of observations for state exceed this number

### A.2.11 make_quests

#### Tool Description

Description:
This is an implementation of Dr. Rita Singh's automatic question generation. (Copied from Rita's comment) The current algorithm clusters CI distributions using a hybrid bottom-up top-down clustering algorithm to build linguistic questions for decision trees.
(From Arthur : I need to do some tracing before understand it what's the internal of the code)

#### Example

Example:
make_quest -moddeffn mdef -meanfn mean -varfn var -mixwfn mixwfn -npermute 8 -niter 1 -qstperstt 20 -tempfn temp -questfn questions

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition file of the ci models

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: means file for tree building using continuous HMMs

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: variances file for tree building using continuous HMMs

- **-varfloor** (Default Value : 1.0e-08)
  Description: The minimum variance

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: PDF's for tree building using semicontinuous HMMs

- **-npermute** (Default Value : 6)
  Description: The minimum variance

- **-niter** (Default Value : 0)
  Description: Number of iterations

- **-qstperstt** (Default Value : 8)
  Description: something per state

- **-tempfn** (Default Value : /tmp/TEMP.QUESTS)
  Description: File to write temprorary results to (important)

- **-questfn** (Default Value : NO DEFAULT VALUE)
  Description: File to write questions to

- **-type** (Default Value : NO DEFAULT VALUE)
  Description: HMM type

### A.2.12 mixw_interp

#### Tool Description

Description:

A routine that provides and ad-hoc way of speaker adaptation by mixture

weight interpolation. SD and SI model's mixture weight are first

determined and they act as an inputs of this program. The output

is the interpolated mixture weight.

The interpolation is controlled by the value lambda (-sillambda)

#### Example

Example:

mixw_interp -SImixwfn si_mixw -SDmixwfn sd_mxiw -outmixwfn final_mixw -SIlambad 0.7

### Command-line Argument Description

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-SImixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The SI mixture weight parameter file name

- **-SDmixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The SD mixture weight parameter file name

- **-outmixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The output interpolated mixture weight parameter file name

- **-SIlambda** (Default Value : 0.5)
  Description: Weight given to SI mixing weights

### A.2.13 mk_flat

#### Tool Description

Description:

(Copied from Rita's web page)

In flat-initialization, all mixture weights are set to be equal for all states, and all state transition probabilities are set to be equal. Unlike in continuous models, the means and variances of the codebook Gaussians are not given global values, since they are already estimated from the data in the vector quantization step. To flat-initialize the mixture weights, each component of each mixture-weight distribution of each feature stream is set to be a number equal to 1/N, where N is the codebook size. The mixture_weights

and transition_matrices are initialized using the executable mk_flat

#### Example

Example:

mk_flat -moddeffn CFS3.ci.mdef -topo CFS3.topology -mixwfn mixture_weights

-tmatfn transition_matrices -nstream 1 -ndensity 1

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III model definition file name

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: An output SPHINX-III mixing weight file name

- **-topo** (Default Value : NO DEFAULT VALUE)
  Description: A template model topology matrix file

- **-tmatfn** (Default Value : NO DEFAULT VALUE)
  Description: An output SPHINX-III transition matrix file name

- **-nstream** (Default Value : 4)
  Description: Number of independent observation streams

- **-ndensity** (Default Value : 256)
  Description: Number of densities per mixture density

### A.2.14 mk_mdef_gen

#### Tool Description

Description:

(Copied from Rita's comment and I think it is a pretty good description.)

Multi-function routine to generate mdef for context-independent

training, untied training, and all-triphones mdef for state tying.

Flow:

if (triphonelist) make CI phone list and CD phone list

if alltriphones mdef needed, make mdef

if (rawphonelist) Make ci phone list,

if cimdef needed, make mdef

Generate alltriphones list from dictionary

if alltriphones mdef needed, make mdef

if neither triphonelist or rawphonelist quit

Count triphones and triphone types in transcript

Adjust threshold according to min-occ and maxtriphones

Prune triphone list

Make untied mdef

#### Example

Example:

Create CI model definition file

mk_mdef_gen -phnlstfn phonefile -ocimdef ci_mdeffile -n_state_pm 3

Create untied CD model definition file

mk_mdef_gen -phnlstfn rawphonefile -dictfn dict -fdictfn filler_dict

-lsnfn transcription -ountiedmdef untie_mdef -n_state_pm 3

-maxtriphones 10000

Create tied CD model definition file

mk_mdef_gen -phnlstfn rawphone -oalltphnmdef untie_mdef -dictfn dict

-fdictfn filler_dict -n_state_pm 3.

