

Harmony in Harmonic Serialism*
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1. Introduction

Assimilation as feature spreading is a central insight of autosegmental phonology (Goldsmith 1976a, b). The idea is that assimilation involves increasing the temporal span of a tone or distinctive feature to encompass more than a single segment. In autosegmental phonology, which coordinates features and segments via association lines, the spreading of a feature's associations expands its scope in the segmental string.

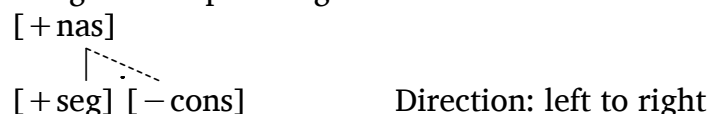
For example, in Johore Malay, nasality spreads rightward affecting vowels and glides:

(1) Nasal harmony in Johore Malay (Onn 1976)

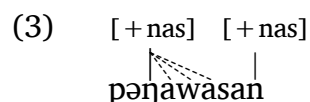
mãʔãp	'pardon'
pəŋãwãsan	'supervision'
mãratappi	'to cause to cry'
baŋõn	'to rise'

In most implementations of autosegmental phonology, spreading is obtained by iterative application of rules like the following:¹

(2) Autosegmental spreading rule



Iterative rules apply to their own output, proceeding directionally until no further changes can be made (Anderson 1980; Howard 1972; Johnson 1972; Kenstowicz & Kisseberth 1977 and others) Spreading therefore continues until it runs out of segments or is blocked by a segment with an incompatible feature specification (e.g., true consonants in Johore Malay):



Although Optimality Theory has no direct equivalent to spreading rules (Prince & Smolensky 1993/2004), OT markedness constraints that favor candidates with spreading have been used in analyses of harmony phenomena. It turns out (section 2) that standard proposals for the pro-spreading markedness constraint make implausible typological predictions (McCarthy 2003; Wilson 2003, 2004, 2006). This leads in section 3 to a new proposal with three main elements:

- (i) Distinctive features are privative (present/absent), not equipollent (positive/negative).

¹In the earliest literature on autosegmental phonology such as Goldsmith (Goldsmith 1976a, b) or Clements and Ford (Clements 1979), spreading was effected by constraints rather than rules. In place of iteration, which makes sense for rules but not constraints, Clements and Ford recruit the Q variable of Halle (Halle 1975).

- (ii) The motive for harmony is a constraint on autosegmental representations, SHARE(F), that is violated by any pair of adjacent segments that are not linked to the same [F] autosegment.
- (iii) Harmony and all other phonological processes occur serially rather than in parallel. This assumption is a consequence of adopting Harmonic Serialism as the overall analytic framework.

I'll refer to the theory with this constellation of assumptions as *Serial Harmony* (SH), not to be confused with Harmonic Serialism (HS).

After explaining these assumptions in section 3, I go on in section 4 to show how this system accounts for various 'pathologies' identified by Wilson. These pathologies are implausible typological predictions that emerge from theories of harmony based on alignment constraints in OT. The move to SH eliminates these unwelcome predictions.

Subsequent sections address some issues that arise when SH is extended to vowel harmony (section 5) and confront some potential challenges to this theory (section 6).

Throughout this article, I often illustrate problems and results by using variations on the Johore Malay nasal harmony pattern in (1). This is just a matter of convenience. Neither the problems that I address nor SH as a whole are specific to nasal harmony. Rather, they are far more general, involving phenomena like vowel harmony, assimilation of tongue root advancement or retraction, and of course tone spreading.

Conversely, the scope of this article is also less general than the broad topic of harmony processes. For example, I will not be saying anything about the agreement-by-correspondence approach to long-distance assimilation (Hansson 2001; Rose & Walker 2004).

2. Problems with current approaches to spreading in OT

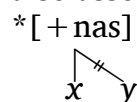
If unimportant details are set aside, then there are only two main approaches to the pro-spreading markedness constraint in OT, local AGREE and long-distance ALIGN. Both have serious problems.

2.1. Local AGREE

The constraint AGREE is perhaps closest conceptually to iterative rules like (2). AGREE(F) says that, if a segment bears the feature-value [F], then the immediately preceding/following segment must also bear that feature value (Bakovic 2000b; Eisner 1999; Lombardi 1999, 2001; Pulleyblank 2004). A directional version of AGREE, appropriate for Johore Malay, appears in (4):

(4) AGREE-R([nasal])

In a sequence of adjacent segments xy , if x is associated with [nasal], then y is also associated with [nasal]. I.e.,



The [ŋa] sequence in *[pəŋawasan] violates this constraint because the [nasal] feature of the [ŋ] is not shared with the immediately following [a].

The problem with AGREE arises in languages where harmony is blocked. Nasal harmony is often blocked by featural cooccurrence restrictions that, in general, discountenance nasality in lower-sonority segments (Cohn 1993; Piggott 1992; Pulleyblank 1989; Schourup 1972; Walker 1998). Walker formalizes these restrictions in OT with the following universally fixed constraint hierarchy:

(5) Nasalizability constraint hierarchy (Walker 1998: 36)

*NASOBSSTOP >> *NASFRICATIVE >> *NASLIQUID >> *NASGLIDE >>
 *NASVOWEL >> *NASSONSTOP

For example, *NASFRICATIVE is violated by [s̃]. If AGREE-R([nasal]) is ranked below *NASFRICATIVE, then fricatives will not undergo harmony. Under the further assumption that nasal spreading cannot skip over segments, fricatives will block the propagation of nasality. In Johore Malay, where nasal spreading affects only vowels and glides, AGREE-R([nasal]) is ranked between *NASLIQUID and *NASGLIDE.

AGREE doesn't work because it has a sour-grapes property:² it favors candidates with spreading that is fully successful, but it gives up on candidates where spreading is blocked (McCarthy 2003; Wilson 2003, 2004, 2006). For this reason, it predicts for Johore Malay that hypothetical /mawa/ will become [mãwã], with total harmony, but hypothetical /mawasa/ will become [mawasa], with no harmony at all. The tableaux in (6) and (7) illustrate this prediction. When all AGREE violations can be eliminated (tableau (6)), then they are. But when a blocking constraint prevents complete spreading (tableau (7)), there is no spreading at all. (The sequences that violate AGREE have been underlined to make them easy to find. Tableaux are in comparative format (Prince 2002a).)

(6) AGREE without blocker

/mawa/	*NASFRIC	AGREE-R([nas])	IDENT([nas])
a. → m̃ãw̃ã			3
b. <u>m</u> awa		1 W	L
c. m̃ <u>aw</u> a		1 W	1 L
d. m̃ã <u>w</u> ã		1 W	2 L

² The phrase “sour grapes property”, due to Jaye Padgett, refers to Aesop's fable of the fox and the grapes. When the fox can't reach the grapes, he walks away in disgust saying, “Those grapes are probably sour anyway!”

(7) Sour grapes effect of AGREE with blocker

/mawasa/	*NASFRIC	AGREE-R([nas])	IDENT([nas])
a. → <u>m</u> awasa		1	
b. m <u>ã</u> wasa		1	1 W
c. m <u>ã</u> <u>~</u> wasa		1	2 W
d. m <u>ã</u> <u>~</u> <u>ã</u> sa		1	3 W
e. m <u>ã</u> <u>~</u> <u>ã</u> <u>~</u> sa	1 W	1	4 W
f. m <u>ã</u> <u>~</u> <u>ã</u> <u>~</u> <u>ã</u> sa	1 W	L	5 W

The intended winner in (7) is [mã~ãsa], but it is harmonically bounded by the candidates with no spreading and total spreading, [mawasa] and [mã~ãã]. Therefore, the intended winner cannot actually win under *any* ranking of these constraints.

Clearly, this AGREE constraint is unable to account for real languages like Johore Malay. Worse yet, it predicts the existence of languages with sour-grapes spreading like the one in (6) and (7), and such languages are not attested. This problem is fatal to this approach to harmony.

A devotee of AGREE might offer to solve this problem by building the blocking effect into the AGREE constraint itself, instead of deriving this effect from interaction with higher-ranking constraints like *NASFRICATIVE. In Johore Malay, for instance, the AGREE constraint would have to prohibit any sequence of a nasal segment immediately followed by an oral vowel or glide: *[+nasal][-cons, -nasal]. Since [mã~ãsa] satisfies this constraint but no candidate with less spreading does, it would do the job.

This seemingly innocent analytic move really seems to miss the whole point of OT (Wilson 2003, 2004). The fundamental descriptive goals of OT are to derive complex patterns from the interaction of simple constraints and to derive language typology by permuting rankings. If AGREE in Johore Malay is defined as *[+nasal][-cons, -nasal], then we are deriving a more complex pattern by complicating a constraint and not by interaction. That becomes apparent when we look at a language with a different set of blockers, such as Sundanese (Anderson 1972; Robins 1957). Because glides are blockers in Sundanese, a slightly different AGREE constraint will be required. If we do this, then we are deriving language typology by constraint parametrization rather than ranking permutation. The move of redefining AGREE to incorporate the blocking conditions, while technically possible, is antithetical to sound explanation in OT.

2.2. Long-distance ALIGN

Alignment constraints require that the edges of linguistic structures coincide (McCarthy & Prince 1993; Prince & Smolensky 1993/2004). When alignment constraints are evaluated gradiently, they discriminate among candidates that are imperfectly aligned.

Gradient alignment constraints have often been used to enforce autosegmental spreading by requiring a distinctive feature to be associated with the leftmost or rightmost segment in some domain (Archangeli & Pulleyblank 1994b; Cole &

Kisseberth 1995a, b; Kirchner 1993; Pulleyblank 1996; Smolensky 1993; and many others). In Johore Malay, for example, the gradient constraint ALIGN-R([nasal], word) ensures that each token of a [nasal] autosegment is linked as far to the right as possible:

(8) ALIGN-R([nasal], word) illustrated

	/mawasa/	*NASFRIC	ALIGN-R([nasal], word)	IDENT([nasal])
a.	mawasa		5 W	W
b.	māwasa		4 W	1 W
c.	māw̃asa		3 W	2 W
d. →	māw̃āsa		2	3
e.	māw̃āšā	1 W	1 L	4 L
f.	māw̃āšā̃	1 W	L	5 L

Candidate (8)d wins because its [nasal] autosegment is linked to a segment that is only two segments away from the right edge of the word. In candidates with more ALIGN violations, [nasal] hasn't spread as far, whereas candidates with fewer violations contain the forbidden segment *[š̃].

Gradient alignment constraints are not without their problems (McCarthy 2003), and the problems are particularly serious when gradient alignment is applied to harmony processes (Wilson 2003, 2004, 2006). Wilson has identified a broad range of 'pathologies' — unwelcome predictions that derive from ranking constraints like ALIGN-R([nasal], word) in ways other than just (8). I will reserve discussion of most of the pathologies for section 4, after SH has been presented, but meanwhile it is useful to get some sense of why gradient alignment is not a sound basis for the theory of harmony.

One pathology is the ability of featural alignment constraints to block epenthesis. ALIGN-R([nasal], word) is violated by any segments that are to the right of a nasal segment, unless [nasal] can spread onto them. If a potential locus of epenthesis is inaccessible to spreading because of a blocking effect like (8), then ALIGN-R([nasal], word) can prevent epenthesis in that position.

For instance, suppose there is a language that satisfies NO-CODA by epenthesizing the vowel [i]. Obviously, NO-CODA dominates DEP. Suppose further that NO-CODA is ranked below ALIGN-R([nasal], word) in a hierarchy like (8). In that case, epenthesis will be blocked if the epenthetic vowel is inaccessible to nasal harmony because of an intervening blocking segment:

(9) ALIGN-R([nasal], word) preventing epenthesis

/mas/	*NASFRIC	ALIGN-R([nasal], word)	NO-CODA	DEP
a. → mās		1	1	
b. māsɪ		2 W	L	1 L
c. māsĩ	1 W	L	L	1 L

Since words that contain no nasals vacuously satisfy ALIGN-R([nasal], word), that constraint is irrelevant, and so NO-CODA is satisfied by vowel epenthesis:

(10) No nasal trigger: /pas/ → [pasɪ]

/pas/	*NASFRIC	ALIGN-R([nasal], word)	NO-CODA	DEP
a. → pasɪ				1
b. pas			1 W	L

Likewise, words that contain a nasal but no blockers will undergo epenthesis, since epenthesis does not subvert ALIGN-R([nasal], word) in these words:

(11) No blocker: /maw/ → [māsĩ]

/mas/	*NASFRIC	ALIGN-R([nasal], word)	NO-CODA	DEP
a. → māsĩ				1
b. mās			1 W	L

The language illustrated in (9), (10), and (11) would match the following description: final consonants become onsets by vowel epenthesis, unless the word contains, at any distance, a nasal followed by a true consonant. This is a wildly implausible prediction — truly, it is a pathology.

