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Autosegmental spreading in Optimality Theory¹

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1. Introduction

Nick Clements's contributions to phonological theory have profoundly influenced my own work as well as that of many others. Among these contributions is his formalization of the principles of autosegmental association. The core idea of autosegmental phonology is that the pieces of phonological representation – tones, segments, and features – are separate but coordinated by association lines (Goldsmith 1976a, 1976b). The principles of autosegmental association in Clements and Ford (1979) define an initial or default association that can be altered by subsequent phonological rules.

Among these rules is autosegmental spreading. Spreading of a feature or tone increases its temporal span – in short, spreading is assimilation or harmony. For example, in Johore Malay nasal harmony (1), the feature [nasal] spreads rightward to vowels and glides.

(1) Nasal harmony in Johore Malay (Onn 1980)

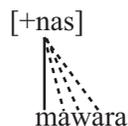
mãĩãp	'pardon'
pəŋãwãsan	'supervision'
mãratappi	'to cause to cry'
baŋõn	'to rise'

In most implementations of autosegmental phonology, spreading is obtained by iterative application of rules like (2), whose effect in Johore Malay is schematized in (3):²

(2) Autosegmental spreading rule



(3) /mawara/ → [mãwãra]



Iterative rules apply to their own output, proceeding directionally until no further changes can be made (Anderson 1980; Howard 1972; Johnson

1972; Kenstowicz and 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 (Prince and Smolensky 1993/2004) has no direct equivalent to spreading rules, 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. This leads in section 3 to a new proposal with two novel elements:

- (i) 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.
- (ii) 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 will refer to this theory as *Serial Harmony* (SH). After explaining these assumptions in section 3, I go on in sections 4 and 5 to show how this system eliminates the problems with previous approaches described in section 2.

Throughout this chapter, 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 pertain to the range of phenomena attributable to iterative autosegmental spreading.

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 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 2000; Eisner 1999; Lombardi 1995/2001, 1999; 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].

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 (after Walker 1998: 36)

*NASPLO >> *NASFRIC >> *NASLIQ >> *NASGLI >> *NASVOW

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

AGREE fails because it has a “sour-grapes” property: 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 /mawara/ will become [mawara], with no harmony at all. The tableaux in (6) and (7) illustrate this prediction. When all AGREE violations can be eliminated (6), then they are. But when a blocking constraint prevents complete spreading (7), there is no spreading at all. (The sequences that violate AGREE have been italicized to make them easy to find. Tableaux are in comparative format (Prince 2002).)

(6) AGREE without blocker

/mawa/	*NASLIQ	AGREE-R([nas])	IDENT([nas])
a. → mǎwǎ			3
b. mawa		1 W	L
c. mǎwa		1 W	1 L
d. mǎwǎ		1 W	2 L

(7) Sour-grapes effect of AGREE with blocker

/mawara/	*NASLIQ	AGREE-R([nas])	IDENT([nas])
a. → mawara		1	
b. mǎwara		1	1 W
c. mǎwǎra		1	2 W
d. mǎwǎra		1	3 W
e. mǎwǎrǎ	1 W	1	4 W
f. mǎwǎrǎ	1 W	L	5 W

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

Clearly, AGREE is unable to account for real languages like Johore Malay. Worse yet, it predicts the existence of languages with sour-grapes spreading like (6) and (7), and such languages are not attested.

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 *NASLIQ. 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 [mǎwǎra] satisfies this constraint but no candidate with less spreading does, it would do the job.

This seemingly innocent analytic move misses the point of OT (Wilson 2003, 2004). The fundamental descriptive and explanatory goals of OT are

(i) to derive complex patterns from the interaction of simple constraints and (ii) 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 adopt this constraint, 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 and Prince 1993; Prince and Smolensky 1993/2004). When alignment constraints are evaluated gradiently, they can discriminate among candidates that are imperfectly aligned.

