# The UCLA Phonotactic Learner

# Draft manual, August 2006

## 1. The program

- This is in Java, and consists of many dozen files with the suffix .class (i.e., Java executables.)
- The source code is also given, consisting of the same files with the suffix .java.
- The usual business about installing Java and putting access to java.exe in the Path command, is in effect.
- The Shell program (see below), automatically runs the command
  - > path C:\Program Files\Java\jre1.5.0 02\bin

But if you are running it on your own you should type this first, so that Java can be found.

• The batch file can be made with Notepad or any other simple text editor.

### 2. The Shell

- Bruce has written a Windows shell, which checks input files for many, many, possible errors, prepares certain files that would otherwise have to be prepared by hand, and makes prettier output files.
- Directions thus come in two flavors: Pure Java, and Windows Shell.

## **DIRECTIONS WITH PURE JAVA**

## 3. The Algorithm

- includes a stochastic element: the salad selection routine starts each sequence of n salad items with a new random seed
- Hence there is no guarantee that multiple runs will yield identical results.

# 4. Making Sure the Program can Access Downloaded Code

- Colin uses fancy downloaded Java routines that have to be accessed when the program runs.
- This is a bit tricky because they are sitting inside .jar files, similar to .zip.
- Generally, the way to do it with a command line is to put this stuff:

java -Xms650m -Xmx650m -classpath uclapl.jar;colt.jar;datafile.jar;jas.jar;pal-1.5.jar;commons-math-1.0.jar;fsm.jar;trove.jar

up front in the command; after which comes the name of the program, UCLAPhonotacticLearner, followed by all of the Java command-line options.

# 5. A Sample RunMe.bat file

from Bruce's setup. This ran the learner on a Shona vowel harmony simulation. Note the path command to tell Windows where Java is.

cd C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\Java7-21

Path C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\MyJava\bin\

java -Xms650m -Xmx650m -classpath uclapl.jar;colt.jar;datafile.jar;jas.jar;pal-1.5.jar;commons-math-1.0.jar;fsm.jar;trove.jar UCLAPhonotacticLearner -gui -maximumPathLength 8 -tiers

 $C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\Inputs\FeatureList.txt\ -phonemes\ C:\AR\PhonotacticS\UCLAPhonotacticLearner\VBInterface\Inputs\FeatureChart.txt\ -naturalClasses$ 

 $C: \AR\Phonotactics \UCLAPhonotactic Learner \VBInterface \Inputs \Natural Classes. txt-trigram \Natural Classes$ 

C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\Inputs\TrigramLimitationFile.txt - corpus C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\Inputs\TrainingData.txt - select -maximumFieldSize 30 -sampleType graphical -sigma2 1 -maximumGramSize C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\Inputs\TierGramSize.txt - complementClasses -weighting ConjugateGradient -weightingIteration 10 -sampleDiameter 3 - oeThreshold .35 -projections

 $\label{lem:condition} C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\Inputs\Projections.txt\ -test\\ C:\AR\Phonotactics\UCLAPhonotacticLearner\VBInterface\Inputs\TestingData.txt\ -sample > ProgramTrace.txt\\$ 

## 6. Input files and parameter specification

- All files can be named whatever you please.
- The name is entered on the command line interface, preceded by a -n entry that says which file it is.
- You need to include a path, unless it is in the same folder that contains the program (i.e., the batch of .class files). The path can be relative to the main folder, if it's in a subfolder.

### 6.1 Obligatory Input Files

#### 6.1.1 The Feature File

- Access it on the command line with **-tiers filename**.
- Internal format:
  - > First line should be

Tiers

NO COLON!

• Then, list the features, one per line.

- It is crucial that feature names not have spaces. Use or whatever.
- Java is case-sensitive.
- The first feature must always be word boundary.