This pathology reflects a larger issue confronting alignment-based harmony. The combination of gradient alignment with blocking constraints like *NASFRICATIVE creates an impetus to minimize the number of peripheral segments that are inaccessible to harmony because of an intervening blocker. The effects of this minimization can include failure of epenthesis, as in (9), triggering of deletion, selection of short allomorphs, less reduplicative copying, and repositioning of affixes (see section 4). A related prediction is that the count of peripheral segments will not be minimized when the word contains no harmony trigger or when no blocker intervenes between the harmony trigger and the domain edge designated in the alignment constraint. These predictions are all wrong, as far as we know.

These unwanted predictions of ALIGN are part of a larger problem usually referred to as ‘too many repairs’ (TMR) or ‘too many solutions’ (Blumenfeld 2006; Lombardi 1995/2001; Pater 1999; Steriade 2001, 2001/2008; Wilson 2000, 2001). In a TMR problem, the observed ways of satisfying a markedness constraint by an unfaithful mapping are a proper subset of the ways that are predicted by free permutation of

faithfulness constraints. There are many ways of satisfying ALIGN-R([nasal], word), but only one is actually attested: spreading [nasal] as far to the right as possible.

2.3. Summary

Local AGREE constraints aren't powerful enough to compel harmony when a blocking segment makes perfect harmony impossible. Long-distance ALIGN constraints are too powerful, since they predict avoidance of segments that are inaccessible to harmony. Something different is required.

3. The proposal: Serial Harmony

The theory of Serial Harmony (SH) has three elements: privative features (section 3.1); a proposal about the constraint that favors autosegmental spreading (section 3.2) and a derivational approach to phonological processes (section 3.4).

3.1. Privative features

Privative features mark contrasts by their presence or absence. For example, the representation of [m] includes a token of the feature [nasal], but the representation of [b] does not. Equipollent features have two values. For example, the representation of [m] includes the feature value [+nasal], but the representation of [b] includes the feature value [−nasal]. The terminology comes from Trubetzkoy, though it is clear that Trubetzkoy himself had something very different in mind when he introduced these expressions (Trubetzkoy 1939: 67).

Previous research makes a fairly compelling case for privativity. The argument rests on the not entirely uncontroversial claim that assimilation processes are asymmetric: they only ever target one value of a feature. Steriade (1993a, b, 1995) and Trigo (1993) propose that no language spreads [−nasal], though plenty of languages spread [+nasal]. This observation finds an immediate explanation if [nasal] is privative. Earlier, Lombardi (1991) argued on these grounds for privative laryngeal features, and Steriade (1995: 147-149) extends the privativity hypothesis to [round].

The best cases against privativity can be made for [ATR] and [back] (Archangeli & Pulleyblank 1994a). but it in both cases we are probably dealing with two binary features (Steriade 1995: 150): [ATR] versus [RTR], and [back] versus [front]. The [ATR]/[RTR] question is addressed by Backley (1997), Goad (1991, 1993), Pulleyblank (1995), and Rose (1996: 89-90). Evidence demonstrating the need for [front] as well as [back] is assembled (though not presented as such) in Ladefoged and Maddieson (1996: 290-292).

Obviously, the argument for privativity from assimilation asymmetries only works with features that participate in assimilation; it says nothing about whether typically non-assimilating features like [continuant] are privative or not. But since this paper is about assimilation, it does not matter for present purposes whether these other features are privative or not.

3.2. Autosegmental spreading in SH

We saw in section 2 that the markedness constraint favoring autosegmental spreading is a crucial weakness of previous approaches to harmony in OT. My proposal

looks somewhat like one of those earlier constraints, AGREE, but there are important differences as a result of other assumptions I make.

The constraint SHARE(F) requires adjacent segments (or other harmony-bearing units) to be linked to the same [F] autosegment:

(12) SHARE(F)

Assign one violation mark for every pair of adjacent segments that are not linked to the same token of [F].

When SHARE(F) is combined with the assumption that features are privative, there is only one way that a pair of adjacent segments can satisfy this constraint. Example (13) illustrates satisfaction of SHARE([nasal]):

(13) Example: SHARE([nasal]) obeyed

[nas]
 ↙
 mā

There are several ways that a pair of adjacent segments can violate this constraint: a [nasal] autosegment is linked to one but not the other, as in (14)a; each segment is linked to a different [nasal] autosegment, as in (14)b; or neither segment is linked to a [nasal] autosegment, as in (14)c.

(14) Examples: SHARE([nasal]) violated

a. [nas] b. [nas] [nas] c.
 | ↘ ↙ ba
 ma mā

In the rest of this article, I will be using a simplified notation for autosegmental structures with privative features that allows easy detection of SHARE(F) violations. When two segments are separated by a vertical line, they are not linked to the same [F] autosegment. (Whether [F] is [nasal] or some other feature will usually be clear from context.) For example, [m|a] (= (14)a) violates SHARE([nasal]) because [m] is linked to a [nasal] autosegment and [a] is not. The form [m|ã] (= (14)b) also violates SHARE([nasal]), though in this case the segments are linked to different [nasal] autosegments. In [b|a] (= (14)c), neither is linked to a [nasal] autosegment, and again SHARE([nasal]) is violated. Finally, [mã] satisfies SHARE([nasal]) because a single [nasal] autosegment is linked to both segments. When reckoning violations of SHARE, a simple trick is to count | symbols.

Unlike ALIGN, SHARE has no inherent directionality. Instead, directionality of spreading is obtained through constraint interaction — specifically, interaction with faithfulness constraints. If [nasal] only spreads to the right in some language, then the leftmost segment in a sequence of segments associated with some [nasal] autosegment must be its underlying host. If the leftmost segment associated with some [nasal] autosegment is *required* to be its underlying host, then spreading must be strictly

rightward, as in Johore Malay. This faithfulness-based approach directionality is formalized by the constraints in (15) and (16):³

(15) INITIAL(F)

Let input F tier = $f_1f_2\dots f_m$.

Let input segmental tier = $s_1s_2\dots s_n$.

Let output F tier = $f_1f_2\dots f_o$.

Let output segmental tier = $s_1s_2\dots s_p$.

Assign one violation mark for every $s_i \Re s_j$, where:

$f_k \Re f_i$,

f_k is associated with s_i , and there is no s_x that precedes s_i and is also associated with f_k , and

f_i is associated with s_j , and there is some s_y that precedes s_j and is also associated with f_i .

(16) FINAL(F)

Let input F tier = $f_1f_2\dots f_m$.

Let input segmental tier = $s_1s_2\dots s_n$.

Let output F tier = $f_1f_2\dots f_o$.

Let output segmental tier = $s_1s_2\dots s_p$.

Assign one violation mark for every $s_i \Re s_j$, where:

$f_k \Re f_i$,

f_k is associated with s_i , and there is no s_x that follows s_i and is also associated with f_k , and

f_i is associated with s_j , and there is some s_y that follows s_j and is also associated with f_i .

These definitions are obviously quite a mouthful, but the concept they embody is quite simple. Leftward spreading of, say, [nasal] violates INITIAL([nasal]) the leftmost segment linked to nasal in the output precedes the (correspondent of) the leftmost segment linked to it in the input.⁴

Finally, I will assume a version of IDENT(F) that is violated whenever a segment loses or gains an association with an [F] autosegment.

³ The closest analogue to these constraints in the earlier literature is ANCHOR in McCarthy & Prince (McCarthy & Prince 1995, 1999).

⁴ Because the definition of INITIAL(F)/FINAL(F) in (15) includes the antecedent clause ' $s_i \Re s_j$ ', spreading cannot have a directional bias when the underlying segmental host of [F] has been deleted but [F] itself has been left behind. This prediction is exemplified in Capanahua (Loos 1969; Safir 1982). Nasality spreads leftward from an intact nasal consonant, affecting vowels and glides: [pōjān] 'arm'; [bīmi] 'fruit'. Nasal consonants delete from coda position, except when followed by a stop. Spreading of nasality from a deleted nasal is bidirectional: /wuranwu/ → [wurañwū] 'push it'.

(17) IDENT(F)

Let input F tier = $f_1f_2\dots f_m$.

Let input segmental tier = $s_1s_2\dots s_n$.

Let output F tier = $f_1f_2\dots f_o$.

Let output segmental tier = $s_1s_2\dots s_p$.

Assign one violation mark for every pair $s_i \mathfrak{R} s_j$, where:

f_k is associated with s_i , and

there is no f_l such that $f_k \mathfrak{R} f_l$ and f_l is associated with s_j ,

or

f_l is associated with s_j , and

there is no f_k such that $f_k \mathfrak{R} f_l$ and f_k is associated with s_i .

This way of defining IDENT lumps four different ways of being unfaithful: delinking of a feature; deletion of a feature; spreading of a feature; and insertion of a feature. It is likely that more than one faithfulness constraint is involved here. This issue merits further exploration, but I defer it in the interest of forging ahead on the topic of this paper.

I will conclude this subsection by applying these constraints and representational assumptions to nasal harmony in Johore Malay. We'll start with the phonemic inventory. Since nasality is only contrastive in the nasal stops, the faithfulness constraint IDENT([nasal]) must be ranked below *NASVOWEL and all of the other constraints that are higher in the nasalizability constraint hierarchy (5):

(18) /bãt/ → [bat] (hypothetical)

	b ã t	*NASVOWEL	IDENT([nas])
a. →	b a t		1
b.	b ã t	1 W	L

Harmony occurs at the expense of unfaithfulness to underlying orality. Therefore, IDENT([nasal]) is dominated by SHARE([nasal]). Furthermore, because glides and vowels can become nasalized as a result of harmony, SHARE([nasal]) must dominate the constraints at the bottom of the nasalizability hierarchy, *NASGLIDE and *NASVOWEL:

(19) /maʔap/ → [mãʔãp]

	m a ʔ a p	SHARE([nas])	*NASGLI	*NASVOW	IDENT([nas])
a. →	mãʔãp	1	1	2	3
b.	m a ʔ a p	4 W	L	L	L

Spreading of [nasal] is blocked by *NASLIQUID and the other nasalizability constraints that dominate SHARE([nasal]):

(20) /məratappi/ → [m̃əratappi]

m ə r a t a pp i	*NASLIQ	SHARE([nas])	*NASGLI	*NASVOW	IDENT([nas])
a. → m̃ə r a t a pp i		6		1	1
b. m̃ə̃r̃ã t a pp i	1 W	4 L		2 W	3 W

Spreading that skips over some segments, as in *[m̃ə̃r̃ãt̃ãpp̃i], is arguably ruled out universally (Gafos 1999; Ní Chiosáin & Padgett 2001; Walker 1998). For more about general problem of neutral segments in harmony systems, see section 5.1.

Finally, the observation that nasality only spreads rightward in Johore Malay is obtained by ranking INITIAL([nasal]) above SHARE([nasal]) and FINAL([nasal]) below it:

(21) /pəŋawasan/ → [pəŋãwãsan]

p ə ŋ a w a s s a n	INIT([nas])	SHR([nas])	FINAL([nas])	*NASGLI	*NASVOW	ID([nas])
a. → p ə ŋãwã s a n		5	1	1	2	3
b. p ə̃ŋãwã s ã̃n	2 W	3 L	1	1	4 W	5 W
c. p ə ŋ a w a s a n		8 W	L	L	L	L

INITIAL([nasal]) is violated in (21)b because /ŋ/'s underlying [nasal] autosegment has an output correspondent that has spread leftward to the [ə] that precedes /ŋ/'s output correspondent. (The final /n/ is also involved in a violation of this constraint.) Since (21)a lacks this fault, it wins. Candidate (21)c satisfies FINAL([nasal]), but only at the expense of failure to spread rightward, with bad consequences for satisfaction of SHARE([nasal]).

3.3. No sour grapes

The SHARE constraint does not have AGREE's sour grapes problem. Succinctly, the sour grapes problem is the existence of rankings that map /mawa/ to [mãwã] and /mawara/ to [mawara] — total spreading whenever possible, otherwise no spreading. To show that the problem has been solved under the new set of assumptions, we need to assemble all of the ranking data for these two mappings (the ERCs, in the sense of Prince (2002b, 2006)) and demonstrate that they are inconsistent.

The ranking data for [mãwã] to beat a candidate with no spreading are given in (22), and the ranking data for [mawara] to beat candidates with spreading are given in (23).

