# Trimming Phonetic Alignments Improves the Inference of Sound Correspondence Patterns from Multilingual Wordlists 

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## Goals

## Trimming Phonetic Alignments

- Improve the regularity of automatically inferred correspondence patterns among cognate sets from related languages
- Eliminate noisy data: morphemes and non-cognate elements
- Shorten long-tail distribution of correspondence patterns with few occurrences


## Correspondence Patterns in Linguistics

Language $A$
Language $B$
Language C
Language D

| 1 |  | II |  | II |  | I |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| t | a | h | e | h | i | t | U |
| $\mathrm{t}^{\text {h }}$ | a | x | e | x | u | $\mathrm{t}^{\text {b }}$ |  |
| t | a | x | e | x | u | t |  |
| ts | a | x | e | x | u | ts |  |

Figure: Corresponding alignment sites in a set of four fictitious languages.

## Correspondence Patterns

- Patterns are formed by a set of sound correspondences
- Shared between multiple languages, not language pairs
- Recurring correspondence patterns form the basis for the reconstruction of proto-languages


## Trimming in Historical Linguistics

| Pacaraos | w | a | n | u | +k |
| :--- | :--- | :--- | :--- | :--- | :--- |
| u |  |  |  |  |  |
| Napo | w | a | n | u | +n |
| a |  |  |  |  |  |
| Pastaza | w | a | n | u | +n |
| a |  |  |  |  |  |
| Ayacucho | w | a | n | u |  |
| Jauja | w | a | n | u |  |
| Lamas | w | a | n | u |  |
|  |  |  |  |  |  |

Figure: Trimming morphemes in Quechua. The root is combined with different morphemes in some varieties.

## Trimming in Historical Linguistics



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## Examples for trimming

- Trimming is often practiced without being made explicit
- Explicit examples are Payne (1991) and Cayón \& Chacon (2022)


## Trimming of Alignment Sites in Computational Biology

How does the trimming proceed?

- Trimming DNA sequence alignments
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## Methods for trimming

- Removing sites with many gaps (Capella-Gutiérrez et al. 2009)
- Removing sites based on entropy values (Criscuolo \& Gribaldo 2010)


## Datasets Used in the Study

| Data set | Lang. | Conc. | Cog.-Sets | Words | Source |
| :--- | :---: | :---: | :---: | :--- | :--- |
| CONSTENLACHIBCHAN | 25 | 106 | 213 | 1216 | Constenla Umaña (2005) |
| CROSSANDEAN | 20 | 150 | 223 | 2789 | Blum et al. (forthcoming) |
| DRAVLEX | 20 | 100 | 179 | 1341 | Kolipakam et al. (2018) |
| FELEKESEMITIC | 21 | 150 | 271 | 2622 | Feleke (2021) |
| HATTORIJAPONIC | 10 | 197 | 235 | 1710 | Hattori (1973) |
| HOUCHINESE | 15 | 139 | 228 | 1816 | Hóu (2004) |
| LEEKOREANIC | 15 | 206 | 233 | 2131 | Lee (2015) |
| ROBINSONAP | 13 | 216 | 253 | 1424 | Robinson \& Holton (2012) |
| WALWORTHPOLYNESIAN | 20 | 205 | 383 | 3637 | Walworth (2018) |
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## Standardized datasets

- Lexibank-datasets (List et al. 2022) are openly available
- Cognacy annotated manually by dataset creators


## Trimming Strategies

Language
Language A Language B Language C Language D Gap proportion

Core-oriented

| s | - | t | e | r | b | - |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| m | e | $\mathrm{t}^{\mathrm{h}}$ | e | - | - | - |
| - | a | t | e | - | b | u |
| - | - | t | e | - | b | - |
| 0.5 | 0.5 | 0.0 | 0.0 | 0.75 | 0.25 | 0.75 |

Gap-oriented

| s | - | t | e | r | b | - |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| m | e | $\mathrm{t}^{\mathrm{h}}$ | e | - | - | - |
| - | a | t | e | - | b | u |
| - | - | t | e | - | b | - |
| 0.5 | 0.5 | 0.0 | 0.0 | 0.75 | 0.25 | 0.75 |

Figure: Artificial example for the computation of gap profiles followed by trimming using the core-oriented (left) and the gap-oriented strategy (right).

## Computational Details

- Minimal CV/VC skeleton is preserved in all settings
- Sites with more than $50 \%$ gaps are trimmed


## Regularity thresholds

How do we measure regularity?

