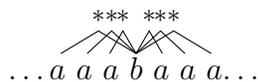


Majority Rule in Harmonic Serialism - General Case

- Define output constraint AGREE-GLOBAL as assigning violations to subsequences $a \dots b$ and $b \dots a$
- Every pair of segments in the word is a potential locus of violation; picture shows six loci associated with one b



- Let A represent the total number of a 's in a candidate and B represent the total number of b 's
- Each a violates AGREE-GLOBAL B times, giving $A \times B$ total violations
- AGREE-GLOBAL disprefers candidates with more violations: $\# \text{ vios by } C_i < \# \text{ vios by } C_j \iff C_i \succ_{\text{AGREE-GLOBAL}} C_j$
- Define faithfulness constraint IDENT as penalizing changes $/a/ \rightarrow [b]$ and $/b/ \rightarrow [a]$
- With AGREE-GLOBAL \gg IDENT, it is always optimal to assimilate a member of the smallest class to the largest class

– Consider an input made of A a 's and B b 's ($A + B = n$), where there are more a 's than b 's: $A > B$

– Three relevant candidates:

- C_{faithful} fully faithful
- $C_{a \rightarrow b}$ one $/a/$ changed to $[b]$
- $C_{b \rightarrow a}$ one $/b/$ changed to $[a]$ (Majority Rule candidate)

– Total violations of each candidate:

Candidate	No. of a 's	No. of b 's	Violations of AGREE-GLOBAL	Violations of IDENT
C_{faithful}	A	B	$A \times B = AB$	0
$C_{a \rightarrow b}$	$A - 1$	$B + 1$	$(A - 1) \times (B + 1) = AB + A - B - 1$	1
$C_{b \rightarrow a}$	$A + 1$	$B - 1$	$(A + 1) \times (B - 1) = AB - A + B - 1$	1

– Majority Rule candidate violates AGREE-GLOBAL the least: $C_{b \rightarrow a} \succ C_{\text{faithful}} \succeq C_{a \rightarrow b}$

$$AB - A + B - 1 < AB \leq AB + A - B - 1$$

$$B - A < 1 \leq A - B$$

- For any A, B where $A > B$, Majority Rule candidate is preferred by AGREE-GLOBAL over faithful candidate and other unfaithful candidate, and is therefore optimal
- Given an input of length $n = A + B$, we can write the number of violations of the faithful candidate as $A \times (n - A) = nA - A^2$. We know $n > A$, so $nA > A^2$. While A grows linearly with the length of the input, the total violations of AGREE-GLOBAL grow quadratically.

Alphabetical Sorting in Harmonic Serialism

See Lamont (2018) for an argument that sorting in HS crucially depends on subsequence constraints.

The Midpoint Pathology

- Eisner (1997b) gives the following tableau for the Midpoint Pathology using a single ALIGN constraint; each column records the number of violations contributed by that syllable, with the total violations in the right column

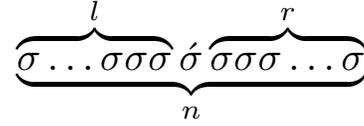
$/\sigma\sigma\sigma\sigma\sigma\sigma/ + /H/$	σ_1	σ_2	σ_3	σ_4	σ_5	σ_6	σ_7	Total violations
a. $\acute{\sigma}\sigma\sigma\sigma\sigma\sigma$		1	2	3	4	5	6	W 21
b. $\sigma\acute{\sigma}\sigma\sigma\sigma\sigma$	1		1	2	3	4	5	W 16
c. $\sigma\sigma\acute{\sigma}\sigma\sigma\sigma$	2	1		1	2	3	4	W 13
→ d. $\sigma\sigma\sigma\acute{\sigma}\sigma\sigma$	3	2	1		1	2	3	12
e. $\sigma\sigma\sigma\sigma\acute{\sigma}\sigma$	4	3	2	1		1	2	W 13
f. $\sigma\sigma\sigma\sigma\sigma\acute{\sigma}$	5	4	3	2	1		1	W 16
g. $\sigma\sigma\sigma\sigma\sigma\acute{\sigma}$	6	5	4	3	2	1		W 21

- With some reverse engineering, we can see that the ALIGN constraint assigns violations to four marked subsequences: $\acute{\sigma} \dots \sigma$, $\acute{\sigma} \dots \sigma \dots \sigma$, $\sigma \dots \acute{\sigma}$, $\sigma \dots \sigma \dots \acute{\sigma}$