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-phnlstfn** (Default Value : NO DEFAULT VALUE)
  Description: List of phones

- **-inCImdef** (Default Value : NO DEFAULT VALUE)
  Description: Input CI model definition file.

- (Default Value : If)
  Description: nored

- (Default Value : NO DEFAULT VALUE)
  Description:

- **-triphnlstfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III triphone file name.

- (Default Value : If)
  Description: incimdef ignored

- (Default Value : NO DEFAULT VALUE)
  Description:

- **-inCDmdef** (Default Value : NO DEFAULT VALUE)
  Description: Input CD model definition file.

- (Default Value : If)
  Description: phnlstfn, -incimdef ignored

- (Default Value : NO DEFAULT VALUE)
  Description:

- **-dictfn** (Default Value : NO DEFAULT VALUE)
  Description: Dictionary

- **-fdictfn** (Default Value : NO DEFAULT VALUE)
  Description: Filler dictionary

- **-lsnfn** (Default Value : NO DEFAULT VALUE)
  Description: Transcripts file

- **-n_state_pm** (Default Value : 3)
  Description: No. of states per HMM

- **-ocountfn** (Default Value : NO DEFAULT VALUE)
  Description: Output phone and triphone counts file

- **-ocimdef** (Default Value : NO DEFAULT VALUE)
  Description: Output CI model definition file

- **-oalltphnmdef** (Default Value : NO DEFAULT VALUE)
  Description: Output all triphone model definition file

- **-ountiedmdef** (Default Value : NO DEFAULT VALUE)
  Description: Output untied model definition file

- **-minocc** (Default Value : 1)
  Description: Min occurances of a triphone must occur for inclusion in mdef file

- **-maxtriphones** (Default Value : 100000)
  Description: Max. number of triphones desired in mdef file

### A.2.15 mk_mllr_class

#### Tool Description

Description:

Create the senone to mllr class mapping.

#### Example

Example:

mk_mllr_class -nmap mapfile -nclass 4 -cb2mllrfn out.cb2mllr

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-nmap** (Default Value : NO DEFAULT VALUE)
  Description: # of codebook -> MLLR class mappings

- **-nclass** (Default Value : NO DEFAULT VALUE)
  Description: # of MLLR classes to map into

- **-cb2mllrfn** (Default Value : NO DEFAULT VALUE)
  Description: Codebook-to-MLLR mapping file to create

### A.2.16 mk_model_def

#### Tool Description

Description:
(Copied from Eric Thayers' comment)
Make SPHINX-III model definition files from a variety
input sources. One input source is a SPHINX-II senone mapping
file and triphone file. Another is a list of phones (in which
case the transition matrices are tied within base phone class
and the states are untied)

#### Example

Example:
[Under construction]

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool
- **-example** (Default Value : no)
  Description: Shows example of how to use the tool
- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III model definition file name
- **-triphonefn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-II triphone file name
- **-phonelstfn** (Default Value : NO DEFAULT VALUE)
  Description: List of phones (first 4 columns of phone def'ns)
- **-mapfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-II senone mapping file name
- **-n_cdstate** (Default Value : NO DEFAULT VALUE)
  Description: total # of CD senones/tied_states (even though mapfn may reference fewer)
- **-n_cistate** (Default Value : NO DEFAULT VALUE)
  Description: # of CI senones/tied_states
- **-n_tmat** (Default Value : NO DEFAULT VALUE)
  Description: # of tied transition matrices
- **-n_state_pm** (Default Value : 5)
  Description: # of states/model

### A.2.17 mk_s2cb

#### Tool Description

Description:
Convert s3 means and variances to s2 codebook format.
cepstrum, delta, delta-delta and power cepstrum basename could be changed by uers.