Gradient alignment constraints have often been used to enforce autosegmental spreading by requiring an autosegment to be associated with the leftmost or rightmost segment in some domain (Archangeli and Pulleyblank 2002; Cole and Kisseberth 1995a, 1995b; Kirchner 1993; Pulleyblank 1996; Smolensky 1993; and many others). In Johore Malay, the gradient constraint ALIGN-R([nasal], word) ensures that every [nasal] autosegment is linked as far to the right as possible:

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

/mawara/	*NASLIQ	ALIGN-R([nasal], word)	IDENT([nasal])
a. mawara		5 W	W
b. māwara		4 W	1 W
c. māw̃ara		3 W	2 W
d. → māw̃āra		2	3
e. māw̃ā̃ra	1 W	1 L	4 L
f. māw̃ā̃ā̃	1 W	L	5 L

Candidate (8d) wins because its [nasal] autosegment is linked to a segment

that is only two segments away from the right edge of the word. (Diagram (3) illustrates.) In candidates with more ALIGN violations, [nasal] has not spread as far, whereas candidates with fewer ALIGN violations contain the forbidden segment *[ɾ].

The blocking situation illustrated in (8) is the source of ALIGN's problems as a theory of spreading in OT, as Wilson (Wilson 2003, 2004, 2006) has shown. ALIGN creates an impetus to minimize the number of peripheral segments that are inaccessible to harmony because of an intervening blocker. Many imaginable ways of doing that – such as deleting segments, forgoing epenthesis, or choosing shorter allomorphs – are unattested but predicted to be possible under ranking permutation. These wrong predictions will be discussed in section 5, after SH has been presented.

3. The proposal: Serial Harmony

The theory of Serial Harmony (SH) has two novel elements: a proposal about the constraint that favors autosegmental spreading (section 3.1), and a derivational approach to phonological processes (section 3.2).

The proposal is worked out here under the assumption that distinctive features are privative, since this seems like the most plausible view (see Lombardi 1991; Steriade 1993a, 1993b, 1995; Trigo 1993; among others). Whether this proposal can be made compatible with equipollent features remains to be determined.

3.1. 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. SH's constraint 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 elements (here, segments) to be linked to the same [F] autosegment.³

(9) SHARE(F)

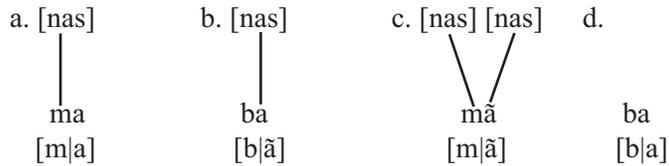
Assign one violation mark for every pair of adjacent elements that are not linked to the same token of [F].

Example (10) illustrates the only way that a pair of adjacent segments can satisfy this constraint, while example (11) shows the several ways that a pair of segments can violate it. Below each form I show the simplified notation I will be using in the rest of this chapter.

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



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



The three kinds of SHARE violation exemplified in (11) are: (a), (b) a [nasal] autosegment is linked to one segment but not the other; (c) each segment is linked to a different [nasal] autosegment; (d) neither segment is linked to a [nasal] autosegment. In the simplified notation, these violations are indicated by a vertical bar between the offending segments.

Like ALIGN-R([nasal], word), which it replaces, SHARE([nasal]) favors (10) over (11a), c. Unlike ALIGN-R([nasal], word), SHARE([nasal]) also favors (10) over (11d), the form with no [nasal] feature to spread. This difference is addressed in section 3.2. And because it has no inherent directional sense, SHARE([nasal]) disfavors (11b) as much as (11a), whereas ALIGN-R([nasal], word) finds (11b) inoffensive. Limitations of space do not permit me to present SH's theory of directionality, which is an obvious extension of recent proposals that the source segment in autosegmental spreading is the head of the featural domain (Cassimjee and Kisseberth 1997; Cole and Kisseberth 1995a; McCarthy 2004; Smolensky 1995, 1997, 2006).