- The tableau below makes this explicit, again, the right column records the total

/σσσσσσσ/ + /H/	acute...σ	acute...σ...σ	σ...acute	σ...σ...acute	Total violations
a. acuteσσσσσσ	6	15			W 21
b. σacuteσσσσσσ	5	10	1		W 16
c. σσacuteσσσσ	4	6	2	1	W 13
→ d. σσσacuteσσ	3	3	3	3	12
e. σσσσacuteσσ	2	1	4	6	W 13
f. σσσσσacuteσ	1		5	10	W 16
g. σσσσσσacute			6	15	W 21

- Consider candidates of length n with one high-toned syllable. Let l and r be the number of syllables to the left and right of the high-toned syllable, respectively. $l + r = n - 1$



- For $l > 0$, there are l subsequences $\sigma \dots \acute{\sigma}$: $\binom{l}{1} = \frac{l!}{1!(l-1)!} = l$. Likewise, there are r subsequences $\acute{\sigma} \dots \sigma$ for $r > 1$.
- There are $l + r = n - 1$ subsequences $\sigma \dots \acute{\sigma}$ and $\acute{\sigma} \dots \sigma$ regardless of where the high tone is placed. Because these subsequences do not affect the constraint's preference, we can ignore them, simplifying the tableau above:

/σσσσσσσσ/ + /H/	acute...σ...σ	σ...σ...acute	Total violations
a. acuteσσσσσσ	15		W 15
b. σacuteσσσσσσ	10		W 10
c. σσacuteσσσσ	6	1	W 7
→ d. σσσacuteσσ	3	3	6
e. σσσσacuteσσ	1	6	W 7
f. σσσσσacuteσ		10	W 10
g. σσσσσσacute		15	W 15

- We only need the subsequences $\acute{\sigma} \dots \sigma \dots \sigma$ and $\sigma \dots \sigma \dots \acute{\sigma}$ to center the high tone. The Midpoint Pathology obtains when $l \geq 2$, $r \geq 2$, and $n \geq 6$. As above, the ALIGN constraint disfavors candidates with more violations.

- For $l \geq 2$, there are $\frac{l^2-l}{2}$ subsequences $\sigma \dots \sigma \dots \acute{\sigma}$: $\binom{l}{2} = \frac{l!}{2!(l-2)!} = \frac{l(l-1)}{2} = \frac{l^2-l}{2}$, and 0 for $l \leq 1$.
- Likewise, there are $\frac{r^2-r}{2}$ subsequences $\acute{\sigma} \dots \sigma \dots \sigma$ for $r \geq 2$ and 0 for $r \leq 1$.
- We have $\frac{l^2-l+r^2-r}{2}$ total subsequences $\sigma \dots \sigma \dots \acute{\sigma}$ and $\acute{\sigma} \dots \sigma \dots \sigma$. This is minimized when $l = r$ (i.e. when the high tone is centered):
 - * When $l = r$, we have $\frac{l^2-l+l^2-l}{2} = \frac{2(l^2-l)}{2} = l^2 - l$ total violations
 - * When $l < r$, we have $\frac{l^2-l+(n-l-1)^2-(n-l-1)}{2} = \frac{2l^2+2l+n^2-2ln-3n+2}{2}$ total violations

$$l^2 - l < \frac{2l^2 + 2l + n^2 - 2ln - 3n + 2}{2}$$

$$2l^2 - 2l < 2l^2 + 2l + n^2 - 2ln - 3n + 2$$

$$0 < 4l + n^2 - 2ln - 3n + 2$$

$$0 < 4(2) + (6)^2 - 2(2)(6) - 3(6) + 2 \leq 4l + n^2 - 2ln - 3n + 2$$

$$0 < 4 \leq 4l + n^2 - 2ln - 3n + 2$$

- * By symmetry, when $l = r$, there are fewer violations than when $l > r$
- The candidate where the high tone is centered violates ALIGN the least, and is optimal.
- Again, we see quadratic growth in the number of possible violations of ALIGN relative to the length fo the input

The take away

Assuming constraints simply add up violations, the total number of violations an output constraint can assign grows quadratically if it is defined over subsequences (Eisner, 1997a; Bíró, 2003). This is not true for constraints over substrings, which can assign at most $n - k + 1$ violations to a candidate of length n where k is the length of the locus of violation (tiers are irrelevant). The three pathologies discussed here depend on constraints defined over subsequences. Removing them from CON begins to rein in the computational power of HS.

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