#### Example

Example:
mk_s2cb -meanfn s3mean -varfn s3var -cbdir s2dir -varfloor 0.00001

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III mean density parameter file name

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III variance density parameter file name

- **-cbdir** (Default Value : NO DEFAULT VALUE)
  Description: A directory containing SPHINX-II 1PD codebooks

- **-varfloor** (Default Value : NO DEFAULT VALUE)
  Description: Minimum variance value

- **-cepcb** (Default Value : cep.256)
  Description: Basename of the cepstrum codebook

- **-dcepcb** (Default Value : d2cep.256)
  Description: Basename of the difference cepstrum codebook

- **-powcb** (Default Value : p3cep.256)
  Description: Basename of the power codebook

- **-2dcepcb** (Default Value : xcep.256)
  Description: Basename of the 2nd order difference cepstrum codebook

- **-meanext** (Default Value : vec)
  Description: Mean codebook extension

- **-varext** (Default Value : var)
  Description: Variance codebook extension

### A.2.18 mk_s2hmm

#### Tool Description

Description:

Convert s3 model definition file, mixture weight and transition matrices to s2 hmm format.

#### Example

Example:

mk_s2hmm -meanfn s3mdef -varfn s3mixw -tmat s3tmat -hmmdir s2dir

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition file for the S3 models

- **-tmatfn** (Default Value : NO DEFAULT VALUE)
  Description: S3 transition matrix parameter file name

- **-tpfloor** (Default Value : 0.0001)
  Description: Transition probability smoothing floor

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: S3 mixing weight parameter file name

- **-hmmdir** (Default Value : NO DEFAULT VALUE)
  Description: S2 model output directory

- **-hmmext** (Default Value : chmm)
  Description: Extension of a SPHINX-II model file.

- **-cepsenoext** (Default Value : ccode)
  Description: Extension of cepstrum senone weight file

- **-dcepsenoext** (Default Value : d2code)
  Description: Extension of difference cepstrum senone weight file

- **-powsenoext** (Default Value : p3code)
  Description: Extension of power senone weight file

- **-2dcepsenoext** (Default Value : xcode)
  Description: Extension of 2nd order difference cepstrum senone weight file

- **-mtype** (Default Value : sdm)
  Description: Model type sdm,dhmm

### A.2.19 mk_s2phone

#### Tool Description

Description:
(Copied from Eric Thayer's comment)
* Make a SPHINX-II phone file given a list of phones (in SPHINX-III
* format). Ok, this sounds like a bizarre fn, but I did need it
* once.

#### Example

Example:
mk_s2phone -s2phonefn s2.phone -phonelstfn s3.phone

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-s2phonefn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-II phone file name

- **-phonelstfn** (Default Value : NO DEFAULT VALUE)
  Description: List of phones

- (Default Value : NO DEFAULT VALUE)
  Description:

### A.2.20 mk_s2phonemap

#### Tool Description

Description:

Convert s3 model definition file to s2 phone and map files.

#### Example

Example:

mk_s2phonemap -moddeffn s3mean -phonefn s2/phone -mapfn s2/map

### Command-line Argument Description

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: The model definition file for the model to be converted

- **-phonefn** (Default Value : NO DEFAULT VALUE)
  Description: Output phone file name

- **-mapfn** (Default Value : NO DEFAULT VALUE)
  Description: Output map file name

### A.2.21 mk_s2sendump

#### Tool Description

Description:

Convert s3 model definition file and s3 mixture weight file to a s2 senddump file.

#### Example

Example:

mk_s2sendump -moddeffn s3mdef -mixwfn s3mixw -tpfloor 0.0000001

-feattype s2_4x -sendumpfn s2dir/sendump

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: The model definition file for the model inventory to train

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The mixture weight parameter file name

- **-sendumpfn** (Default Value : NO DEFAULT VALUE)
  Description: Output sendump file name

- **-feattype** (Default Value : NO DEFAULT VALUE)
  Description: Feature type e.g. s2_4x

- **-tpfloor** (Default Value : 0.0001)
  Description: Transition probability smoothing floor

### A.2.22 mk_s3gau

#### Tool Description

Description:

Conversion from sphinx 2 codebook to sphinx3 means and variances

#### Example

Example:

mk_s3gau -meanfn s3mean -varfn s3var -cbdir s2dir -feat 4s_12c_24d_3p_12dd

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III mean density parameter file name

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III variance density parameter file name

- **-cbdir** (Default Value : NO DEFAULT VALUE)
  Description: A directory containing SPHINX-II 1PD codebooks

- **-varfloor** (Default Value : NO DEFAULT VALUE)
  Description: Minimum variance value

- **-cepcb** (Default Value : cep.256)
  Description: Basename of the cepstrum codebook