3.2. 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. Lately, I and others have begun to reexamine HS, finding that it has a number of attractive properties (see

Jesney to appear; Kimper to appear; McCarthy 2000, 2002, 2007a, 2007b, 2007c, 2008a, 2008b; Pater to appear; Pruitt 2008; 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 chapter, but before analysis can proceed it is necessary to adopt *some* assumptions about how GEN manipulates autosegmental structures:

(12) Assumptions about GEN for autosegmental phonology in HS⁴

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.

b. 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 differs 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).

3.3. SH exemplified

We now have sufficient resources to work through an example in SH. The grammar of Johore Malay maps /mawara/ to [mãwãra] by the succession of derivational steps shown in (13). At each step, the only candidates that are considered are those that differ from the step's input by at most one GEN-imposed change. The grammar evaluates this limited set of candidates in exactly the same way as in parallel OT. The optimal form then becomes the input to another pass through GEN, and so on until the unchanged candidate wins (“convergence”).

(13) SH derivation of /mawara/ → [mãwãra] (cf. (8))

Step 1

m a w a r a	*NASLIQ	SHARE ([nasal])	*NASGLI	*NASVOW	IDENT ([nas])
a. → mã w a r a		4		1	1
b. m a w a r a		5 W		L	L
c. b a w a r a		5 W		L	1

Step 2

mã w a r a	*NASLIQ	SHARE ([nasal])	*NASGLI	*NASVOW	IDENT ([nas])
a. → mãw̃ a r a		3	1	1	1
b. mã w a r a		4 W	L	1	L

Step 3

mãw̃ a r a	*NASLIQ	SHARE ([nasal])	*NASGLI	*NASVOW	IDENT ([nas])
a. → mãw̃ã r a		2	1	2	1
b. mãw̃ a r a		3 W	1	1 L	L

Step 4 – Convergence

mãw̃ã r a	*NASLIQ	SHARE ([nasal])	*NASGLI	*NASVOW	IDENT ([nas])
a. → mãw̃ã r a		2	1	2	
b. mãw̃ãr̃ a	1 W	1 L	1	2	1 W

3.4. A difference between HS and parallel OT

HS's architecture imposes limitations on the kinds of mappings that languages can perform. Recall that SHARE([nasal]) favors [mã] over [b|a]. In parallel OT, SHARE([nasal]) can compel insertion and spreading of

[nasal] to change /b|a/ into [mã], as shown in tableau (14).

(14) Spontaneous nasalization with SHARE([nasal]) in parallel OT

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

This prediction is obviously undesirable; languages with nasal harmony do not also have spontaneous nasalization in oral words.

HS cannot produce this mapping with these constraints. (This claim has been verified using OT-Help 2, which is described in section 5.) The winning candidate [mã] differs from the input /ba/ by two changes: nasalization of one of the segments and spreading of [nasal] to the other. In HS, these two changes cannot be effected in a single pass through GEN. Starting with input /b|a/, 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. Tableau (15) shows that SHARE([nasal]) does not favor either of these unfaithful candidates over [b|a].

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

	/b a/	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. HS has no capacity to look ahead to the more favorable result that can be achieved by spreading once [nasal] has been inserted. 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 form the basis for most arguments in support of HS in the literature cited at the beginning of this section. This difference is also key to SH's ability to avoid the problems of AGREE and ALIGN, as we will now see.

4. SH compared with AGREE

SH does not share AGREE's sour-grapes problem described in section 2.1. This problem is AGREE's inability to compel spreading that is less than complete because of an intervening blocking segment. AGREE has this problem because it is not satisfied unless the feature or tone spreads all the way to the periphery.

That SHARE does not have this problem is apparent from (13). The mapping /mawara/ → [mãwãra] is exactly the kind of situation where AGREE fails, since faithful [mawara] and the intended winner [mãwãra] each violate AGREE once. But SHARE deals with this situation successfully because [m|a|w|a|r|a] has more violations than [mãwã|r|a].