(22) Ranking data for /mawa/ → [mãwã]

m a w a	*NASLIQ	INIT([nas])	SHR([nas])	FIN([nas])	*NASGLI	*NASVOW	ID([nas])
a. → m̃ãwã				1	1	2	3
b. m a w a			3 W	L	L	L	L

(23) Ranking data for /mawara/ → [mawara]

m a w a r a	*NASLIQ	INIT([nas])	SHR([nas])	FIN([nas])	*NASGLI	*NASVOW	ID([nas])
a. → m a w a r a			5				
b. mãwã r a			2 L	1 W	1 W	2 W	3 W

The ranking data in (22) show that the winner-favoring constraint SHARE([nasal]) has to dominate all four of the loser-favoring constraints FINAL([nasal]), *NASGLIDE, *NASVOWEL, and IDENT([nasal]). The ranking data in (23) show that at least one of the four winner-favoring constraints FINAL([nasal]), *NASGLIDE, *NASVOWEL, and IDENT([nasal]) has to dominate SHARE([nasal]). There's an obvious contradiction here, proving, as desired, that no single language can get both of these mappings with this constraint set.

The reason for this success is that SHARE([nasal]) counts non-harmonizing segments. Performance is therefore improved whenever any segment is brought into harmony. Furthermore, since [nasal] is privative, the only way of satisfying SHARE([nasal]) is to spread nasality — spreading orality is not an option.

Another advantage of SHARE over both AGREE and ALIGN is that it does not predict 'harmony' by feature deletion. The problem is that AGREE([nasal]) or ALIGN([nasal]) can be vacuously satisfied by denasalization. This leads to a tie between candidates with spreading and candidates with denasalization:

(24) AGREE or ALIGN triggering denasalization

ma	AGREE-R([nasal]) or ALIGN-R([nasal], word)	IDENT([nasal])
a. → ba		1
b. → mã		1
c. ma	1 W	L

Worse yet, the candidate with denasalization will win if spreading is blocked. So both the AGREE and ALIGN approaches predict the existence of a language where [nasal] spreads rightward (/ama/ → [amã]), but it deletes if a blocking segment follows (/amsa/ → [absa]). No such language exists.

SHARE([nasal]) does not make this prediction. That's because denasalization does not improve performance on this constraint; only spreading does. The candidates [m|a] and [b|a] each have one violation of SHARE([nasal]), while [mã] has none.

Although the new constraints and representational assumptions offer some improvement over the AGREE and ALIGN approaches, they are not unproblematic. For one thing, they do not solve the problem with ALIGN blocking epenthesis (see (9) in section 2.2). If SHARE([nasal]) dominates NO-CODA, which itself dominates DEP, then epenthesis will always be prevented in an oral context, because adding an oral segment

inevitably adds a SHARE([nasal]) violation. The result is that epenthesis is blocked except when the epenthetic vowel is in a nasal harmony context, as it is in /maw/ → [mãwĩ]:

(25) Epenthesis problem with new constraints

a. /mas/ → [mã|s]

m a s	*NASFRIC	SHARE([nas])	NO-CODA	DEP
i. → m ã s		1	1	
ii. m ã s i		2 W	L	1 W
iii. m ã ĩ	1 W	L	L	1 W

b. /pas/ → [p|a|s]

p a s	*NASFRIC	SHARE([nas])	NO-CODA	DEP
i. → p a s		2	1	
ii. p a s i		3 W	L	1 W

c. /maw/ → [mãwĩ]

m a w	*NASFRIC	SHARE([nas])	NO-CODA	DEP
i. → m ã wĩ				1
ii. m ã w ĩ		1 W		1
iii. m ã w			1 W	L

Although the pattern predicted by this ranking is somewhat different from the pattern obtained in section 2.2, they are equally implausible. We do find languages where vowel epenthesis — or any other process that alters segment count — depends on whether or not the added segments can undergo harmony.

Another liability of the new constraints and representational assumptions is that they predict the possibility of spontaneous nasalization simply to satisfy SHARE([nasal]):

(26) Spontaneous nasalization

b a	SHARE([nas])	IDENT([nas])
a. → m ã		2
b. b a	1 W	L
c. m a	1 W	1 L

This implausible prediction follows because oral segments have no other way of satisfying SHARE([nasal]). Whatever reasons there may be for oral segments to become nasal, SHARE([nasal]) is not among them.

Solving these and other problems requires another theoretical refinement: harmonic serialism.

3.4. SH and Harmonic Serialism

Harmonic serialism (HS) is a version of OT in which GEN is limited to making one change at a time. Since inputs and outputs may differ in many ways, the output of each pass through HS's GEN and EVAL is submitted as the input to another pass through GEN and EVAL, until no further changes are possible. HS was briefly considered by Prince and Smolensky (1993/2004), but then set aside. It is explored at length in McCarthy (2000, 2002, 2007a, b, c, 2008a, b), Kimper (2008), Pruitt (2008), and Wolf (2008). Besides Prince and Smolensky's work, HS also has connections with other ideas about serial optimization (e.g., Black 1993; Chen 1999; Goldsmith 1990: 319ff., 335-336, 1993; Kenstowicz 1995; Kiparsky 2000; Norton 2003; Rubach 1997; Tesar 1995).

An important aspect of the on-going HS research program is determining what it means to make 'one change at a time'. Answering this question for the full range of phonological phenomena is beyond the scope of this paper, but before analysis can proceed it is necessary to adopt *some* assumptions about how GEN manipulates autosegmental structures:

(27) Assumptions about GEN for autosegmental phonology in HS⁵

GEN's set of operations consists of:

a. Insertions:

-A feature and a single association line linking it to some pre-existing structure.

-A single association line linking two elements of pre-existing structure.

a. Deletions:

-A feature and a single association line linking it to some pre-existing structure.

-An association line linking two elements of pre-existing structure.

Under these assumptions, GEN cannot supply a candidate that differ from the input by virtue of, say, spreading a feature from one segment and delinking it from another. This means that feature 'flop' processes require two steps in an HS derivation (McCarthy 2007a: 91-93).

We now have enough background to make headway on the issues raised at the end of the previous section. One of the problems was the possibility of spontaneous nasalization to satisfy SHARE([nasal]), as in (26). The winning candidate [mã] differs from the input /ba/ by two changes: nasalization of [b] and spreading of [nasal] to /a/. In HS, these two changes cannot be effected in a single pass through GEN and EVAL. Starting with input /ba/, the candidate set after the first pass through GEN includes faithful [b|a] and nasalized [m|a] or [b|ã] — but not [mã], which has both inserted [nasal] and spread it. This limited candidate set is submitted to EVAL, which applies the same constraint hierarchy as in the parallel OT tableau (26):

⁵ Under the assumptions about GEN in (27), feature spreading is an iterative process, affecting one segment at a time. Nothing in this paper depends on that assumption, though Pruitt (2008) has argued that stress assignment must iterate in HS, while Walker (2008) presents evidence from Romance metaphony against iterative spreading.

(28) Convergence to [b|a] on first pass through GEN and EVAL

/ba/	SHARE([nas])	IDENT([nas])
a. → b a	1	
b. m a	1	1 W
c. b ã	1	1 W

Clearly, there is no danger of SHARE([nasal]) causing spontaneous nasalization, since all three candidates violate this constraint equally.

This example typifies the difference between parallel OT and HS. In parallel OT, the (spurious) advantage of spontaneous nasalization and spreading is realized immediately, and so the unwanted /ba/ → [mã] mapping is possible. In HS, however, any advantage accruing to spontaneous nasalization must be realized without the benefit of spreading, which comes later. Since none of the constraints under discussion favors spontaneous nasalization, the /ba/ → [mã] mapping is impossible in HS with exactly the same constraints and representational assumptions that made it possible in parallel OT. Differences like this between parallel OT and HS are typical and form the basis for most arguments in support of HS in the literature cited at the beginning of this section.

The other problem raised at the end of section 3.3 is that SHARE([nasal]) can block epenthesis except in a context where the epenthetic vowel is [nasal] in harmony with the preceding segment. This analysis relies on the ability of parallel OT to epenthesize a vowel and to spread [nasal] onto that vowel simultaneously, in a single pass through GEN and EVAL. The situation is different in HS.

Epenthesis of a vowel and spreading of a feature onto that vowel are separate changes, so HS's GEN cannot impose them simultaneously on a candidate. Rather, epenthesis and spreading must take place in separate steps, and so EVAL judges the consequences of epenthesis without knowing how spreading might subsequently affect the epenthetic vowel.

To illustrate this result, I return to the examples in (25):

In tableau (25)a, the input is /mas/. HS's GEN offers the candidates [m|a|s], [m|a|s|i], and [mã|s]. The form [mã|s|i] is not yet included in the candidate set, since it differs from the input to GEN by the effect of more than one change. A constraint hierarchy identical to the one in (25) selects [mã|s] as optimal:

(29) /mas/ → [mã|s] on first pass through GEN and EVAL

/mas/	*NASFRIC	SHARE([nas])	NO-CODA	DEP
a. → mã s		1	1	
b. m a s		2 W	1	
c. m a s i		3 W	L	1 W

Although the form [mãsi] is included in the candidate set on the next pass through GEN and EVAL, it is not optimal because SHARE([nasal]) dominates NO-CODA. Instead, the derivation converges on [mã|s]:

(30) Convergence to [mã|s] on second pass through GEN and EVAL

/mas/ [mã s]	*NASFRIC	SHARE([nas])	NO-CODA	DEP
a. → mã s		1	1	
b. mã s i		2 W	L	1 W
c. mãĩ i	1 W	1	L	1 W

In tableau (25)b, the input is /pas/. The candidates available on the first pass through Gen are [p|a|s] and [p|a|s|i]. Since SHARE([nasal]) dominates NO-CODA, [p|a|s] wins:

(31) Convergence to [p|a|s] on first pass through GEN and EVAL

/pas/ [p a s]	*NASFRIC	SHARE([nas])	NO-CODA	DEP
a. → p a s		2	1	
b. p a s i		3 W	L	1 W

The input and output are identical, so the derivation has already converged and [p|a|s] is the final output.

In tableau (25)c, the input is /maw/. On the first pass through HS's GEN and EVAL, the winning candidate is the one with nasal spreading, for the same reason as in (29):

(32) /maw/ → [mã|w] on first pass through GEN and EVAL

/maw/ [mã w]	*NASFRIC	SHARE([nas])	NO-CODA	DEP
a. → mã w		1	1	
b. m a w		2 W	1	
c. m a w i		3 W	L	1 W

On the next pass, nasal spreading is once again optimal:

(33) /maw/ → [mã|w] → [mãĩw] on second pass

/maw/ [mãĩw]	*NASFRIC	SHARE([nas])	NO-CODA	DEP
a. → mãĩw			1	
b. mã w		1 W	1	
c. mã w i		2 W	L	1 W

The derivation then converges:

(34) Convergence to [mãĩ] on third pass

/maw/	*NASFRIC	SHARE([nas])	NO-CODA	DEP
a. → mãĩ			1	
b. mãĩ i		1 W	L	1 W

At no point is [mãĩ] even among the candidates under consideration, much less optimal. That's because the derivation never gets far enough for [mãĩ] to be an input to GEN.

Under this ranking, where SHARE([nasal]) dominates NO-CODA, the parallel OT and HS analyses derive different languages. In the parallel OT analysis (25), epenthesis is blocked with the inputs /mas/ and /pas/, but allowed with /maw/. This difference emerges because only input /maw/ allows the epenthetic vowel to undergo nasal spreading, yielding [mãĩ]. The problem is that no known language behaves this way — vowel epenthesis is never contingent on the epenthetic vowel's ability to undergo nasal harmony. In the HS analysis (29)–(34), however, SHARE([nasal]) blocks epenthesis across the board, regardless of what precedes the locus of epenthesis. Ranking SHARE([nasal]) above NO-CODA might seem like a peculiar way of ruling out epenthesis— if a language has no epenthesis, why not just rank DEP above NO-CODA? — but it is completely unproblematic typologically, since there are certainly languages that don't have epenthesis.

From this discussion, it would appear that parallel OT predicts an implausible interaction between nasal harmony and vowel epenthesis, whereas HS does not, given identical constraints and the ranking in (25) and (29)–(34). To secure the argument, it is necessary to show that HS does not allow this implausible interaction under *any* ranking of these constraints. In other words, we need to establish a result about factorial typology in HS.

Specifically, we need to show that no grammar that produces the underlying → surface mappings /mas/ → [mã] and /pas/ → [pas] will also produce the mapping /maw/ → [mãĩ]. As above, we assemble all of the ranking data for the /mas/ → [mã] and /pas/ → [pas] mappings, and then compare it with the ranking data for the /maw/ → [mãĩ] mapping.