#### 6.1.2 The Phoneme File

- This currently is needed, but according to the revised spec, it should merely be read off the feature chart, since it's redundant.
- Access it on the command line with **-phonemes filename**.
- Internal format: this is the format that Bruce has been passing on to Colin, viz.
  - ➤ Line 1: Segments
  - Line 2: #TAB{SPACE+word boundary,SPACE[values for features (0/+,-)Feature,SPACE]<sub>0</sub>}
  - Line 3+: SymbolTAB{SPACE-word\_boundary,SPACE[values for features (0/+,-)Feature,SPACE]<sub>0</sub>}
  - Colin has been replacing spaces with underscores to conform with the restriction above.
- If the file includes a feature not in the feature list, the program will merrily proceed onward, so exercise caution.

#### 6.1.3 The Natural Classes File

- This, too, should ultimately not be an input file, but should be calculated.
- Access it on the command line with -naturalClasses filename.
- This is exactly the output of SimilarityByKie.exe, with two changes:
  - Remove the final two lines that give information about how many classes.
  - > Remove the **null natural class**, which often comes up with the first privative feature in the list.
  - It appears necessary to remove the natural class [-word\_boundary], i.e. no natural class that encompasses all segments.

## 6.1.4 An Obligatory Parameter: -gui

- At present, this must be included in the command line; perhaps future versions will make it optional.
- March 2006: no longer needed

### 6.2 Optional Input Files

### 6.2.1 Trigram Limitation File (UG)

- This implements a bit of UG. It is supposed that languages cannot promiscuously use trigram constraints, but must limit themselves to a coarse subset of the feature system.
- The option is used when the user is not doing the UG herself, but is relying on the UCLA Phonotactic Learner to fabricate the constraints.
- The file is simply a list of features, each with a plus minus value, such that:

The Learner will not use a trigram constraint, unless (at least) one of the matrices it contains is a single-feature matrix, consisting of one of the feature values given on the list.

- Hence it will normally contain "primal" features like [syllabic] and [word\_boundary], or the so-called "Root" features.
- Access it on the command line with **-trigramNaturalClasses filename**.
- Format (example):

- +syllabic -syllabic
- +word\_boundary
- To cancel this aspect of UG (while still letting the program fabricate the constraints), place the following on the command line: **-trigramNaturalClasses all**
- If the user wishes to provide her own constraints in a file, simply omit -trigramNaturalClasses from the command line. (You can leave it in, but in the presence of a user-specific constraint file, it will have no effect.)

# 6.2.2 The Training Data

- Access it on the command line with **-corpus filename**.
- Format:
  - > Just transcriptions (no annotations)
  - ➤ Phonetic symbols solely from the phoneme list.
  - ➤ Phonetic symbols are to be separated with spaces.
  - ➤ No leading or trailing spaces.
  - > Frequency is designated with repetition
- If the file includes a symbol not in the phoneme list, the program will identify it.

# 6.2.3 Testing data

- For test using these words, access it on the command line with **-test filename**.
- The set of blick words should have the same format as the training set.
- See detailed spec, for the need for comments on each testing items (such comments can be frequencies, or categories, etc.)
- This will only make sense provided you have in hand (either computed, or in a file whose existence is pointed out in the command line options covered above):
  - Constraints
  - Weights

## 6.2.4 List of User-Defined Constraints

- from which selection takes place
- Access it on the command line with **-constraintList filename**.
- Format: see example

### 6.2.5 File of Evaluation Order

- Bruce never implemented this. I think it should not exist; the program should just use the order given in the constraint file.
- This determines the order in which the constraints are pulled out of their file and inspected.
- The program will keep inspecting, following this order, until it finds a constraint that satisfies the Accuracy Criterion.
- This file consists of a single column; a real number for each constraint; the program considers the constraints in *ascending* order of these numbers.

- Do not use scientific notation.
- Access it on the command line with **-constraintOrder filename**.
- Tiers will be considered in file order.

#### 6.3 Parameters

# 6.3.1 The **Select** Parameter

- Set this parameter by including **-select** in the command line.
- It means "find the constraints, either from an input file, or from the default UG, that best model the data".
- It is left out if you are blick-testing, or if the constraint set is meant to be used completely.

## 6.3.2 The Parameter -constraints filename

• This means, "use *all* of the constraints in the filename specified".