- **-dcepcb** (Default Value : d2cep.256)
  Description: Basename of the difference cepstrum codebook

- **-powcb** (Default Value : p3cep.256)
  Description: Basename of the power codebook

- **-2dcepcb** (Default Value : xcep.256)
  Description: Basename of the 2nd order difference cepstrum codebook

- **-meanext** (Default Value : vec)
  Description: Mean codebook extension

- **-varext** (Default Value : var)
  Description: Variance codebook extension

- **-fixpowvar** (Default Value : false)
  Description: Fix the power variance to the SPHINX-II standards

- **-feat** (Default Value : 4s_12c_24d_3p_1)
  Description: 2dd Defines the feature set to use

- **-ceplen** (Default Value : 13)
  Description: Defines the input feature vector (e.g. MFCC) len

### A.2.23 mk_s3mix

#### Tool Description

Description:
Conversion from sphinx 2 hmms to sphinx3 mixture weights

#### Example

Example:
(By Arthur: Not sure, may be obsolete)
mk_s3mixw -mixwfn s3mixw -moddeffn s3mdef -hmmdir s2hmmdir

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III mixture weight parameter file name

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III model definition file name

- **-floor** (Default Value : NO DEFAULT VALUE)
  Description: Floor weight value to apply before renormalization

- **-ci2cd** (Default Value : false)
  Description: CD weights initialized to CI weights (-hmmdir is to a set of CI models)

- **-hmmdir** (Default Value : NO DEFAULT VALUE)
  Description: A directory containing SPHINX-III models consistent with -moddeffn

- **-cepsenoext** (Default Value : ccode)
  Description: Extension of cepstrum senone weight file

- **-dcepsenoext** (Default Value : d2code)
  Description: Extension of difference cepstrum senone weight file

- **-powsenoext** (Default Value : p3code)
  Description: Extension of power senone weight file

- **-2dcepsenoext** (Default Value : xcode)
  Description: Extension of 2nd order difference cepstrum senone weight file

### A.2.24 mk_s3tmat

#### Tool Description

#### Example

**Command line Argument Decription**

### A.2.25 mk_ts2cb

#### Tool Description

Description:

(copied from Eric's comments)

* Create a tied-state-to-codebook mapping file for semi-continuous,

* phone dependent or fully continuous Gaussian density tying.

#### Example

Example:

(By Arthur: Not sure, may be obsolete)

mk_ts2cb -moddeffn semi -ts2cbfn ts2cb

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-ts2cbfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III tied-state-to-cb file name

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-III model definition file name

- **-tyingtype** (Default Value : semi)
  Description: Output a state parameter def file for fully continuous models

- **-pclassfn** (Default Value : NO DEFAULT VALUE)
  Description: A SPHINX-II phone class file name

### A.2.26 mllr_solve

#### Tool Description

Description:

Given a set of mean accumulator, mllr_solve can compute the transform

matrix based on the maximum likelihood criteria.

The mean vand variance are required to be input in arguements -meanfn and -varfn

For linear regression equation y=Ax+b,

If you specific only -mllrmult, then only A will be estimated.

If you specific only -mllradd, then only b will be estimated.

#### Example

Example:

The simplest case:

mllr_solve -outmllrfn output.matrix -accumdir accumdir -meanfn mean -varfn var

Adapt based on only CD-senones

mllr_solve -outmllrfn output.matrix -accumdir accumdir -meanfn mean -varfn var -cdonly yes -moddeffn mdef.

Only adapt on A :

mllr_solve -outmllrfn output.matrix -accumdir accumdir -meanfn mean -varfn var -mllrmult yes -mllradd no

help and example:

mllr_solve -help yes -example yes

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-outmllrfn** (Default Value : NO DEFAULT VALUE)
  Description: Output MLLR regression matrices file

- **-accumdir** (Default Value : NO DEFAULT VALUE)
  Description: Paths containing reestimation sums from bw

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: Baseline Gaussian density mean file

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: variance (baseline-var, or error-var) file

- **-cb2mllrfn** (Default Value : .1cls.)
  Description: Codebook to mllr class mapping index file (If it is given, ignore -cdonly)

- **-cdonly** (Default Value : no)
  Description: Use only CD senones for MLLR (If yes, -moddeffn should be given.)