First, the ranking data for the non-epenthetic mappings:

(35) Ranking data for /mas/ → [mās] and /pas/ → [pas]

	*NASFRIC	SHARE([nas])	NO-CODA	DEP
a. [mā s] ~ *[m a s]		W		
b. [mā s] ~ *[m a s i]		W	L	W
c. [mā s] ~ *[mā s i]		W	L	W
d. [mā s] ~ *[māš i]	W		L	W
e. [p a s] ~ *[p a s i]		W	L	W

This table contains all of the crucial candidate comparisons in tableaux (29)–(31). By simple ranking logic, it establishes a disjunction: NO-CODA is dominated by DEP or by both *NASFRICATIVE and SHARE([nasal]).

To determine which rankings would be necessary for the /maw/ → [māwĩ] underlying → surface mapping, we need to consider all of the logically possible derivational paths from /maw/ to [māwĩ]. They are not very numerous:

(36) Derivational paths from /maw/ to [māwĩ]

- a. <maw, mawi, māwi, māwĩ, māwĩ>
- b. <maw, māw, māwi, māwĩ, māwĩ>
- c. <maw, māw, māw̃, māwĩ, māwĩ>

To prove the typological result, I need to show that each of these derivational paths, considered separately, has ranking requirements that are inconsistent when taken together with the ranking data in (35). We will consider each in turn, starting with the path in (36)a:

(37) Ranking requirements for (36)a <maw, mawi, māwi, māwĩ, māwĩ>

Pass #		*NASFRIC	SHARE([nas])	NO-CODA	DEP
1	[m a w i] ~ *[m a w]		L	W	L
1	[m a w i] ~ *[mā w]		L	W	L
2	[mā w i] ~ *[m a w i]		W		
3	[māw̃ i] ~ *[mā w i]		W		
4	[māwĩ] ~ *[māw̃ i]		W		

The derivational path from /maw/ to [māwĩ] in (37) requires NO-CODA to dominate both SHARE([nasal]) *and* DEP. That is inconsistent with (35), which requires NO-CODA to be dominated by SHARE([nasal]) *or* DEP.

Next, the ranking requirements for (36)b, <maw, māw, māwi, māwĩ, māwĩ>. It is clear from (38) that this derivational path is simply impossible under this constraint set, since it imposes internally inconsistent ranking requirements. For example, the [mā|w] ~ [m|a|w|i] comparison in pass 1 requires SHARE([nas]) *or* DEP to dominate

NO-CODA, but the [mã|w|i] ~ [mã|w] comparison in pass 2 requires NO-CODA to dominate SHARE([nas]) and DEP.

(38) Ranking requirements for (36)b < maw, mǎw, mǎwi, mǎwi, mǎwĩ >

Pass #		*NASFRIC	SHARE([nas])	NO-CODA	DEP
1	[mã w] ~ [m a w]		W		
1	[mã w] ~ [m a w i]		W	L	W
2	[mã w i] ~ [mã w]		L	W	L
2	[mã w i] ~ [mãw̃]		L	W	L
3	[mãw̃ i] ~ [mã w i]		W		
4	[mãw̃ĩ] ~ [mãw̃ i]		W		

The derivational path in (36)c < maw, mǎw, mǎw̃, mǎwi, mǎwĩ > is also possible because it imposes internally inconsistent ranking requirements (the rows with W-L-W matching a row with L-W-L).

(39) Ranking requirements for (36)c < maw, mǎw, mǎw̃, mǎwi, mǎwĩ >

Pass #		*NASFRIC	SHARE([nas])	NO-CODA	DEP
1	[mã w] ~ [m a w]		W		
1	[mã w] ~ [m a w i]		W	L	W
2	[mǎw̃] ~ [mã w]		W		
2	[mǎw̃] ~ [mã w i]		W	L	W
3	[mǎw̃ i] ~ [mǎw̃]		L	W	L
4	[mǎw̃ĩ] ~ [mǎw̃ i]		W		

In summary, only one of the derivational paths from /maw/ to [mǎw̃ĩ] is internally inconsistent, but it is inconsistent with the ranking data in (35). Therefore, HS with this constraint set cannot produce a language that obeys the generalization that vowel epenthesis is blocked unless the epenthetic vowel is accessible to nasal harmony. Since parallel OT can produce such a language with the same constraints, and such a language does not seem to exist, HS is apparently necessary to ensure a typologically restrictive theory of harmony.

4. SH and other pathologies of ALIGN(feature)

As I noted earlier, the problematic interaction of harmony by alignment with epenthesis is one of several pathological predictions of featural alignment identified by Wilson (2003, 2004, 2006). In section 3.4, we saw that the problematic interaction of harmony with epenthesis does not arise when HS is combined with the constraints and

representational assumptions in section 3.2. We'll now look at the other pathologies that Wilson discusses, and I will show that they also disappear under the new regime.

4.1. Harmony by affix repositioning

By dominating affixal alignment constraints, markedness constraints can compel infixation (Prince & Smolensky 1991; 1993/2004 and others). They can even cause affixes to switch between prefixal and suffixal position (Fulmer 1997; Noyer 1993).

ALIGN-R([nasal], word) is among the markedness constraints that could in principle have this effect. Its influence on affix placement is much like its influence on epenthesis. When the stem contains a nasal consonant followed by a blocker like [s], then an oral affix can be forced out of suffixal position to improve alignment of [nasal] (see (40)a). But if the stem contains no [nasal] segments, then there is no threat of improper alignment, and so the affix can be a suffix, as it its wont (see (40)b). The affix will also be suffixed if it is itself permeable to nasal harmony and no blocker precedes in the stem (see (40)c).

(40) ALIGN-R([nasal], word) affecting affix placement

a. Prefixation when inaccessible to harmony

/mas, o/	*NASFRIC	ALIGN-R([nasal], word)	ALIGN-R(-o, word)
i. → omãs		1	3
ii. māsō		2 W	L
iii. māsõ	1 W	L	L

b. Suffixation with no nasal to harmonize

/pas, o/	*NASFRIC	ALIGN-R([nasal], word)	ALIGN-R(-o, word)
i. → paso			
ii. opas			3 W

c. Suffixation when accessible to harmony

/maw, o/	*NASFRIC	ALIGN-R([nasal], word)	ALIGN-R(-o, word)
i. → mǎwõ			
ii. omǎw			3 W

Nothing like this has been observed among the known cases of phonologically-conditioned affix placement. It is presumptively impossible.

We will now look at how cases like this play out in the new system. We first need a theory of phonology-morphology interaction in HS to serve as the basis for analyzing affix displacement phenomena like (40)a. To this end, I adopt the framework of Wolf (2008). Wolf assumes that the input to the phonology consists of abstract morphemes represented by their morphosyntactic features — e.g., /DOG-PLURAL/. Spelling out each morpheme requires a single step of a HS derivation: <DOG-PLURAL, dɔg-PLURAL, dɔgz>.

Spell-out is compelled by the constraint MAX-M, which is satisfied when a feature is spelled out by some formative. (On the relationship of this work to previous proposals about morphology and its interface with phonology, see Wolf (2008: chapter 1).)

Affix displacement phenomena show that the location where a feature is spelled out is not predetermined. Thus, [dɔgz], [dɔzg], [dzɔg] etc. are all legitimate candidates that satisfy MAX-M. The actual output [dɔgz] is selected by the constraint MIRROR (an evocation of the Mirror Principle of Baker (1985)). It favors candidates where the phonological spell-out of a feature matches its location in morphosyntactic structure. (In this way, Wolf answers Horwood's (2002, 2004) objections to the previous OT analysis with constraints like ALIGN-R(-o, word).) Affix displacement is violation of MIRROR to satisfy some higher-ranking constraint.

We now have the resources necessary to study the consequences of the new system for this example. For the morphosyntactic representations of the roots, I'll use small capitals — MAS, PAS, MAW — and I'll assume that the suffix is PLURAL. The simplest case is PAS, so I'll begin there. The input is the morphosyntactic structure [PAS PLURAL]. The first derivational step spells out the morphosyntactic representation PAS as the phonological string [pas]. This change improves performance on the constraint MAX-M (see (41)), but because it introduces phonological structure where previously there was none, it brings violations of phonological markedness constraints, including SHARE([nas]). (When I turn to the other examples, I will elide this first derivational step, where the root gets spelled out.)

(41) First step: [PAS PLURAL] → [pas PLURAL]

[PAS PLURAL]	*NASFRIC	MAX-M	SHARE([nas])
a. → [p a s PLURAL]		1	2
b. [PAS PLURAL]		2 W	L

Further improvement on MAX-M is possible by spelling out PLURAL as [o]. GEN offers candidates that differ in where PLURAL is spelled out, and MIRROR chooses the correct one. MIRROR is shown as separated from the rest of the tableau because its ranking cannot be determined by inspecting these candidates:

(42) Second step: [pas PLURAL] → [paso]

[pas PLURAL]	*NASFRIC	MAX-M	SHARE([nas])	MIRROR
a. → [p a s o]			3	
b. [p a s PLURAL]		1 W	2 L	
c. [o p a s]			3	3 W
d. [p o a s]			3	2 W
e. [p a o s]			3	1 W

Since no further harmonic improvement is possible (relative to the constraints under discussion), the derivation converges on [paso] at the third step.

When the input to the second step contains a nasal, like [mas PLURAL], there is a choice between spelling out PLURAL or spreading [nasal]. Since MAX-M is ranked higher, spell-out takes precedence:

(43) Second step: [mas PLURAL] → [maso]

[mas PLURAL]	*NASFRIC	MAX-M	SHARE([nas])	MIRROR
a. → [m a s o]			3	
b. [m a s PLURAL]		1 W	2 L	
c. [mã s PLURAL]		1 W	1 L	
d. [o m a s]			3	3 W
e. [m o a s]			3	2 W
f. [m a o s]			3	1 W

This is the crucial tableau. It shows that SHARE([nasal]), unlike ALIGN in (40)b, is unable to affect the placement of the affix. All placements of the affix [o] equally affect performance on SHARE([nasal]), adding one violation of it. Thus, there is no advantage to shifting this affix out of the position preferred by the constraint MIRROR.

It might seem that SHARE([nasal]) could affect affix placement by favoring results like [õm|a|s] or [mõ|a|s], but these are not legitimate candidates at the affix spell-out step. HS's one-change-at-a-time GEN cannot simultaneously spell out a morpheme and spread a feature onto it. Although SHARE([nasal]) would make it advantageous to spell out [o] next to [m], that advantage cannot be discovered until it is too late, when the location of the affix has already been determined.

Spreading does finally occur at the third step of the derivation because no further improvement on top-ranked MAX-M is possible:

(44) Third step: [maso] → [mãso]

[maso]	*NASFRIC	MAX-M	SHARE([nas])	MIRROR
a. → [mã s o]			2	
b. [m a s o]			3 W	

At the fourth step, further spreading of [nasal] is blocked by *NASFRICATIVE, and the derivation converges:

(45) Fourth step: convergence on [mãso]

[maso]	*NASFRIC	MAX-M	SHARE([nas])	MIRROR
a. → [mã s o]			2	
b. [maš o]	1 W		1 L	

The remaining example in (40) contains a nasal consonant with no following blockers. Succinctly, the derivation is <MAW PLURAL, maw PLURAL, mawo, mãwo, mãwo,

mãwõ>. As in the other two cases, MIRROR determines the location of the affix, and spreading follows spell-out because MAX-M dominates SHARE([nasal]). Tableaux would be superfluous, since this example is so straightforward.

As we have seen, SHARE([nasal]) cannot affect affix placement under the HS regime, given Wolf's independently motivated theory of the morphology-phonology interface in HS. The shift to SHARE([nasal]) from ALIGN(+nasal) rules out effects like (40)a, where a suffix is displaced because of a preceding nasal consonant. Regardless of where the suffix goes, it has the same effect on SHARE. The shift to HS from parallel OT rules out examples like *[mõās] or *[õmās], where an affix is displaced to make it accessible to autosegmental spreading. The affix's accessibility to autosegmental spreading is irrelevant to its placement, because the effect of spreading and the location of spell-out cannot be decided simultaneously, since it is impossible under HS for competing candidates to differ in both of these characteristics together.