## 6.3.3 The Parameter -weights filename

- Read in a list of predetermined weights, one for each constraint in the file mention in §6.3.2.
- Format: simply a column of weights.
- These must be nonpositive.
- Do not use scientific notation.

## 6.3.4 The Parameter -train

- Use this in conjunction with the command line option **-constraints filename**.
- When it is present, the system will find the best weights for the complete set of constraints in the file specified in **-constraints filename**.
- Note that the presence of **-constraints filename** will *not* by itself cause weights to be learned for this file.
- Not needed if you are using the default primitive UG.

# 6.4 Parameter Governing the Length of the Run

- Add the command line option **-maximumFieldSize n**, where *n* is an integer.
- The current default is unbounded (keeps learning until no selected constraint can satisfy the accuracy criterion).
  - The accuracy criterion is currently set to follow a schedule, viz.
    - .01 where "accuracy" is defined as

.1

violations in training set/violations in current salad .2

.9

• If **-maximumFieldSize n** is selected, and the program reaches a point where no selected constraint can satisfy the accuracy criterion, it halts, even if *n* constraints have no yet been installed in the grammar.

# 6.5 Parameter Governing Salad - NOT SURE IF THIS IS OBSOLETE; ASK COLIN

### 6.5.1 Size

- Add the command line option **-sampleSize n**, where *n* is an integer.
- The current default is about 3000.
- In principle (no guarantees) larger salads could increase learning accuracy (and, of course, increase run time).
- The program does not give *exactly* this value, but probably something within the same order of magnitude.
  - > Specifically, if the user asks for a salad bigger than the corpus, the actual salad will be of the length which the closest integer multiple of the training set size.
  - ➤ If the user asks for a *smaller* salad than the training set, the program will return a salad of approximately that size.
  - ➤ The program creates salads that are of approximately the same length distribution as the training set.

# 6.5.2 Type **PROBABLY OBSOLETE**; **CHECK WITH COLIN**

- Add one of the following command line options:
  - > -sampleType sequential. This will cause the program to generate samples that match the length distribution of the training data, but are otherwise unconstrained. This seems to be the best choice...
  - > -sampleType monosyllables. This will cause the program to use a sample-generation program that insists on there being exactly one vowel per sample item.
  - > -sampleType onsets. This will cause the program to behave quite similarly to when you select sequential, but with different code. Stay tuned for clarification or deletion.
  - > xxx graphical
- To run the **monosyllables** option, some conditions must be met:
  - There must be both consonants and vowels in the segment inventory.
  - There must a feature [syllabic] to distinguish the two.
  - ➤ The consonants (i.e. [-syllabic]) must form a contiguous bloc in the feature chart, as must the vowels. Either consonant-vowel, or vowel-consonant order is acceptable.

## 6.6 Assessing the result

## 6.6.1 The Parameter -sample

- This causes the program to create an output file with salad in it.
- This is the terminal, best salad.

• Like blick testing, this needs a constraints file and a weights file.

### 6.6.2 Summary: How To Blick Test

you need these options to be selected:

- -tiers filename
- -phonemes filename
- -naturalClasses filename
- -test filename

the blick test data

- -constraints filename
- -weights filename

# 7. Output Files

#### 7.1 Grammar.txt

- This is a list of constraints and weights.
- The constraints might be concocted (using the default UG), or selected from (user-supplied UG, or just the list you gave it; see options above.
- See detailed spec for further information that should be included in this file.

### 7.2 BlickTestResults.txt

- For each blick word, the summed weights of the violations.
- See detailed spec for further information that should be included in this file.

## 7.3 SampleSalad.txt

- This is the salad created if you include **-sample**; see above.
- The salad, as well as the training data, can be resubmitted to the program as a set of blick items.
- See detailed spec for further information that should be included in this file.

## 8. Polysyllabic Salad Creation PROBABLY OBSOLETE; CONSULT COLIN

Word  $\rightarrow$  (Syllable)\*

Syllable → Onset Nucleus Coda

Onset  $\rightarrow$  C<sub>0</sub>, where C is defined in the feature system with the feature [-syllabic].

Nucleus  $\rightarrow$  V<sub>0</sub>, where V is defined in the feature system with the feature [+syllabic].

