Evaluating the Efficacy of Prosody-lab Aligner for a Study of Vowel Variation in Cantonese

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Presentation Goals

- To demonstrate the use of Prosodylab Aligner as a tool for a large scale project examining vowel variation and change in Toronto Heritage Cantonese
- To address the effectiveness of Prosody-lab aligner for this purpose
- To assess the best source for training new Models
 - Data from all speakers together (ALL)?
 - Data from each generational group separately (GEN)?
 - Data from each speaker individually (SOLO)?



- Large-scale project investigating variation and change in Toronto's heritage languages.
- Includes sociolinguistic interview data from 7+ heritage languages spoken by immigrants and 2 or 3 generations of their descendants
- The corpus makes it possible to investigate contact effects on a wide variety of variables across all languages using the same methodology



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A Sample of Linguistic Variables

	Cantonese	Faetar	Italian	Korean	Polish	Russian	Ukrainian
VOT	1		1	1		1	1
Ø-subject	1	1	1		1	1	
Borrowing	1	1					
Classifiers	WICL-1/3			WICL-3			
Vowels	WICL-3						

GEN 1	GEN 2
Born and raised in HK, Immigrated to Canada as adults	Grew up in Toronto
L1 Cantonese, Some L2 English	Simultaneous (Early) Bilingual in Cantonese and Toronto English

Methodological Issues

- Hour-long interviews (spontaneous speech) from each of ~ 40 speakers
 - 40 speakers X 8 vowels X 6 tones X 10+ tokens/each = 19200!!!



- Forced Alignment Tools
 - FAVE (Rosenfelder et al 2011)
 - Now widely used for sociolinguistic studies of English dialects
 - But only works on English
 - Prosodylab-Aligner (Gorman et al 2011)
 - Can train new models from raw data making it customizable for any language
 - However, its efficacy for Cantonese unknown





More About Prosodylab

- ProsodyLab (Gorman et al. 2011) is based on the Hidden Markov Toolkit (HTK), a speech recognition toolkit based on Hidden Markov Models, developed at Cambridge University
- Requires
 - Python 2.6 or above
 - SoX (Sound Exchange)
 - HTK (Hidden Markov Model Toolkit)
- Can be downloaded from
 - <u>https://github.com/kylebgorman/Prosodylab-Aligner</u>
 - More info
 - <u>http://prosodylab.org/tools/aligner/</u>

What is Forced Alignment?

- Forced alignment automates the process of time-aligning transcription with audio signal
- Permits automated measure of variable, e.g. formant values



About Acoustic Models

- Uses machine-learning to perform transcript to audio time-alignment
- Speech models map phone lists to audio signal
- Will vary in how well they fit the data, how well they demarcate boundaries etc. Hence our study!

Questions

- Is Prosody-lab aligner effective at producing sufficiently accurate transcript alignment to permit automated measurement of vowel data?
- What is the best data source for training models?
 - All speakers together (ALL)?
 - More robust model, but does it work as well with the variation present in a HL variety
 - Each generational group separately (GEN)?
 - Tse (2015) suggest inter-generational phonological differences
 - Each speaker individually (SOLO)?
 - Requires a large percentage of data, but would it be as accurate?

Pre-processing

- 1. Interviews transcribed by native speakers of Cantonese using Jyutping Romanization in ELAN
 - Manual sentence-level alignment



2. To create input readable by Prosodylab-Aligner, PRAAT script used to create smaller .wav files with matching .txt files for each annotation.

PRAAT Script (Labber)



Forced alignment needs a custom dictionary

<u>Orthography</u>	<u>Phonemes</u>
GU1	GU
GU2	GU
GU3	G U 🦛
GU4	GU
GU5	GU
GU6	GU
TUB	TAH1 B
TUBA	TUW1 BAHO
TUBAL	TUW1 BAHO L
TUBB	TAH1 B
TUBBS	TAH1 B Z
TUBBY	TAH1 BIYO
TUBE	TUW1 B
TUBE	TYUW1B

To train an acoustic model:

- pronouncing bilingual dictionary (~ currently 3.6 MB)
- important b/c program can't run when there are unrecognized words in the transcript
- program needs to convert orthography to phonemic segment as established by custom dictionary

Training and Evaluation

0	Θ	CAN_dict_4.txt
ZUNG3	Z U NG	
ZUNG4	Z U NG	
ZUNG5	Z U NG	
ZUNG6	7 U NG	
7UT1	7 II T	
ZUT2	7 II T	
ZUT3	7 II T	
71174	7 II T	
ZUTS	Z U T	
ZUT6	7 U T	
ZYU1	Z YU	
ZYU2	Z YU	
ZYU3	Z YU	
ZYU4	Z YU	
ZYU5	Z YU	
ZYU6	Z YU	
ZYUN1	Z YU N	
ZYUN2	Z YU N	
ZYUN3	ZYUN	
ZYUN4	Z YU N	
ZYUN5	Z YU N	
ZYUN6	Z YU N	
ZYUT1	Z YU T	
ZYUT2	Z YU T	
ZYUT3	Z YU T	
ZYUT4	Z YU T	
ZYUT5	Z YU T	