4.2. Harmony by allomorph selection

This is another of Wilson's examples of pathologies that come from assuming that featural alignment constraints drive harmony. The phenomenon in question is phonologically conditioned allomorphy (PCA). In PCA, a morpheme has two or more surface alternants that are selected for phonological reasons but cannot be derived from a common underlying form. In Korean, for example, the nominative suffix has two alternants, [i] and [ka]. There is no reasonable way of deriving them from a single underlying representation, but their occurrence is determined phonologically: [i] follows vowel-final stems and [ka] follows consonant-final stems:

- (46) Korean nominative suffix allomorphy
- | | |
|---------------------|-------------|
| cib-i | 'house-NOM' |
| c ^h a-ga | 'car-NOM' |

Research in OT has led to the development of a theory of phonologically conditioned allomorphy based on the following premises (Burzio 1994; Hargus 1995; Hargus & Tuttle 1997; Mascaró 1996; Mester 1994; Tranel 1996a, b; 1998; and others):

- (i) The allomorphs of a morpheme are listed together in the underlying representation: /cip-{i, ka}/, /c^ha-{i, ka}/.
- (ii) GEN creates candidates that include all possible choices of an allomorph: [cib-i], [cip-ka], [c^ha-i], [c^ha-ga]. (Intervocalic voicing is an allophonic alternation that I will not be discussing here.)
- (iii) Faithfulness constraints like MAX and DEP treat all allomorph choices equally.
- (iv) So markedness constraints determine which allomorph is most harmonic. In Korean, the markedness constraints ONSET and NO-CODA correctly favor [cib-i] and [c^ha-ga].

The following tableaux illustrate:

(47) Allomorph selection in Korean

a.

/cip-{i, ka}/	ONSET	NO-CODA
i. → ci.bi		
ii. cip.ka		1 W

b.

/c ^h a-{i, ka}/	ONSET	NO-CODA
i. → c ^h a.ga		
ii. c ^h a.i	1 W	

The pathology emerges when $\text{ALIGN-R}([\text{nasal}], \text{word})$ is allowed to participate in allomorph selection. This constraint has the peculiar property of preferring the shorter suffix allomorph when the stem contains a nasal and $[\text{nasal}]$ has not spread onto the suffix. Furthermore, it will exercise this preference even in a language that has no nasal harmony at all, since the potential effect of $\text{ALIGN-R}([\text{nasal}], \text{word})$ on allomorph selection is independent of its ranking with respect to faithfulness to $[\text{nasal}]$.

The pseudo-Korean example in (48) illustrates. Although ONSET favors the allomorph $[-ga]$ after vowel-final stems, its effect is overridden by $\text{ALIGN-R}([\text{nasal}], \text{word})$ when the stem contains a nasal consonant:

(48) Allomorph selection pathology

/mi-{i, ka}/	$\text{ALIGN-R}([\text{nasal}], \text{word})$	ONSET
a. → mi.i	2	1
b. mi.ga	3 W	L

In a language with the ranking in (48), the choice between $[i]$ and $[ka]$ will be determined by ONSET *except when the stem contains a nasal consonant*, in which case the shorter allomorph will win despite the marked syllable structure it creates. Furthermore, this effect has nothing to do with the ranking of $\text{IDENT}([\text{nasal}])$ or any similar faithfulness constraint. It is therefore possible for $\text{ALIGN-R}([\text{nasal}], \text{word})$ to have this effect in languages without an inkling of nasal harmony. This prediction is surely an implausible one.

$\text{SHARE}([\text{nasal}])$ does not make these predictions.⁶ It simply favors the shorter allomorph, $[i]$, since this allomorph introduces one $\text{SHARE}([\text{nasal}])$ violation while the

⁶ Wilson also points out a related prediction. If it dominates MAX-BR , $\text{ALIGN-R}([\text{nasal}], \text{word})$ can cause a reduplicative suffix to copy fewer segments when the stem contains a nasal consonant: $/\text{pataka-RED}/ \rightarrow [\text{pataka-taka}]$ versus $/\text{makasa-RED}/ \rightarrow [\text{makasa-sa}]$. This behavior is also unattested. Details of the analysis will depend on how reduplication is analyzed in HS, especially in relation to Wolf's (2008) theory. This is a topic of on-going research by Wendell Kimper.

longer allomorph [k|a] introduces two. SHARE([nasal]) has this effect regardless of whether the stem contains a nasal consonant:

(49) No pathology with SHARE([nasal])

a. No nasal in stem

/c ^h a-{i, ka}/	SHARE([nas])	NO-CODA	ONSET
i. → c ^h a i	2		1
ii. c ^h a g a	3 W		L

b. Nasal in stem

/nami-{i, ka}/	SHARE([nas])	NO-CODA	ONSET
a. → n a m i i	4		1
b. n a m i g a	5 W		L

This prediction might seem odd, but a little reflection shows that it is harmless in much the same way as the prediction about epenthesis in section 3.4. What we have here is simply a case where there is no allomorphy: the suffix always surfaces as [i] because SHARE([nasal]) favors the shorter allomorph consistently. Presumably the learner would be content to represent this suffix as just /i/ instead of taking the roundabout route in (49). But a language without allomorphy is a possible human language, so there is no pathological prediction being made.

To claim assurance that there are no lurking pathologies in the new system, we also need to consider the potential effects of SHARE and HS on allomorph selection in languages that actually have nasal harmony. As it turns out, there are none. The reasoning is as follows:

- (i) In Wolf's (2008) system, allomorph selection is done at the point of spell-out. In section 4.1, we saw that HS's GEN cannot spell-out a morpheme and spread a feature onto it simultaneously.
- (ii) Hence, spell-out of a segmental morpheme inevitably introduces violations of SHARE([nasal]). This means that MAX-M must dominate SHARE([nasal]) for spell-out to occur at all (see (41), (42)).
- (iii) Hence, it is more harmonic to spell-out all morphemes before attempting to spread (see (43)).
- (iv) This means that allomorphs cannot be chosen for their ability to undergo nasal spreading. An allomorph has already been chosen by the point in the HS derivation when spreading first occurs.

Consider, for example, a plural suffix with two allomorphs, [sa] and [wa]. If *NASFRICATIVE dominates SHARE([nasal]), which in turn dominates *NASGLIDE, then [sa] is opaque to nasal harmony but [wa] will undergo it. Nonetheless, SHARE([nasal]) will favor neither one of them, regardless of whether they are suffixed to a stem that undergoes nasal spreading (/ma/ → [mã]) or not (/pa/ → [pã]). The tableaux in (50)

illustrate this by showing the candidates available at the second step of the derivation, after the root has been spelled out.

(50) No allomorphy pathology with SHARE([nasal]) in HS

a. Stem /ma/

[m a PLURAL]	MAX-M	*NASFRIC	SHARE([nas])	IDENT([nas])
a. → [m a w a]			3	
b. → [m a s a]			3	
c. [mã PLURAL]	1 W		L	1 W
d. [m a PLURAL]	1 W		1 L	

b. Stem /pa/

[p a PLURAL]	MAX-M	*NASFRIC	SHARE([nas])	IDENT([nas])
a. → [p a w a]			3	
b. → [p a s a]			3	
c. [p a PLURAL]	1 W		1 L	

Because a morpheme cannot simultaneously be spelled out and undergo harmony, harmony-favoring markedness constraints like SHARE will not affect the choice of allomorph. In (50), this choice is shown as indeterminate, but in real grammars the choice is made by some other markedness constraint.

The results developed in this section are very similar to the results in section 4.1. HS's GEN is limited to doing one thing at a time. In Wolf's (2008) theory, morpheme spell-out is one of the things that HS's GEN can do. Since spell-out and spreading cannot occur simultaneously, the possible consequences of spreading cannot influence spell-out, so an allomorph's amenability to spreading does not improve its chances. In general, SHARE([nasal]) favors shorter allomorphs, but it does so in a non-pathological way: it does not distinguish between bases that contain nasals and those that do not, so it cannot produce the odd long-distance affix-minimizing effect that ALIGN predicts.

4.3. Harmony by deletion

ALIGN-R([nasal], word) is violated by any non-harmonizing segment that follows a nasal. In the last two sections, we saw how this aspect of alignment could in principle — though never in fact — cause affix displacement or selection of shorter affix allomorphs. Unsurprisingly, it can also cause deletion in another pathology discovered by Wilson:

(51) Harmony by deletion pathology with ALIGN

/mawasa/	*NASFRIC	ALIGN-R([nasal], word)	MAX	IDENT([nas])
a. → māwã			2	3
b. māwãsa		2 W		3
c. mā			4 W	1 L

A language with this ranking would be expected to show truncation in words containing a nasal followed by a blocker. There would be no truncation in words with no nasals and words with no blockers. No such language has been observed.

In parallel OT, SHARE([nasal]) would make a somewhat different but equally bizarre prediction. Because orality does not spread, the only way to bring an oral segment into conformity with SHARE([nasal]), other than nasalizing it, is to delete it. With a ranking similar to (51), we would get the following:

(52) Harmony by deletion pathology with SHARE in parallel OT

a. [nasal] spreads to all accessible segments; others delete

/mawasa/	*NASFRIC	SHARE([nas])	MAX	IDENT([nas])
i. → māwã			2	3
ii. māwã s a		2 W		3
iii. mā			4 W	1 L

b. Words containing no nasal segments delete entirely

/pat/	*NASFRIC	SHARE([nas])	MAX	IDENT([nas])
a. → ∅			3	
b. p a t		3 W		

c. Unless they are monosegmental

/a/	*NASFRIC	SHARE([nas])	MAX	IDENT([nas])
a. → a				
b. ∅			1 W	

Clearly, SHARE without HS no panacea for the ALIGN pathologies discovered by Wilson.

HS eliminates this problem, however. One consequence of adopting an autosegmental view of distinctive features is that segmental deletion can be regarded as a gradual process of attrition, in which deleting a segment is the result of deleting its component parts in separate steps of an HS derivation. In McCarthy (2008a), I argue that deletion-as-attrition accounts for an asymmetry in how deletion affects heterosyllabic consonant clusters VC₁.C₂V: the coda consonant C₁ is targeted for deletion, not the onset consonant C₂ (Steriade 2001/2008; Wilson 2000, 2001).

Because segments have multiple structural components, a single markedness constraint is typically not going to be enough to force deletion. For instance, deleting /d/ from coda position requires that separate markedness constraints against [coronal] and [voice] in codas be ranked above their respective faithfulness constraints. Total segmental deletion is the result of ‘telescoping’ (Wang 1968) a series of feature-deleting, reductive neutralization processes.

Under these assumptions, it is clear why SHARE([nasal]) cannot cause segmental deletion. When given the step-four input [mãwã|s], HS’s GEN will not offer the candidate [mãwã] that improves performance on SHARE([nasal]). It will produce candidates where different features of [s] have been deleted, such as [mãwã|t] or [mãwã|h], but none of them satisfies SHARE([nasal]) any better than the faithful candidate does.

The deletion pathology arises in parallel OT because GEN produces candidates that differ from the underlying representation in many ways — for instance, from /mawasata/, it directly produces [mãwã], which is optimal under the ranking in (52)a. Given the ranking in (52) and the underlying representation /mawasata/, [mãwã] is the *global minimum* of potential for further harmonic improvement. Parallel OT always finds this global minimum. HS’s GEN is incapable of such fell-swoop derivations. As a result, HS derivations sometimes get stuck at a *local minimum* of harmonic improvement potential. The evidence here and elsewhere (McCarthy 2007b, 2008a) shows that it is sometimes a good thing to get stuck.

4.4. Harmony by stress shift

The starting point of this pathology is Guaraní. In Guaraní, stressed syllables block nasal harmony. Beckman (1998) attributes this phenomenon to the positional faithfulness constraint IDENT_o([nasal]), which prevents segments in stressed syllables from changing between oral and nasal. To illustrate the pathology, we will assume the existence of a language with penultimate stress represented by a trochaic foot assigned at the right edge of the word: [ga(ˈwata)]. As Wilson points out, by ranking IDENT_o([nasal]) and ALIGN-R([nasal]) above FOOT=TROCHEE, it is possible to force a right-aligned iambic foot as a way of permitting nasal spreading :

(53) Stress shift pathology

a. Stress shifts to accommodate nasal spreading

/mawasa/	IDENT _o ([nas])	ALIGN-R([nasal], word)	FOOT = TROCHEE
i. → mā(ṽā'sa)		2	1
ii. mā('wāsa)	2 W	2	L
iii. mā('wasa)		4 W	L

b. But not otherwise

/gawata/	IDENT _o ([nas])	ALIGN-R([nasal], word)	FOOT = TROCHEE
i. → ga('wata)			
ii. ga(wa'ta)			1 W

No known language assigns stress in this way.

HS eliminates this pathological prediction. To see why, we will need to consider two possible derivational paths starting at /mawasa/, one where [nasal] spreads and then stress is assigned, and another where stress is assigned and then [nasal] spreads. (See Jesney 2008 for a much broader discussion of how HS can eliminate positional faithfulness pathologies.)