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model Definition file (to get CD starting point for MLLR)

- **-mllrmult** (Default Value : yes)
  Description: Reestimate full multiplicative term of MLLR adatpation of means (yes/no)

- **-mllradd** (Default Value : yes)
  Description: Reestimate shift term of MLLR adaptation of means (yes/no)

- **-varfloor** (Default Value : 1e-3)
  Description: var floor value

### A.2.27 mllr_transform

#### Tool Description

Description:

Given a set of MLLR transform, mllr_transform can transform the mean according to formulat y=Ax+b.

The output and input files are specified by -outmeanfn and -inmeanfn respectively. You may also transform the context-dependent model using the option -cdonly. In that case you need to specify a model definition using -moddeffn.

#### Example

Example:

The simplest case:

mllr_transform -inmeanfn inMeans -outmeanfn outMeans -mllrmat matrix

Adapt only on CD phones:

mllr_transform -inmeanfn inMeans -outmeanfn outMeans -mllrmat matrix -cdonly yes -moddeffn mdef

Help and example:

nmllr_transform -help yes -example yes

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-inmeanfn** (Default Value : NO DEFAULT VALUE)
  Description: Input Gaussian mean file name

- **-outmeanfn** (Default Value : NO DEFAULT VALUE)
  Description: Output Gaussian mean file name

- **-mllrmat** (Default Value : NO DEFAULT VALUE)
  Description: The MLLR matrix file

- **-cb2mllrfn** (Default Value : .1cls.)
  Description: The codebook-to-MLLR class file. Override option -cdonly

- **-cdonly** (Default Value : no)
  Description: Use CD senones only. -moddeffn must be given.

- **-varfloor** (Default Value : 1e-2)
  Description: Value of the variance floor. Mainly for smoothing the mean.

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model Definition file.

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: Gaussian variance file name. For smoothing.

- —— (Default Value : Compiled)
  Description: 23 2004, 02:51:07

- (Default Value : NO DEFAULT VALUE)
  Description:

### A.2.28 norm

#### Tool Description

Description:
compute the HMM's parameter generated by bw.

#### Example

Example:
norm
-accumdir accumdir
-mixwfn mixw
-tmatfn tmat
-meanfn mean
-varfn variances

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-accumdir** (Default Value : NO DEFAULT VALUE)
  Description: Paths containing reestimation sums from bw

- **-oaccumdir** (Default Value : NO DEFAULT VALUE)
  Description: Path to contain the overall reestimation sums

- **-tmatfn** (Default Value : NO DEFAULT VALUE)
  Description: Transition prob. matrix file to produce (if any)

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: Mixing weight file to produce (if any)

- **-meanfn** (Default Value : NO DEFAULT VALUE)
  Description: Gaussian density mean file to produce (if any)

- **-varfn** (Default Value : NO DEFAULT VALUE)
  Description: Gaussian density variance file to produce (if any)

- **-regmatfn** (Default Value : NO DEFAULT VALUE)
  Description: MLLR regression matrices file to produce (if any)

- **-dcountfn** (Default Value : NO DEFAULT VALUE)
  Description: Gaussian density count file to produce

- **-inmixwfn** (Default Value : NO DEFAULT VALUE)
  Description: Use mixing weights from this file if never observed

- **-inmeanfn** (Default Value : NO DEFAULT VALUE)
  Description: Use mean from this file if never observed

- **-invarfn** (Default Value : NO DEFAULT VALUE)
  Description: Use var from this file if never observed

- **-feat** (Default Value : NO DEFAULT VALUE)
  Description: The feature set to use.

- **-ceplen** (Default Value : NO DEFAULT VALUE)
  Description: The vector length of the source features (e.g. MFCC)

### A.2.29 param_cnt

#### Tool Description

Description:
Find the number of times each of the triphones listed
in a given model definition file (by -moddeffhn) occured in a set
of transcription, specified by -lsnfn

#### Example

Example :
param_cnt -moddeffn mdef -ts2cbfn .cont. -ctlfn controlfile -lsnfn
transcripts -dictfn dict -fdictfn fillerdict -paramtype phone

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Model definition file for the single density HMM's to initialize

- **-ts2cbfn** (Default Value : NO DEFAULT VALUE)
  Description: Tied-state-to-codebook mapping file

- **-ctlfn** (Default Value : NO DEFAULT VALUE)
  Description: Control file of the training corpus

- **-part** (Default Value : NO DEFAULT VALUE)
  Description: Identifies the corpus part number (range 1..NPART)

- **-npart** (Default Value : NO DEFAULT VALUE)
  Description: Partition the corpus into this many equal sized subsets

- **-nskip** (Default Value : NO DEFAULT VALUE)
  Description: # of lines to skip in the control file

- **-runlen** (Default Value : NO DEFAULT VALUE)
  Description: # of lines to process in the control file (after any skip)

- **-lsnfn** (Default Value : NO DEFAULT VALUE)
  Description: All word transcripts for the training corpus (consistent order w/ -ctlfn!)