Another advantage of SHARE over AGREE is that it does not support feature deletion as an alternative to spreading. The violation of AGREE in /mawara/ could be eliminated by denasalizing the /m/. Thus, AGREE predicts the existence of a language where nasal harmony alternates with denasalization: /mawa/ → [mãwã] vs. /mawara/ → [bawara]. No such language exists, and SHARE makes no such prediction. Step 1 of (13) shows that the mapping /mawara/ → [bawara] (candidate (c)) is harmonically bounded by the faithful mapping. Therefore, the constraints in (13), including SHARE([nasal]), can never cause denasalization under any ranking permutation.

5. SH compared with ALIGN

As I noted in section 2.2, a constraint like ALIGN-R([nasal], word) could in principle be satisfied not only by spreading [nasal] onto segments to its right but also by other methods. Wilson (2003, 2004, 2006) has identified several such methods, none of which actually occur. These "pathologies", as he calls them, are problematic for a theory of harmony based on ALIGN, though, as I will argue, they are no problem in SH.

All of the pathologies have one thing in common: they minimize the number of segments between the rightmost (or leftmost) segment in the [nasal] span and the edge of the word. Deleting a non-harmonizing segment

comes to mind as one way of accomplishing that, but there are several others, including metathesis, affix repositioning, blocking of epenthesis, and selection of shorter allomorphs.⁵

All of the claims in this section about what SH can and cannot do have been verified with OT-Help 2 (Becker et al. 2009). There are principled methods for establishing the validity of typological claims in parallel OT (Prince 2006), but no such techniques exist for HS. Thus, typological claims in HS, such as those in this section, can be confirmed only by following all derivational paths for every ranking. OT-Help 2 implements an efficient algorithm of this type. Moreover, it does so from a user-defined GEN and CON, so it calculates and evaluates its own candidates, starting only with user-specified underlying representations. In the present instance, the typologies were calculated using all of the SH constraints in this chapter and operations equivalent to autosegmental spreading, deletion, metathesis, epenthesis, and morpheme spell-out, as appropriate.

5.1. Segmental deletion

This is the first of the pathologies that we will consider. Because ALIGN-R([nasal], word) is violated by any non-harmonizing segment that follows a nasal, it can be satisfied by deletion as well as spreading. Tableau (16) gives the ranking for a language that deletes non-harmonizing /r/ (and perhaps the vowel that follows it, depending on how ONSET is ranked). This type of harmony has never been observed, to my knowledge.

(16) Harmony by deletion pathology with ALIGN

/mawara/	*NASLIQ	ALIGN-R ([nasal], word)	MAX	IDENT([nas])
a. → mãwã.ã			1	4
b. mãwãra		2 W		3 L
d. mãwãã	1 W		L	5 W

SH does not make this prediction. It does not by virtue of the hypothesis that segmental deletion is the result of gradual attrition that takes place over several derivational steps (McCarthy 2008a). This assumption is a very natural one in light of developments in feature geometry (Clements 1985) and parametric rule theory (Archangeli and Pulleyblank 1994). GEN can perform certain operations on feature-

geometric class nodes, among which is deletion of feature-geometric class nodes. A segment has been deleted when all of its class nodes have been deleted, one by one. Thus, what we observe as total segmental deletion is the “telescoped” (Wang 1968) result of a series of reductive neutralization processes. This proposal explains why segmental deletion is observed in coda position: codas are independently subject to deletion of the Place and Laryngeal nodes.

With this hypothesis about segmental deletion, SH does not allow SHARE (or ALIGN) to compel segmental deletion. The argument is similar to the one in section 3.4: the first step in deleting a segment does not produce immediate improvement in performance on SHARE, and HS has no look-ahead ability. Imagine that the derivation has reached the point where [mãwã|r|a] is the input to GEN. The form [mãwã|a], with outright deletion of [r] and consequent elimination of a SHARE([nasal]) violation, is not among the candidates that GEN emits. There is a candidate in which [r] has lost its Place node, but the resulting Place-less segment still violates SHARE([nasal]).