The first route — spreading then stress — requires SHARE([nasal]) to dominate the constraint that requires assignment of stress, HEADEDNESS(word) (Selkirk 1995). At the first step, [nasal] spreading beats stress assignment because of this ranking:⁷

(54) /mawasa/ → [māwasa] at first step

m a w a s a	IDENT _o ([nas])	*NASFRIC	SHARE([nasal])	HEAD(word)	FT = Tr
a. → mā w a s a			4	1	
b. m a ('w a s a)			5 W	L	
c. m a w a s a			5 W	1	

The derivation continues in a similar vein for two more steps, until [māṽāsa] is the result. Then once again further spreading competes against stress assignment and stress assignment finally wins, since spreading is blocked by *NASFRICATIVE:

⁷ The constraint FOOT = TROCHEE is shown at the bottom of the hierarchy in (54)–(57) not because of any ranking argument — there is none — but simply to emphasize that SH will not produce the stress-shift pathology even if this constraint is ranked low.

(55) Fourth step

mãwã s a	IDENT _o ([nas])	*NASFRIC	SHARE([nasal])	HEAD(word)	FT = TR
a. → mã('wã s a)			2		
b. mã(wã 's a)			2		1 W
c. mãwãs a		1 W	1 L	1 W	
d. mãwã s a			2	1 W	

After this, the derivation converges.

Why does trochaic stress beat iambic stress in the HS analysis (55) but not in the parallel OT analysis (53)a? The short answer is that this language is, by assumption, trochaic, so FOOT=TROCHEE dominates FOOT=IAMB. The longer answer is that IDENT_o([nasal]), which is the source of the pathology, is irrelevant in (55), whereas it is active and doing mischief in (53)a. This constraint is irrelevant in the HS analysis because the syllable [wã] is already nasalized in the input to (55), so there is no unfaithfulness. In HS, each pass through GEN and EVAL has a new input against which faithfulness is assessed. The candidate [mã('wã|s|a)] is not unfaithful to input nasality, so IDENT_o([nas]) is satisfied.

Now we will look at the result of assigning stress before spreading [nasal]. For stress assignment to take precedence, HEADEDNESS(word) has to dominate SHARE([nasal]):

(56) /mawasa/ → [ma('wasa)] at first step

m a w a s a	IDENT _o ([nas])	*NASFRIC	HEAD(word)	SHARE([nasal])	FT = TR
a. → m a ('w a s a)				5	
b. mã w a s a			1 W	4 L	
c. m a w a s a			1 W	5	
d. m a (w a 's a)					1 W

Once stress has been assigned, HEADEDNESS(word) is satisfied, and then spreading can occur. After a step where [nasal] spreads to the first [a], the input to GEN is [mã|('w|a|s|a)]. The output of EVAL is the same, because IDENT_o([nasal]) blocks further spreading:

(57) Convergence on [mã|('w|a|s|a)]

mã ('w a s a)	IDENT _o ([nas])	*NASFRIC	HEAD(word)	SHARE([nasal])	FT = TR
a. → mã ('w a s a)				4	
b. mã ('w ã s a)	1 W			3 L	
c. mã (w a 's a)				4	1 W

In this situation, the positional faithfulness constraint $\text{IDENT}_o([\text{nasal}])$ is active, ruling out a candidate that is unfaithful to [nasal] in a syllable that bears stress. This is no pathology; it is Guaraní.

The pathology would re-emerge, however, if it were possible to shift the previously assigned stress in order to accommodate [nasal] spreading. That cannot happen, however, because of the one-change-at-a-time property of HS's GEN. A form with spreading and stress shift — that is, $[\text{mã}(\tilde{\text{wã}}|\text{'s|a})]$ — would beat all contenders in (57). But this form is not a legitimate candidate in (57) because it differs from the input in two distinct ways, nasalization of [w] and stress shift. Of course, a candidate with stress shift in hopeful anticipation of further spreading — that is, $[\text{mã}|\text{(w|a|'s|a)}]$ in (57) — is a sure loser because EVAL only sees its current state, not its potential for further improvement.

4.5. Summary

When SHARE and its associated representational assumptions are combined with HS, many of the pathologies identified by Wilson (2003, 2004, 2006) are resolved. The shift to SHARE eliminates the long-distance segment-counting effect of ALIGN, where a nasal anywhere in the word could affect the possibility of epenthesis, the location of an affix, or the selection of an allomorph. HS addresses the deletion and stress-shift pathologies, and it also explains why epenthesizing [nasal] is not a legitimate way of improving performance on $\text{SHARE}([\text{nasal}])$. Furthermore, HS denies SHARE the power to have even local effects on epenthesis or allomorph selection.

5. Extending SH to vowel harmony

5.1. Neutral segments

So far, SH has been illustrated only with nasal harmony of the Johore Malay type. This avoids dealing with the problem of neutral segments — those that are (or appear to be) skipped by the harmonizing feature. This problem needs to be addressed, however, before we can look at other kinds of harmony.

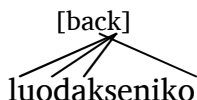
Finnish is a typical language where this issue arises. The feature [back] spreads from the last root vowel onto the suffixes. Intervening consonants and the vowels [i] and [e] seem to be ignored by the harmony process:

(58) Finnish vowel harmony

tuva-ta	'meet-INF'	cf. tykæ-tæ	'like-INF'
tul-nut	'come-PPL'	cf. syø-nyt	'eat-PPL'
ark-u:s	'timidity'	cf. syv-y:s	'depth'
luo-da-kse-ni-ko	'for me to create?'	cf. lyø-dæ-kse-ni-kø	'for me to hit?'

The standard view in autosegmental phonology is that spreading skips over the consonants, [i], and [e] in Finnish, so [luodakseniko] is represented as follows:

(59) Standard autosegmental analysis of neutrality



An important critique of (59) is that autosegmental representation is — or perhaps ought to be — a representation of the timing of actual articulatory gestures, such as raising and retracting the tongue body (= [back]). Considerations like this lead Ní Chiosáin & Padgett (2001) to argue that the intervening consonants are non-contrastive participants in spreading. Recent research has also questioned the assumption that neutral vowels are non-participants (Benus & Gafos 2005, 2007; Benus, Gafos, & Goldstein 2003; Gick et al. 2006).

SH is compatible with either approach to neutral segments. If the gestural theorists are right, then the formulation of SHARE(F) in (12) can be retained unaltered. If the standard autosegmental approach is right, then SHARE(F) will need to be changed to incorporate a more elaborate notion of adjacency than just contiguous segments. For example, the ideas about adjacency parameters in Archangeli & Pulleyblank (1987, 1994a) could be readily adapted for this purpose.⁸

In the balance of this paper, when discussing vowel harmony, I will only indicate the SHARE violations that involve vowels (e.g., [pe|tu|ki] if [back] is the harmonizing feature). At least these violations are common to all of the theories of neutral segments.

5.2. Root-controlled and dominant/recessive harmony

In root-controlled vowel harmony, the harmonizing feature spreads from roots onto affixes. Finnish, seen in (58), is a typical example. Root-controlled harmony can be analyzed with preferential faithfulness to roots over affixes (McCarthy & Prince 1995), expressed by the constraints $\text{IDENT}([\text{back}]_{\text{root}})$ and $\text{IDENT}([\text{back}])$. Since [back] spreads from roots to suffixes, $\text{SHARE}([\text{back}])$ must dominate the more general of these two constraints, $\text{IDENT}([\text{back}])$:

(60) $\text{SHARE}([\text{back}]) \gg \text{IDENT}([\text{back}])$

	tu lnyt	SHARE([back])	IDENT([back])
a. →	tulnut		1
b.	tu lnyt	1 W	L

On the other hand, $\text{IDENT}([\text{back}]_{\text{root}})$ must dominate $\text{SHARE}([\text{back}])$. One piece of evidence for this ranking comes from the existence of disharmonic roots like [kamy:] ‘Camus’, [vulgæ:ri] ‘vulgar’, [analy:si] ‘analysis’, etc. These examples show that one root vowel cannot impose its [back] feature on another:

⁸ It remains to be seen whether the proposal in this paper can be reconciled with the agreement-by-correspondence theory of long-distance assimilation (Hansson 2001; Rose & Walker 2004).

(61) IDENT([back])_{root} >> SHARE([back])

ka my:	IDENT([back]) _{root}	SHARE([back])	IDENT([back])
a. → ka my:		1	
b. kamu:	1 W	L	1 W

Since suffixes harmonize, any [back] specifications that they bear must be ignored. In particular, an underlying [back] suffix cannot surface intact when attached to a front-voweled root. This requires an additional constraint, *[back], that assigns a mark for each back vowel. It has to be ranked between SHARE([back]) and IDENT([back]), since it does not prevent spreading of [back] but it can cause loss of a [back] feature in suffixes. The following tableau uses a hypothetical back-voweled suffix [-tul] to illustrate this ranking:

(62) IDENT([back])_{root} >> SHARE([back]) >> *[back] >> IDENT([back])

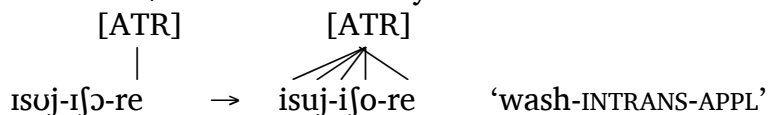
tykæ tul	IDENT([back]) _{root}	SHARE([back])	*[back]	IDENT([back])
a. → tykætyl		3		1
b. tykæ tul		3	1 W	L
c. tukatul	2 W	L	3 W	3 W

Because it is ranked below SHARE([back]) and IDENT([back])_{root}, *[back] does not affect the results in (60) and (61), which relied on these higher ranking constraints.

Tableau (62) shows precisely what it means for Finnish to have root-controlled harmony. There are no suffixes in Finnish that have the ability to control the root by imposing their [back] feature on it. The ranking in (62) shows why there can be no such suffixes: IDENT([back])_{root} dominates SHARE([back]), so spreading will never change a root vowel to make it conform with a suffix vowel.

In dominant/recessive harmony systems, on the other hand, an affix vowel can affect the root. In these systems, a feature on any vowel — root or affix — spreads to all other vowels — root or affix. Maasai is a typical case (Archangeli & Pulleyblank 1994a; Bakovic 2000b, 2002; Hall & et al. 1974; Levergood 1984; Tucker & Mpaayei 1955). An [ATR] specification on any morpheme spreads bidirectionally throughout the word:

(63) Dominant/recessive harmony in Maasai



Words containing no [ATR] morphemes show up with non-advanced vowels throughout: /ki-idim-u/ → [ki-idim-u] ‘1PL-be able-EF’.⁹

⁹ I disregard the hiatus resolution process that changes [kl.idimʊ] to [kɪdimʊ].

The basic properties of dominant/recessive harmony follow directly from SH's main premises. [ATR] spreads bidirectionally to satisfy SHARE([ATR]). The constraints that might affect direction of spread — IDENT([ATR])_{root}, INITIAL([ATR]), and FINAL([ATR]) — are all ranked below SHARE:

(64) Spreading of [ATR] in dominant/recessive harmony

	SHARE([ATR])	ID([ATR]) _{root}	ID([ATR])	INIT([ATR])	FIN([ATR])
a. → i su j ɔ re		2	4	1	
b. i su j ɔ re	4 W	L	L	L	

In (64), I have conflated the intermediate steps involved in spreading [ATR] one vowel at a time. The full HS derivation is <i|su|j|ɔ|re, i|su|j|i|ɔ|re, i|su|ji|ɔ|re, i|suji|ɔ|re, isuji|ɔ|re>, with each step eliminating another violation of SHARE([ATR]).

With an underlying representation like /kɪ|ɪ|dɪ|mu/, there is no [ATR] feature to spread, and so the SHARE([ATR]) violations are unavoidable. Why not insert [ATR] in order to spread it and thereby eliminate the violations? Recall the explanation in (28) for why violations of SHARE([nasal]) are not resolved in totally oral words by inserting a [nasal] autosegment and spreading it: under HS, insertion and spreading have to be separate derivational steps, and insertion alone does not improve performance on SHARE([nasal]). The same reasoning applies to dominant/recessive harmony. To get from /kɪ|ɪ|dɪ|mu/ to *[ki.idimu], it would be necessary first to insert [ATR] and then to spread it: <kɪ|ɪ|dɪ|mu, kɪ|ɪ|dɪ|mu, kɪ|ɪ|dimu, kɪ|idimu, ki.idimu>. That is impossible with this constraint system, since no active markedness constraint favors that first step:

(65) Harmonic bounding of /kɪ|ɪ|dɪ|mu/ → [ki|ɪ|dɪ|mu] at first step

	SHARE([ATR])	ID([ATR]) _{root}	ID([ATR])	INIT([ATR])	FIN([ATR])
a. → kɪ ɪ dɪ mu	3				
b. kɪ ɪ dɪ mu	3		1 W		

5.3. Trigger conditions

In some harmony systems, only certain bearers of the harmonizing feature are able to initiate spreading of it. These 'trigger conditions' have been analyzed as restrictions on the focus of a spreading rule (Archangeli & Pulleyblank 1994a), as constraints on the heads of spreading domain, and as demands that the feature spread (only) from segments whose other properties make it hard to perceive (Kaun 1995, 2004).