- **-dictfn** (Default Value : NO DEFAULT VALUE)
  Description: Dictionary for the content words

- **-fdictfn** (Default Value : NO DEFAULT VALUE)
  Description: Dictionary for the filler words

- **-segdir** (Default Value : NO DEFAULT VALUE)
  Description: Root directory of the training corpus state segmentation files.

- **-segext** (Default Value : v8_seg)
  Description: Extension of the training corpus state segmentation files.

- **-paramtype** (Default Value : state)
  Description: Parameter type to count 'state', 'cb', 'phone'

### A.2.30 printp

#### Tool Description

Description:

Display numerical values of resources generated by Sphinx

Current we supoort the following formats

-tmatfn : transition matrix

-mixwfn : mixture weight file

-gaufn : mean or variance

-gaucntn : sufficient statistics for mean and diagonal covariance

-lambdafn : interpolation weight

Currently, some parameters can be specified as intervals such as mixture weight.

You can also specified -sigfig the number of significant digits by you would like to see.

and normalize the parameters by -norm

#### Example

Example:

Print the mean of a Gaussian:

printp -gaufn mean

Print the variance of a Gaussian:

printp -gaufn var

Print the sufficient statistic:

printp -gaucntfn gaucnt:

Print the mixture weights:

printp -mixw mixw

Print the interpolation weight:

printp -lambdafn lambda

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-tmatfn** (Default Value : NO DEFAULT VALUE)
  Description: The transition matrix parameter file name

- **-mixwfn** (Default Value : NO DEFAULT VALUE)
  Description: The mixture weight parameter file name

- **-mixws** (Default Value : NO DEFAULT VALUE)
  Description: Start id of mixing weight subinterval

- **-mixwe** (Default Value : NO DEFAULT VALUE)
  Description: End id of mixing weight subinterval

- **-gaufn** (Default Value : NO DEFAULT VALUE)
  Description: A Gaussian parameter file name (either for means or vars)

- **-gaucntfn** (Default Value : NO DEFAULT VALUE)
  Description: A Gaussian parameter weighted vector file

- **-regmatcntfn** (Default Value : NO DEFAULT VALUE)
  Description: MLLR regression matrix count file

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: The model definition file

- **-lambdafn** (Default Value : NO DEFAULT VALUE)
  Description: The interpolation weight file

- **-lambdamin** (Default Value : 0)
  Description: Print int. wt. >= this

- **-lambdamax** (Default Value : 1)
  Description: Print int. wt. <= this

- **-norm** (Default Value : yes)
  Description: Print normalized parameters

- **-sigfig** (Default Value : 4)
  Description: Number of significant digits in 'e' notation

### A.2.31 prunetree

#### Tool Description

Description:
Using prunetree, the bifurcations in the decision trees which resulted in the minimum increase in likelihood are progressively removed and replaced by the parent node. The selection of the branches to be pruned out is done across the entire collection of decision trees globally.

#### Example

Example:
prunetree
-itreedir input_tree_dir
-nseno 5000
-otreedir output_tree_dir
-moddefn mdef
-psetfn questions
-minocc 100

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-moddeffn** (Default Value : NO DEFAULT VALUE)
  Description: CI model definition file

- **-psetfn** (Default Value : NO DEFAULT VALUE)
  Description: Phone set definition file

- **-itreedir** (Default Value : NO DEFAULT VALUE)
  Description: Input tree directory

- **-otreedir** (Default Value : NO DEFAULT VALUE)
  Description: Output tree directory

- **-nseno** (Default Value : NO DEFAULT VALUE)
  Description: # of senones defined by the output trees

- **-minocc** (Default Value : 0.0)
  Description: Prune nodes w/ fewer than this # of observations

### A.2.32 tiestate

#### Tool Description

Description :

Create a model definition file with tied state from model definition file without tied states.