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- All patterns with at least three occurrences are considered to be 'regular'
- How many patterns in a cognate set are above this threshold?
- All words with more than $75 \%$ of regular patterns are analyzed as 'regular'


## Results

|  | Original |  | Core |  | Gap |  |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: |
| Dataset | P | W | P | W | P | W |
| CONSTENLACHIBCHAN | 0.71 | 0.50 | 0.69 | 0.46 | $\mathbf{0 . 7 6}$ | $\mathbf{0 . 5 1}$ |
| CROSSANDEAN | 0.73 | 0.58 | 0.74 | 0.60 | $\mathbf{0 . 7 5}$ | $\mathbf{0 . 6 4}$ |
| DRAVLEX | 0.56 | 0.23 | 0.57 | 0.27 | $\mathbf{0 . 6 1}$ | $\mathbf{0 . 3 1}$ |
| FELEKESEMITIC | 0.55 | 0.22 | 0.58 | 0.25 | $\mathbf{0 . 6 2}$ | $\mathbf{0 . 2 9}$ |
| HATTORIJAPONIC | 0.58 | 0.33 | 0.57 | 0.33 | $\mathbf{0 . 5 9}$ | $\mathbf{0 . 3 8}$ |
| HOUCHINESE | 0.65 | 0.40 | 0.65 | 0.42 | $\mathbf{0 . 6 9}$ | $\mathbf{0 . 4 5}$ |
| LEEKOREANIC | 0.44 | 0.21 | 0.47 | 0.20 | $\mathbf{0 . 5 2}$ | $\mathbf{0 . 2 2}$ |
| ROBINSONAP | 0.64 | 0.36 | 0.65 | 0.37 | $\mathbf{0 . 6 7}$ | $\mathbf{0 . 4 1}$ |
| WALWORTHPOLYNESIAN | 0.66 | 0.40 | 0.66 | 0.40 | $\mathbf{0 . 7 2}$ | $\mathbf{0 . 4 8}$ |
| ZHIVLOVOBUGRIAN | 0.57 | 0.24 | 0.58 | 0.26 | $\mathbf{0 . 6 1}$ | $\mathbf{0 . 2 8}$ |

Table: Proportion of regular correspondence patterns ( P ) and regular words (W) across all datasets after trimming.

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## Summary

- Gap-oriented trimming shows the best results for all datasets
- Datasets with low internal diversity show the fewest improvements


## Comparing the Random Model

| Dataset | Core | Gap |
| :--- | :---: | :---: |
| CONSTENLACHIBCHAN | 0.58 | 0.00 |
| CROSSANDEAN | 0.02 | 0.00 |
| DRAVLEX | 0.00 | 0.00 |
| FELEKESEMITIC | 0.17 | 0.01 |
| HATTORIJAPONIC | 0.40 | 0.00 |
| HOUCHINESE | 0.05 | 0.00 |
| LEEKOREANIC | 0.54 | 0.06 |
| ROBINSONAP | 0.34 | 0.00 |
| WALWORTHPOLYNESIAN | 0.11 | 0.00 |
| ZHIVLOVOBUGRIAN | 0.12 | 0.05 |

Table: Percentage of models with random deletion of alignment sites that achieved higher regularity than the respective trimming model.

## Successful Removal of Irregular Patterns



Figure: Distribution of alignment sites per pattern with gap-oriented trimming and without. Each point on the $x$-axis represents one correspondence pattern.

## Example I: Successful Trimming in Chibchan

| Boruca | - | I | u | - | $\eta$ | - |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Cabecar | - - |  | u | - | I | i | t | 1 |
| Chimila | - - |  | u | h | $\eta$ | a | ? | - |
| Malayo | - - |  | $\dot{\text { i }}$ | - | n | - |  |  |
| Ngabere | 〕 u |  | ш |  |  |  |  |  |
|  |  |  | ũ |  | ${ }^{\text {nd }}$ |  |  |  |

Figure: Gap-oriented trimming for the cognate words of ASHES

## Evaluation

- Reconstruction provided by Pache (2018)
- Trimming identifies problematic alignment sites and removes them


## Example II: Problematic Trimming in Chibchan

| Boruca | d | $i$ | $?$ |
| :--- | :--- | :--- | :--- | :--- |
| Bribri | d | i | ? |
| Buglere | ts | i | - |
| Cogui | n | i | - |
| Ngabere | n | r | - |
| Proto-Chibchan | nd | $i$ | ? |

Figure: Trimming for the cognate words of water

## Evaluation

- Reconstruction provided by Pache (2018)
- Our strategy erroneously eliminates a site that includes reconstructed segments


## Outlook

What we have

- Trimming improves the regularity of inferred correspondence patterns
- Shortening of the distribution tail of patterns with few alignment sites
- Promising transfer of trimming to historical linguistics


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## Where we want to go

- Find the best thresholds for gaps and regularity
- Use inferred correspondence patterns for sound reconstruction


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