Trigger conditions appear to be more common in [ATR] and [round] harmony, but I know of a case in [nasal] harmony that I will use to illustrate here. In Ennemor (also known as Inor), bidirectional [nasal] spreading is initiated only by nasalized continuants, which include [β̃], [w̃], [r̃], and nasalized vowels (Hetzron & Marcos 1966). Spreading is not initiated by the nasal stops:

(66) Nasal harmony in Ennemor (trigger in boldface)

a. Spreading from nasalized continuants

$f\tilde{\Lambda}?\tilde{\Lambda}\beta\tilde{\Lambda}$	‘obstruct’
$\tilde{\Lambda}\tilde{w}\tilde{\Lambda}d$	‘gourd, pipe’
$d\tilde{\Lambda}?\tilde{\Lambda}\tilde{r}\tilde{\Lambda}$	‘hide’
$q^j\tilde{\Lambda}?\tilde{\Lambda}^{10}$	‘thread’

b. No spreading from nasal stops

$an\Lambda q\Lambda$	‘strangled’
$n\Lambda q\Lambda\beta\Lambda$	‘find’
$m\Lambda k\Lambda r\Lambda$	‘advise’
$n\Lambda m\Lambda d\Lambda$	‘like’

Karen Jesney has suggested that trigger conditions could be incorporated into SH by modifying the INITIAL(F) and FINAL(F) constraints in (15) and (16) by adding an argument referring to the class of segments that are barriers to leftward or rightward spreading. The revised constraint, INITIAL(F, X), is defined in (67), with the amendment italicized. FINAL(F, X) can be defined similarly.

(67) INITIAL(F, X)

Let input F tier = $f_1f_2\dots f_m$.

Let input segmental tier = $s_1s_2\dots s_n$.

Let output F tier = $f_1f_2\dots f_o$.

Let output segmental tier = $s_1s_2\dots s_p$.

Assign one violation mark for every $s_i \mathfrak{R} s_j$, where:

$f_k \mathfrak{R} f_i$,

f_k is associated with s_i , and there is no s_x that precedes s_i and is also associated with f_k , and

f_i is associated with s_j , s_j is of type X, and there is some s_y that precedes s_j and is also associated with f_i .

In Ennemor, [nasal] cannot spread to the left or the right of a nasal stop. Therefore, INITIAL([nasal], [stop]) and FINAL([nasal], [stop]) must dominate SHARE([nasal]). Since harmony spreads bidirectionally from continuants, INITIAL([nasal], [continuant]) and FINAL([nasal], [continuant]) (or perhaps just unmodified INITIAL([nasal]) and FINAL([nasal])) have to be ranked below SHARE([nasal]). Tableau (68) shows these rankings at work:

¹⁰ The evidence that the first vowel rather than the second is the harmony trigger in [q^jΛ̃?Λ̃] is purely diachronic: the cognate in Chaha is [qΛntʃ^ʔΛ].

(68) Analysis of triggering condition in Ennemor

$n _{\Delta} q _{\Delta} \tilde{\beta} _{\Delta}$	INITIAL([nas], [stop])	FINAL([nas], [stop])	SHARE([nas])	INITIAL([nas], [cont])	FINAL([nas], [cont])
a. $\rightarrow n _{\Delta} q \tilde{\alpha}\tilde{\beta}\tilde{\alpha}$			3	1	1
b. $n _{\Delta} q _{\Delta} \tilde{\beta} _{\Delta}$			5 W	L	L
c. $n\tilde{\alpha} q \tilde{\alpha}\tilde{\beta}\tilde{\alpha}$		1 W	2 L	1	1

On this view, triggering conditions are actually blocking conditions imposed by the complement of the class of triggering segments. In Ennemor, continuants are the exclusive triggers of spreading because high-ranking INITIAL([nasal], [stop]) and FINAL([nasal], [stop]) prohibit it from non-continuants.

Although this modification of INITIAL and FINAL offers a way of analyzing triggering conditions, it is unlikely to be the last word on the subject. For example, a less general but possibly more accurate approach to the Ennemor triggering condition is to understand it under the rubric “like things interact” (see Hutcheson 1973; Ito, Mester, & Padgett 1995: 600 and additional references there). The triggers of assimilation are more similar to the targets of assimilation, because both are [continuant]. If this is correct, then the closest analogue to Ennemor is parasitic rounding harmony, where trigger and target must have the same height specification (Archangeli & Suzuki 1997; Cole & Trigo 1989; Kaun 2004).

Complicating the picture further is a major inconsistency among attested triggering conditions. As Pater (to appear) observes, Archangeli and Pulleyblank (1994a) and Smolensky (2006) argue that the marked bearers of [ATR] (back and non-high vowels) are the *poorest* triggers of [ATR] harmony, while Kaun (1995, 2004) claims that the marked bearers of [round] (low vowels) are the *best* triggers of [round] harmony. Although (67) may be adequate as a description of triggering conditions, deeper understanding and resolution of this apparent contradiction must await further research.

6. Challenges?

A couple of phenomena initially look like problems for SH. I will argue that they are not, though for different reasons: one is fully compatible with SH, and the other is spurious.

6.1. Re-pairing

This phenomenon was first identified (and so named) by Bakovic (2000a, b, 2002). In some languages, a segment undergoing harmony is altered to bring it into conformity with general restrictions on the inventory. For instance, in Kolokuma Ijo (Williamson 1965, 1987), nasality spreads leftward, affecting vowels, glides, the flap [ɾ], and the lateral [l]. The result of nasalizing [l] is not the expected [l̃], however, but [n]. In Bakovic’s terms, the expected alternating pair [l]~[l̃] is ‘re-paired’ to [l]~[n].

Re-pairing in Kolokuma Ijo is a response to the same nasalizability constraints that block harmony in other languages. In Sundanese (Robins 1957), [l] is opaque because

*NASLIQUID crucially dominates SHARE([nasal]): /molohok/ → [mōlohok]. In Kolokuma Ijo, *NASLIQUID crucially dominates some faithfulness constraint, presumably IDENT([lateral]), that militates against replacing [ĩ] with [n]. Compare the rankings in the following parallel OT tableaux:

(69) Effects of *NASLIQUID

a. Blocking of nasal harmony in Sundanese

m o l o h o k	*NASLIQUID	IDENT([lat])	SHARE([nas])	IDENT([nas])
i. → mō l o h o k			5	1
ii. mō l̃ ō h̃ ō k	1 W		1 L	5 L
iii. mō ñ ō h̃ ō k		1 W	1 L	5 L

b. Re-pairing in Kolokuma Ijo

t ɔ l ĩ	SHARE([nas])	*NASLIQUID	IDENT([nas])	IDENT([lat])
i. → t ɔ̃ nĩ	1		2	1
ii. t ɔ̃ ĩ	1	1 W	2	L
iii. t ɔ l ĩ	3 W		L	L

At first blush, re-pairing looks like a problem for HS. The analysis in (69)b relies on the ability of GEN in parallel OT to simultaneously spread [nasal] onto /l/ and delete /l/'s [lateral] specification. HS's more limited GEN cannot do that. So how is re-pairing possible in HS? The same question arises with the re-pairing examples discussed by Bakovic.

The answer is that spreading of [nasal] and deletion of [lateral] occur at different steps of the HS derivation. Spreading of [nasal] onto [l] creates a violation of *NASLIQUID, and that violation is eliminated by the further change of [ĩ] into [n]. The following tableaux show the full sequence of steps:

(70) Re-pairing in HS

a. Step 1: /tɔ̃lĩ/ → [tɔ̃lĩ]

t ɔ l ĩ	SHARE([nas])	*NASLIQUID	IDENT([nas])	IDENT([lateral])
i. → t ɔ̃ ĩ	2	1	1	
ii. t ɔ l ĩ	3 W			
iii. t ɔ d ĩ	3 W			1 W

b. Step 2: [tɔ̃lĩ] → [tɔ̃lĩ]

t ɔ̃ lĩ	SHARE([nas])	*NASLIQUID	IDENT([nas])	IDENT([lateral])
i. → t ɔ̃lĩ	1	1	1	
ii. t ɔ̃ lĩ	2 W	1	L	
iii. t ɔ̃ nĩ	2 W	L	L	1 W

c. Step 3: [tɔ̃lĩ] → [tɔ̃nĩ]

t ɔ̃lĩ	SHARE([nas])	*NASLIQUID	IDENT([nas])	IDENT([lateral])
i. → t ɔ̃nĩ	1		1	1
ii. t ɔ̃lĩ	1	1 W	1	L

The derivation converges at step 4.

There is an important ranking difference between the HS and parallel OT analyses. In (69)b, the ranking of SHARE([nas]) relative to *NASLIQUID is irrelevant because the optimal form obeys both of them. In (70)b, however, SHARE([nas]) must dominate *NASLIQUID because spreading [nasal] onto /l/ creates [l̃], which is not eliminated until later in the derivation. In general, derivations in HS can require introducing violations of constraints that are obeyed in surface structure (McCarthy 2008b: 538). Finding that constraints are violated in a theory that famously posits violable constraints is hardly surprising, of course.

As it happens, the ranking required in (70)b is independently motivated in this language. Another reason why SHARE([nasal]) has to dominate *NASLIQUID is that /r/ also undergoes nasal harmony, as in [sɔ̃rɔ̃] ‘five’. Some undominated faithfulness constraint prevents [r̃] from also being re-paired to [n] — e.g., IDENT([flap]) will do.

The behavior of /r/ in Kolokuma Ijo points toward a difference in the typological predictions that parallel OT and HS make. In Kolokuma Ijo, both liquids undergo nasal harmony, but only one is re-paired. In parallel OT, it is also possible with this constraint set to analyze a language where one liquid blocks harmony and the other one undergoes it and is re-paired. The trick is to rank *NASLIQUID above SHARE([nasal]), but rank the faithfulness constraints so that only one of the liquids can be re-paired in a way that conforms with *NASLIQUID:

(71) A prediction of parallel OT

a. /r/ blocks harmony

/sɔ̃rɔ̃/	*NASLIQUID	IDENT([flap])	SHARE([nas])	IDENT([nas])	IDENT([cont])
i. → s ɔ̃ r ɔ̃			3		
ii. s ɔ̃r̃ɔ̃	1 W		1 L	2 W	
iii. s ɔ̃nɔ̃		1 W	1 L	2 W	1 W

b. /l/ undergoes harmony and re-pairing

/tɔ̃l̃/	*NASLIQUID	IDENT([flap])	SHARE([nas])	IDENT([nas])	IDENT([cont])
i. → t ̃nĩ			1	2	1
ii. t ̃ĩ	1 W		1	2	L
iii. t ɔ̃ l̃ĩ			3 W	L	L

HS could not analyze such a language with this constraint set. For /r/ to block harmony, *NASLIQUID has to dominate SHARE([nasal]) — exactly as in (71)a. But, as we saw in (70)a, spreading of nasality onto /l/ is the first step toward re-pairing in HS. Spreading of nasality onto /l/ cannot occur if *NASLIQUID dominates SHARE([nasal]).

The constraints of the nasalizability hierarchy establish certain equivalence classes like liquids, fricatives, and so on. All of the segments in a class are predicted to behave alike in blocking or undergoing nasal harmony. In parallel OT, however, a segment can undergo harmony by re-pairing regardless of whether the other members of its class are undergoers or blockers. In HS, a segment can undergo harmony by re-pairing only if the other members of its class are undergoers. This prediction is easily generalized to include other harmony processes, whenever the markedness constraints with harmony-blocking potential partition segments into equivalence classes.

Compared with parallel OT, HS offers the more restrictive typology of re-pairing. It is therefore more readily falsified. I know of no counterexamples.

6.2. Direction-specific blocking

The problem of direction-specific blocking was first identified by Davis (1995). The problem has to do with blocking effects that affect one direction of spreading but not the other. Imagine, for example, a language with bidirectional nasal harmony where *NASFRICATIVE blocks rightward spreading but not leftward spreading, so /asamasa/ becomes [ãšãmāsa].