#### Example

Example:

tiestate -imoddeffn imdef -omoddeffn omdef -treedir trees -psetfn questions

This is an example of the input and output format, I copied from Rita's web page,

This is an hypothetical input of tiestate

# triphone: (null)

# seno map: (null)

#

0.3

5 n_base

34 n_tri

156 n_state_map

117 n_tied_state

15 n_tied_ci_state

5 n_tied_tmat

#

# Columns definitions

#base lft rt p attrib tmat ... state id's ...

SIL - - - filler 0 0 1 2 N

AE - - - n/a 1 3 4 5 N

AX - - - n/a 2 6 7 8 N

B - - - n/a 3 9 10 11 N

T - - - n/a 4 12 13 14 N

AE B T i n/a 1 15 16 17 N

AE T B i n/a 1 18 19 20 N

AX AX AX s n/a 2 21 22 23 N

AX AX B s n/a 2 24 25 26 N

AX AX SIL s n/a 2 27 28 29 N

AX AX T s n/a 2 30 31 32 N

AX B AX s n/a 2 33 34 35 N

AX B B s n/a 2 36 37 38 N

AX B SIL s n/a 2 39 40 41 N

AX B T s n/a 2 42 43 44 N

AX SIL AX s n/a 2 45 46 47 N

AX SIL B s n/a 2 48 49 50 N

AX SIL SIL s n/a 2 51 52 53 N

AX SIL T s n/a 2 54 55 56 N

AX T AX s n/a 2 57 58 59 N

AX T B s n/a 2 60 61 62 N

AX T SIL s n/a 2 63 64 65 N

AX T T s n/a 2 66 67 68 N

B AE AX e n/a 3 69 70 71 N

B AE B e n/a 3 72 73 74 N

B AE SIL e n/a 3 75 76 77 N

B AE T e n/a 3 78 79 80 N

B AX AE b n/a 3 81 82 83 N

B B AE b n/a 3 84 85 86 N

B SIL AE b n/a 3 87 88 89 N

B T AE b n/a 3 90 91 92 N

T AE AX e n/a 4 93 94 95 N

T AE B e n/a 4 96 97 98 N

T AE SIL e n/a 4 99 100 101 N

T AE T e n/a 4 102 103 104 N

T AX AE b n/a 4 105 106 107 N

T B AE b n/a 4 108 109 110 N

T SIL AE b n/a 4 111 112 113 N

T T AE b n/a 4 114 115 116 N

is used as the base to give the following CD-tied model definition file with 39 tied states (senones):

# triphone: (null)

```
# seno map: (null)
#
0.3
5 n_base
34 n_tri
156 n_state_map
54 n_tied_state
15 n_tied_ci_state
5 n_tied_tmat
#
# Columns definitions
#base lft rt p attrib tmat ... state id's ...
SIL - - - filler 0 0 1 2 N
AE - - - n/a 1 3 4 5 N
AX - - - n/a 2 6 7 8 N
B - - - n/a 3 9 10 11 N
T - - - n/a 4 12 13 14 N
AE B T i n/a 1 15 16 17 N
AE T B i n/a 1 18 16 19 N
AX AX AX s n/a 2 20 21 22 N
AX AX B s n/a 2 23 21 22 N
AX AX SIL s n/a 2 24 21 22 N
AX AX T s n/a 2 25 21 22 N
AX B AX s n/a 2 26 21 27 N
AX B B s n/a 2 23 21 27 N
AX B SIL s n/a 2 24 21 27 N
AX B T s n/a 2 25 21 27 N
AX SIL AX s n/a 2 26 21 28 N
AX SIL B s n/a 2 23 21 28 N
AX SIL SIL s n/a 2 24 21 28 N
AX SIL T s n/a 2 25 21 28 N
AX T AX s n/a 2 26 21 29 N
AX T B s n/a 2 23 21 29 N
AX T SIL s n/a 2 24 21 29 N
```

AX T T s n/a 2 25 21 29 N

B AE AX e n/a 3 30 31 32 N

B AE B e n/a 3 33 31 32 N

B AE SIL e n/a 3 34 31 32 N

B AE T e n/a 3 35 31 32 N

B AX AE b n/a 3 36 37 38 N

B B AE b n/a 3 36 37 39 N

B SIL AE b n/a 3 36 37 40 N

B T AE b n/a 3 36 37 41 N

T AE AX e n/a 4 42 43 44 N

T AE B e n/a 4 45 43 44 N

T AE SIL e n/a 4 46 43 44 N

T AE T e n/a 4 47 43 44 N

T AX AE b n/a 4 48 49 50 N

T B AE b n/a 4 48 49 51 N

T SIL AE b n/a 4 48 49 52 N

T T AE b n/a 4 48 49 53 N

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-imoddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Untied-state model definition file