 $Coda \rightarrow C_0$ , where C is defined in the feature system with the feature [-syllabic].

Grammar is statistically annotated according to training set.

Find distribution of syllable lengths of words, where these are counted by finding the number of  $V_1$  sequences.

Find distribution of lengths of Nuclei, where these are counted by finding the number of V's in each  $V_1$  sequence.

Find distribution of lengths of Onsets, where these are counted by finding the number of C's in each *word-initial*  $C_0$  sequence.

Find distribution of lengths of Codas, where these are counted by finding the number of C's in each *word-final*  $C_0$  sequence.

When salads are generated, the following is done:

- (a) Pick a number of syllables from the empirical distribution.
- (b) Pick, for each syllable, an onset length, a nucleus length, and a coda length, from the corresponding empirical distributions.
  - (c) Fill these positions with consonants and vowels as appropriate, in equal frequencies.

This creates seeds.

The seeds are improved by successive migration. However, this migration is constrained: one makes one change, which consists of replacing a C in an Onset or Coda position with a different C, or a V in an Onset or Coda with a different V.

#### 9. New Parameters 11/17/05

### 9.1 -maximumGramSize

This can be 1, 2, 3, or 4. The default is 3.

## 9.2 -weighting PROBABLY OBSOLETE; CONSULT COLIN

This has three possible values.

ConjugateGradient

This is what we had first, and as of 1/31/06, it is compulsory.

ImprovedIterativeScaling

This is out of della Pietra/dP/Lafferty. Retained for possible future use.

ObservedOverExpectedAtDiscovery

Bruce's suggestion. Let t be the time at which constraint C is discovered. Then the weight of C is

> log(numberofviolationsOfCInCorpus/ NumberOfViolationsOfCInSample<sub>t</sub>)

Still works

# 9.3 -accuracySchedule

-accuracySchedule PathAndFileName

The accuracy schedule is an ascending list of numbers, all between 0 and 1, e.g.

- .1
- .6
- .9

See §Error! Reference source not found. above for how this works.

## 10. Projections

# 10.1 Defining projections

- To define a projection, you specify feature values, *all* of which must be satisfied for a segment to be projected.
- Also, you define which features get projected.
- Thus, in the file you put, e.g.:

TierName +Feature1, -Feature2, +Feature3: FeatureA, FeatureB, FeatureC

There *must* be a space here also here, or you will be toast.

where the numbered features are the criterion for projection, and the lettered features are the projected features.

- Examples:
  - > for sibilant harmony,

Sibilant +strident: anterior

For vowel harmony:

Vowel +syllabic : high, low, back, round

(and whatever other vowel features there are)

For stress, based on weight, which is based solely on vowel length:

Rhyme +syllabic : long, stress, main

• If you are doing multiple tiers, then each tier occupies a separate line in the file, like this:

Vowel +syllabic : high, low, back, round

Rhyme +syllabic: heavy, stress, main

## 10.2 Instructions for use

Command line is:

-projections FileName

If omitted, nothing is projected.

## 11. Method for Computing Expectations PROBABLY OBSOLETE; CONSULT COLIN

There are two ways:

- A. preparing a sample of pseudo-words
- B. forming a weighted finite state machine to represent the set of all possible words

Method A imposes no limit on constraint type (relevant for future development). Method B is restricted to n-gram constraints, but is more accurate.

Right now, the code uses B for finding new constraints, and A for weighting.

So, it is important for the launching code to specify the flag

-weighting ConjugateGradient

# 12. Complement Natural Classes

Complement natural classes can be enabled with the **-complementClasses** command line option. This option does the following:

- For each natural classes except [+word\_boundary], the learner creates a complement natural class.
- The complement ^C of class C contains all of the segments that are not in C except the word boundary <plus word boundary> to be decided
- The learner prunes every complement class that is extensionally identical to (contains the same segments as) an original natural class, given the segment inventory
- Constraints can mix original and complement natural classes freely; this makes them more powerful than traditional if ... then ... rules, because both the 'focus' and the 'context' can include complements.
- Notation: [^...]stands for the complement of class [...].