• .wav files and matching .lab files put in a Training directory

 Prosodylab-aligner uses Training directory and **dictionary** to build an acoustic model

Custom dictionary in the format of The CMU Pronouncing Dictionary

Our 3 Models of Training With 50% of data from each speaker:

- Solo-trained model: trained only on data for speaker evaluated 1
- Generation-trained model: Data from all speakers of each Gen. Combined 2. in Training directory
- "All"-trained model: Data from all speakers combined in Training directory 3.

More Training Data (Hours of speech) \rightarrow Better Model **Therefore: More speakers data used in training = Less data lost** from each speaker to training

Output of Prosodylab-Aligner: Time-aligned Textgrid



Assessing Accuracy

- Assessment based on 10 speakers (four GEN 1 and six GEN 2)
- Examined first 10 usable textgrids for each speaker

Gold Standard: Manually identify vowel boundaries for all CAN monophthongs



Assessing Accuracy Procedures

- Record "Gold Standard" vowel boundaries
- Record Auto-aligned vowel boundaries



Assessing Accuracy

	Α	В	С	D	E	F	G	Н	I	J	К	L	М	N	0	Р	Q	R
1	Speaker	Timestam	Vowel	traini	Man. Left	Man. right	Auto left	Auto right	left diff.	right diff.	ABS Left Diff	ABS right diff	Left diff ^2	Right Diff ^2	V IN TARGET?	V. Length - Manual	V. Length - Auto	V. Length Diff.
92	C1F78A	15854	F(U)1	solo	3.53	3.65	3.54	3.67	-0.0100	-0.0200	0.0100	0.0200	0.0001	0.0004	1	0.120000	0.130000	0.010000
93	C1F78A	15897 l	L(OE)NG5	solo	0.35	0.42	0.35	0.46	0.0000	-0.0400	0.0000	0.0400	0.0000	0.0016	1	0.070000	0.110000	0.040000
94	C1F78A	15897 (G(O)3	solo	0.53	0.62	0.53	0.63	0.0000	-0.0100	0.0000	0.0100	0.0000	0.0001	1	0.090000	0.100000	0.010000
95	C1F78A	15897	NG(U)K1	solo	1.64	1.7	1.64	1.7	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1	0.060000	0.060000	0.000000
96	C1F78A	15897 \$	S(A)N1	solo	2.1	2.17	2.11	2.18	-0.0100	-0.0100	0.0100	0.0100	0.0001	0.0001	1	0.070000	0.070000	0.000000
97	C1F78A	15897 (G(AA)1	solo	2.3	2.48	2.3	2.54	0.0000	-0.0600	0.0000	0.0600	0.0000	0.0036	1	0.180000	0.240000	0.060000
98	C1M59A	18070	H(AA)6	solo	2.87	2.95	1.9	1.93	0.9700	1.0200	0.9700	1.0200	0.9409	1.0404	0	0.080000	0.030000	-0.050000
99	C1M59A	18070	G(O)2	solo	3.67	3.75	3.67	3.8	0.0000	-0.0500	0.0000	0.0500	0.0000	0.0025	1	0.080000	0.130000	0.050000
100	C1M59A	18070	G(O)3	solo	3.84	3.92	3.84	3.95	0.0000	-0.0300	0.0000	0.0300	0.0000	0.0009	1	0.080000	0.110000	0.030000
101	C1M59A	18070	G(E)3	solo	4.03	4.24	4.04	5.44	-0.0100	-1.2000	0.0100	1.2000	0.0001	1.4400	0	0.210000	1.400000	1.190000
102	C1M59A	18140	D(I)1	solo	0.35	0.43	0.34	0.4	0.0100	0.0300	0.0100	0.0300	0.0001	0.0009	1	0.080000	0.060000	-0.020000
103	C1M59A	18140	L(E)K1	solo	0.66	0.74	0.67	0.85	-0.0100	-0.1100	0.0100	0.1100	0.0001	0.0121	0	0.080000	0.180000	0.100000
104	C1M59A	18140	G(E)3	solo	0.9	0.98	0.92	0.98	-0.0200	0.0000	0.0200	0.0000	0.0004	0.0000	1	0.080000	0.060000	-0.020000
105	C1M59A	18140	J(A)N4	solo	1.22	1.35	1.24	1.32	-0.0200	0.0300	0.0200	0.0300	0.0004	0.0009	1	0.130000	0.080000	-0.050000
106	C1M59A	18140	C(E)NG2	solo	3.44	3.5	3.14	3.25	0.3000	0.2500	0.3000	0.2500	0.0900	0.0625	0	0.060000	0.110000	0.050000
107	C1M59A	18140	J(A)N4	solo	3.6	3.62	3.45	3.49	0.1500	0.1300	0.1500	0.1300	0.0225	0.0169	0	0.020000	0.040000	0.020000