- **-omoddeffn** (Default Value : NO DEFAULT VALUE)
  Description: Tied-state model definition file

- **-treedir** (Default Value : NO DEFAULT VALUE)
  Description: SPHINX-III tree directory containing pruned trees

- **-psetfn** (Default Value : NO DEFAULT VALUE)
  Description: Phone set definiton file

### A.2.33 wave2feat

#### Tool Description

Description:

Create cepstra from audio file.

The main parameters that affect the final output, with typical values, are:

samprate, typically 8000, 11025, or 16000

lowerf, 130, 200, 130, for the respective sampling rates above

upperf, 3700, 5200, 6800, for the respective sampling rates above

nfilt, 31, 37, 40, for the respective sampling rates above

nfft, 256 or 512

format, raw or nist or mswav

"

#### Example

Example:

This example creates a cepstral file named "output.mfc" from an input audio file named "input.raw", which is a raw audio file (no header information), which was originally sampled at 16kHz.

wave2feat -i input.raw

-o output.mfc

-raw no

-input_endian little

-samprate 16000

-lowerf 130

-upperf 6800

-nfilt 40

-nfft 512

**Command-line Argument Description**

*Usage: [options]*

- **-help** (Default Value : no)
  Description: Shows the usage of the tool

- **-example** (Default Value : no)
  Description: Shows example of how to use the tool

- **-i** (Default Value : NO DEFAULT VALUE)
  Description: Single audio input file

- **-o** (Default Value : NO DEFAULT VALUE)
  Description: Single cepstral output file

- **-c** (Default Value : NO DEFAULT VALUE)
  Description: Control file for batch processing

- **-di** (Default Value : NO DEFAULT VALUE)
  Description: Input directory, input file names are relative to this, if defined

- **-ei** (Default Value : NO DEFAULT VALUE)
  Description: Input extension to be applied to all input files

- **-do** (Default Value : NO DEFAULT VALUE)
  Description: Output directory, output files are relative to this

- **-eo** (Default Value : NO DEFAULT VALUE)
  Description: Output extension to be applied to all output files

- **-nist** (Default Value : no)
  Description: Defines input format as NIST sphere

- **-raw** (Default Value : no)
  Description: Defines input format as raw binary data

- **-mswav** (Default Value : no)
  Description: Defines input format as Microsoft Wav (RIFF)

- **-input_endian** (Default Value : little)
  Description: Endianness of input data, big or little, ignored if

NIST or MS Wav

- **-nchans** (Default Value : 1)
  Description: Number of channels of data (interlaced samples assumed)

- **-whichchan** (Default Value : 1)
  Description: Channel to process

- **-logspec** (Default Value : no)
  Description: Write out logspectral files instead of cepstra

- **-feat** (Default Value : sphinx)
  Description: SPHINX format - big endian

- **-mach_endian** (Default Value : little)
  Description: Endianness of machine, big or little

- **-alpha** (Default Value : 0.97)
  Description: Preemphasis parameter

- **-srate** (Default Value : 16000.0)
  Description: Sampling rate

- **-frate** (Default Value : 100)
  Description: Frame rate

- **-wlen** (Default Value : 0.025625)
  Description: Hamming window length

- **-nfft** (Default Value : 512)
  Description: Size of FFT

- **-nfilt** (Default Value : 40)
  Description: Number of filter banks

- **-lowerf** (Default Value : 133.33334)
  Description: Lower edge of filters

- **-upperf** (Default Value : 6855.4976)
  Description: Upper edge of filters

- **-ncep** (Default Value : 13)
  Description: Number of cep coefficients

- **-doublebw** (Default Value : no)
  Description: Use double bandwidth filters (same center freq)

- **-blocksize** (Default Value : 200000)
  Description: Block size, used to limit the number of samples used at a time when reading very large audio files

- **-dither** (Default Value : no)
  Description: Add 1/2-bit noise

- **-verbose** (Default Value : no)
  Description: Show input filenames