As SH is described in section 3, it could not account for such a language. If *NASFRICATIVE dominates SHARE([nasal]), nasal spreading is blocked by [s]. This interaction will be the same regardless of whether nasal is spreading leftward or rightward. Thus, in a language with bidirectional harmony, if *NASFRICATIVE has a blocking effect in one direction, it must also have that effect in the other direction, and if it does not have a blocking effect in one direction, it cannot have that effect in the other direction. That's because SHARE([nasal]) has no directional sense to it. Instead, directionality is obtained from faithfulness constraints that block spreading, rather than markedness constraints (like ALIGN-R and ALIGN-L) that cause it.

The following tableau develops this argument formally. If blocking can be direction-specific, then there should be some ranking where (72)a will win. Observe, however, that the rankings necessary to get this winner are mutually inconsistent. In fact, (72)a is collectively harmonically bounded by (72)b and (72)c.

(72) Impossibility of direction-specific blocking in SH

/asamasa/	*NASFRIC	SHARE([nas])	ID([nas])	INITIAL([nas])	FINAL([nas])
a. → āṣāmā s a	1	2	4	1	1
b. āṣāmāṣā	2 W	L	6 W	1	1
c. a s āṣāmā s a	L	4 W	2 L	1	1
d. āṣām a s a	1	3 W	3 L	1	L

Since all of SH's relevant constraints are included in (72), there is no trick waiting to be pulled out of one's sleeve. SH predicts that direction-specific blocking is impossible.

ALIGN does not make this prediction. There are two distinct ALIGN constraints, ALIGN-L and ALIGN-R. A markedness constraint like *NASFRICATIVE can be ranked below one of them and above the other. So situated, it will block spreading only in the direction specified by the ALIGN constraint that is ranked lower. Thus, a blocking constraint can be direction-specific: it can block spreading in one direction but not the other.

ALIGN's ability to produce direction-specific blocking effects may not be a significant advantage over SH, however, because the evidence for direction-specific blocking is not entirely secure. I will now review that evidence.

No language with nasal harmony that works like (72) has ever been reported. Indeed, Walker's (1998: 67-80) extensive survey of nasal harmony turned up only one case where nasal spreading might seem to have different blocking conditions in different directions, Epena Pedee. In Harms's (1985, 1994) and Walker's (1998: 51-52) analyses, leftward and rightward nasal spreading treat the voiced stops /b/, /d/, and /g/ differently.¹¹ These consonants are said to undergo leftward nasal spread, changing into the corresponding nasal stops (73)a, and to block rightward spread, surfacing with prenasalization at the nasal-oral boundary (73)b.

(73) Nasal harmony in Epena Pedee

a. Leftward

/p ^h aibā:/	p ^h aimā:	'black'
/ʔipadā/	ʔipanā	'bird'

b. Rightward

/wā-hi-da/	wāhī ⁿ da	'go-PST-PL'
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This example is not probative, however. Although rightward nasal spreading is supported by alternations, leftward spreading does not seem to be. For instance, there is no evidence of suffixes like /-ā/ that attach to consonant-final roots and trigger nasalization: /kab-ā/ → [kamā]. Thus, there is no reason to assume that the underlying representation of [ʔipanā] is /ʔipadā/, as in (73)a, rather than /ʔipana/. And if /ʔipana/ is the underlying form, then there is no leftward spreading of nasality in this

¹¹ In Harms's (Harms 1985) and Walker's (Walker 1998) analyses, leftward and rightward spreading also differ in their treatment of /s/, but according to Harms (1994) /s/ undergoes spreading in both directions. Harms describes the 1994 description as an 'update' of his earlier work, so I take it to be definitive.

language, and hence there is no evidence for direction-specific blocking. If such blocking effects exist, they will have to be found elsewhere.

Two cases of direction-specific blocking that have been cited in the literature involve processes that are categorical in one direction and gradient in the other:

(i) Emphasis spreading (i.e., RTR harmony) in Arabic has been cited as an example of direction-specific blocking (Davis 1995; McCarthy 1997). Leftward spreading is categorical, and no segments are blockers. Rightward spreading is said to be blocked by high front segments like [i], but this is an oversimplification. Even segments that should be inaccessible to rightward spreading because of an intervening blocker are somewhat pharyngealized. Ghazeli (1977: 122-123) compared F2 values of the [l]s in words like [sumi:li] ‘you-FEM price for me’ and [s^humi:li] ‘you-FEM fast for me’. He found a consistent difference of 100-200 Hz in this right direction. So rightward spreading of RTR is a gradient process that is attenuated by antagonistic gestures like [i]’s raising and fronting of the tongue, but it is not blocked entirely.

(ii) In Akan, rightward spreading of ATR is blocked by [a] (Archangeli & Pulleyblank 1994a: 214ff.; Clements 1981). But when [a] precedes an ATR vowel, it undergoes a raising process that might look like leftward ATR spreading, except for the following difference: ‘Vowel Raising is not local to the syllable immediately preceding the conditioning syllable but influences the articulation of preceding syllables as well, causing them to acquire increasingly raised variants in a gradual “crescendo” as the conditioning syllable is approached’ (Clements 1981: 157).

Clearly, there is more difference between leftward and rightward harmony in Arabic and Akan than just the class of blockers; the processes themselves are profoundly different. Although autosegmental spreading is an appropriate model for categorical harmony processes, it is inappropriate for gradient ones, where target-and-interpolation models make more sense (Choi 1992; Cohn 1990; Huffman 1989; Keating 1990; Kirchner 1997; Pierrehumbert 1980; Pierrehumbert & Beckman 1988). On this view, there is no actual rightward spreading of RTR in Arabic or leftward spreading of ATR in Akan. Instead, true phonological spreading is unidirectional in both languages and no issue of direction-specific blocking arises.

Archangeli and Pulleyblank (1994a: 460 fn. 418) cite three other ATR harmony systems that are supposed to exemplify direction-specific blocking but have subsequently been reanalyzed:

(i) Kinande

In Archangeli and Pulleyblank’s (1994a: 200ff.) analysis of Kinande, leftward spreading is unrestricted but rightward spreading can only affect high vowels. In their later reanalysis (Archangeli & Pulleyblank 2002), however, there is no rightward spreading whatsoever. The details would take us rather far afield, so I will not review them here.

(ii) Maasai

In Archangeli and Pulleyblank's (1994a: 304ff.) analysis of Maasai, the low vowel /a/ is opaque to leftward spreading of ATR:

- (74) Maasai leftward ATR spreading (Tucker & Mpaayei 1955)
- | | | |
|------------------|----------------|--------------------------------|
| /ɛ-to-nuk-ar-ie/ | ɛ-to-nuk-ar-ie | 's/he buried it with (s.t.)' |
| /a-ɪput-akin-ie/ | aɪputakiñe | 'I fill it for s.o. with s.t.' |

In contrast, /a/ undergoes rightward ATR spreading, and it is subsequently re-paired by raising to [o]:

- (75) Maasai rightward ATR spreading
- | | | |
|------------|--------------|----------------|
| Underlying | /a-ta-pet-a/ | |
| Spreading | atapeta | |
| Re-pairing | atapeto | 'I smeared it' |

The ATR low vowel [ʌ] is re-paired to [o] as a way of satisfying the constraint ATR/Lo 'if ATR, then not low' (after Archangeli & Pulleyblank 1994a: 176).

There are two reasons to doubt this analysis of Maasai's /a/ → [o] process.¹² First, Noske (1996: 82, 2000) has shown that re-pairing cannot be the explanation for this process in another Eastern Nilotic language with a very similar harmony system, Turkana. Turkana has certain suffixes that idiosyncratically fail to undergo ATR harmony, such as /-ar/ 'relative'. Interestingly, this suffix is realized as [-ɔr] after an ATR vowel: [a-buk-ɔr] 'to pour out', [a-rip-ɔr] 'to skim off' (cf. [a-k-ɪɪp-ar] 'to pray, beg'). This observation shows that /a/ raises to a back round vowel after an ATR vowel *tout court*; raising of /a/ is not a re-pairing process, since it is independent of whether /a/ has undergone harmony.

Second, McCrary (2001) has argued that Maasai's /a/ → [o] process is spurious, that this alternation is actually allomorphic, and thus that /a/ always blocks ATR harmony. Her evidence comes from the observation that /a/ blocks even rightward spreading root-internally in nouns and adjectives, in interrogatives, and in one of the verbal suffixes. Clearly, we are not dealing with a general phonological process here.

(iii) Lango

In Archangeli and Pulleyblank's (1994a: 395ff.) and Smolensky's (2006) analyses of Lango, leftward and rightward spreading of ATR are subject to very different blocking (and triggering) conditions. For example, when leftward spreading across a consonant cluster is triggered by [u], only a high vowel can be affected:

- (76) Lango CVCCu harmony (Bavin-Woock & Noonan 1979; Noonan 1992)
- | | | | |
|------------|---------|--------|--------------|
| nɪŋ | 'name' | nɪŋwú | 'your name' |
| lòt | 'stick' | lòtwú | 'your stick' |
| <i>but</i> | | | |
| dèk | 'stew' | dèkwú | 'your stew' |
| kòm | 'chair' | kòm wú | 'your chair' |

¹² For a cyclic reanalysis of Maasai, see Bakovic (Bakovic 2002).

But in the opposite direction, any vowel can be affected, even /a/: /òpúk-Cá/ → [òpúkké] ‘my cat’. Setting aside the conditions on the triggering vowel and the intervening consonants, the problem for SH is that leftward but not rightward spreading is governed by the constraint ATR/Hi ‘if ATR, then high’ (after Archangeli & Pulleyblank 1994a: 176). Since SHARE([ATR]) has no directional sense, we don’t know whether to rank ATR/Hi above SHARE([ATR]) — thereby allowing spreading only to high vowels and failing to derive /òpúk-Cá/ → [òpúkké] — or to rank ATR/Hi below SHARE([ATR]) — thereby allowing spreading to any vowel and wrongly deriving /dèkwú/ → *[dèkwú].

This synopsis of the problem overlooks an important difference between rightward and leftward spreading, however: rightward spreading iterates (77)a, but leftward spreading does not (77)b.

(77) (Non-)iterative spreading in Lango

a. Rightward — iteration

/ceg-εε/	cegere	‘to be closed’
/cul-mεε/	cullere	‘penis-3SG.ALIEN’

b. Leftward — no iteration (Poser 1982)

/bɔŋɔ-ni/	bɔŋoni	‘your dress’
	*bɔŋoni	
/cɔŋɔ-ni/	cɔŋoni	‘your beer’
	*cɔŋoni	

This observation is key because it shows that the conditions on leftward spreading have nothing to do with how SHARE([ATR]) is ranked. That’s because SHARE([ATR]) is only crucial for iterative spreading, which is strictly rightward in Lango. The leftward spreading process must occur to satisfy some constraint other than SHARE([ATR]), perhaps a constraint requiring ATR to be licensed by association with a root segment (Kaplan 2008a, b).

The languages discussed here exhaust the cases of direction-specific blocking that are known to me. SH would be threatened if some language had leftward and rightward spreading processes that differed *only* in their blockers. As we have seen, in the actually attested cases, either the difference in blockers is spurious (Kinande, Maasai) or the difference in blockers is correlated with some other crucial difference between the leftward and rightward processes: one is gradient and the other is categorical (Arabic, Akan); or one is iterative and the other is not (Lango). In light of these results, the directionless SHARE constraint is not imperiled.

7. Conclusion

Harmonic Serialism has all of OT’s central properties: candidate competition judged by ranked, violable constraints. HS differs from parallel OT in just two related respects: HS’s GEN is limited to making one change at a time, and the output of EVAL is fed back into GEN until convergence. In their original discussion of HS, Prince and Smolensky (1993/2004: 95-96) noted that “[i]t is an empirical question of no little interest how Gen is to be construed” and that “[T]here are constraints inherent in the limitation to a

single operation”. This paper is an exploration of that question and those constraints in the domain of harmony processes.

I have argued that a particular approach to autosegmental spreading, embedded in HS and called Serial Harmony, is superior to alternatives embedded in parallel OT. The parallel OT theories of harmony make incorrect typological predictions, while Serial Harmony does not make these predictions.

Of course, many issues remain unresolved. In the study of harmony generally — not just Serial Harmony — there are unsettled questions about neutral segments, long-distance effects, and trigger and target conditions on harmony. A question specific to Serial Harmony — does spreading iterate or happen all at once? — has been scarcely touched on (though see Pruitt 2008; Walker 2008). Much remains to be done.

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