- Manual ("Gold Standard") Measurements taken of left & Right boundaries of Monopthongs
- Compared to Auto boundaries: Differential on left & right, ABS of diff., diff. of total length

Т	U	V	W	Х	Y	
Solo Model Met	rics	Gen Model Metr	ics	All Model Metrics		
RMSD - LEFT Boundary	0.18527152	RMSD - LEFT Boundary	0.193158	RMSD - LEFT Boundary	0.213991	
RMSD - RIGHT Boundary	0.18690933	RMSD - RIGHT Boundary	0.197117	RMSD - RIGHT Boundary	0.207087	
No. Vowels in Target	383	No. Vowels in Target	368	No. Vowels in Target	382	
% Vowels in Target	81.84%	% Vowels in Target	78.63%	% Vowels in Target	81.62%	
Avg. Auto V. Length	0.126816	Avg. Auto V. Length	0.123650	Avg. Auto V. Length	0.132073	
Avg. V. Length deviation	0.013920	Avg. V. Length deviation	0.010753	Avg. V. Length deviation	0.019176	

- Root-Mean-Square-Deviation taken of each boundary (Chen et al 2004)
- Average Length of vowels for each model
- % of vowels' centres (by "Gold Standard") which fall within the autoaligned boundaries

$$\text{RMSD} = \sqrt{\frac{\sum_{t=1}^{n} (\hat{y}_t - y)^2}{n}}.$$

Transcription Issues



Entirety of "O5 Lam2 Jiu3" within "Gong2" boundaries



Same file: The aligner "Catches up" and aligns later sections with excellent accuracy



Modeling Silence



Aligner places "Hei2 Maa5" audio signal within silence



- The effect is more common in Solo-aligned textgrids
- Hypothesis: Silence modelling is better with more data for model training

Syllable Fusion Issues



Fusion of Seng-Jat--> Set



Fusion of Mei-Je --> Me



Fusion of Za-Hai --> Zei

- Some rare examples cause problems: Seng Jat
- However, when we use a closer transcription, the aligner does well

Wong (2006)

Results Table

In spite of problems, quite accurate:

	SOLO	GEN	ALL
Root Mean Square Deviation – Left Boundary	0.185	0.193	0.214
Root Mean Square Deviation – Right Boundary	0.187	0.197	0.207
# of Vowels in Target	383	368	382
% Vowels in Target	81.84%	78.63%	81.62%
Avg. Auto V. Length	0.127s	0.124s	0.132s
Avg. V. Length Deviation	0.014s	0.011s	0.019s

- Solo-trained model has the lowest deviation from gold-standard boundaries
- All-trained model predicts longer vowels: hence higher % of vowel centres within boundaries, despite high deviation
- Overly-long segment prediction would be bad for studies of length, VOT, etc.

Summary

- Is Prosody-lab aligner effective at producing sufficiently accurate transcript alignment to permit automated measurement of vowel data? YES
- What is the best baseline to start with
 - All speakers together (ALL)?
 - Each generational group separately (GEN)?
 - Each speaker individually (SOLO)?

Discussion

- Is Prosody-lab aligner effective at producing sufficiently accurate transcript alignment to permit automated measurement of vowel data?
 - Yes, Overall, 80% accuracy for all three models
 - Can still be a useful tool in facilitating the vowel measurement process with a preliminary estimate of where the vowel boundaries are
 - Boundaries can be manually adjusted later.

Discussion

- What is the best baseline to start with
 - ALL
 - More data used, but model overgenerates → resulted in high RMSD
 - SOLO
 - Slightly more accurate and smaller RMSD than ALL and GEN models, but not much data / too much data lost to training
 - GEN
 - A reasonable compromise between amount of data used in training vs. general accuracy

Conclusion

- The GEN model works better than ALL (contrary to expectations) possibly because of significant inter-generational differences (cf. Tse 2015)
- Yet, even with as much variation as present, it is still generally accurate, and can be a useful tool for Cantonese corpus-based studies.
- Useful for any study that requires segmental boundary information
 - Ex: VOT, vowel length, vowel formant measures, tone, consonants, etc

감사합니다**дякую Grazie molto ^{Спасибо} 多謝** gratsiə namuor:ə

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- Slides will be available at http://www.pitt.edu/~hbt3/presentations.html
- Thank you!
- 多謝晒!



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