The deletion pathology arises in parallel OT because GEN produces candidates that differ from the underlying representation in many ways – for instance, from /mawara/, it directly produces [mãwã.ã], which is optimal under the ranking in (16). In this tableau, [mãwã.ã] 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.

5.2. Metathesis

Though there are skeptics, metathesis really does seem to be securely attested in synchronic phonology (Hume 2001). Certain factors are known to favor metathesis (Ultan 1978), and it is clear that harmony is not among them. Yet metathesis is a possible consequence of enforcement of ALIGN in parallel OT, as tableau (17) shows. Here, [r] and final [a] have metathesized to make [a] accessible to spreading of [nasal], thereby eliminating a violation of ALIGN.

(17) Metathesis pathology with ALIGN

/mawara/	*NASLIQ	ALIGN-R ([nasal], word)	LINEARITY	ID([nas])
a. → mǎwǎ.ǎr		1	1	4
b. mǎwǎra		2 W	L	3 L
c. mǎwǎrǎ	1 W	L	L	5 W

SH makes no such prediction. Metathesis and spreading are distinct operations that require different derivational steps, so the winner in (17) is never among the candidates under consideration. Imagine once again that the derivation has reached the point where [mǎwǎ|r|a] is the input to GEN. The candidate set includes [mǎwǎ|a|r], with metathesis, and [mǎwǎr|a], with spreading, but [mǎwǎ.ǎr] is not possible at this step, because it differs from the input in two distinct ways. This result is similar to the one in (15): because there is no look-ahead, satisfaction of SHARE in HS will never be achieved with a two-step derivation that first sets up the conditions that make spreading possible and then spreads at the next step.

5.3. Epenthesis

Wilson also points out that parallel OT predicts a pathologic interaction between ALIGN and epenthesis. Because ALIGN disfavors segments that are inaccessible to spreading, epenthesis into an inaccessible position is also disfavored. For instance, suppose a language with nasal harmony also has vowel epenthesis, satisfying NO-CODA by inserting [i]. Obviously, NO-CODA dominates DEP. Suppose further that NO-CODA is ranked below ALIGN-R([nasal], word). In that case, epenthesis will be prevented if the epenthetic vowel is inaccessible to nasal harmony because of an intervening blocking segment:

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

/mar/	*NASLIQ	ALIGN-R([nasal], word)	NO-CODA	DEP
a. → mǎr		1	1	
b. mǎri		2 W	L	1 W
c. mǎrĩ	1 W	L	L	1 W

Words that contain no nasals vacuously satisfy ALIGN-R([nasal], word), so this constraint is irrelevant in such words. Thus, nasalless words are able to satisfy NO-CODA by vowel epenthesis: /pas/ → [pasi]. Furthermore, words that contain a nasal but no blockers will also undergo epenthesis, since the epenthetic vowel is accessible to nasal spreading:

(19) No blocker: /maw/ → [mãwĩ]

/maw/	*NASLIQ	ALIGN-R([nasal], word)	NO-CODA	DEP
a. → mãwĩ				1
b. mãw			1 W	L

A language with this grammar would fit the following description: final consonants become onsets by vowel epenthesis, unless preceded at any distance by a nasal and a true consonant, in that order. This is an implausible prediction.

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 hence the constraint hierarchy evaluates the consequences of epenthesis without knowing how spreading might subsequently affect the epenthetic vowel.

It follows, then, that vowel epenthesis always adds a violation of SHARE([nasal]), regardless of context: [mãr] vs. [mãr|i], [mãw] vs. [mãw|i]. If SHARE([nasal]) is ranked above NO-CODA, then it will simply block epenthesis under all conditions, just as DEP will block epenthesis if ranked above NO-CODA. Ranking SHARE([nasal]) above NO-CODA may be a peculiar way of preventing epenthesis, but there is no pathology. There are languages with no vowel epenthesis, and the grammar just described is consistent with that fact.

5.4. Affix repositioning

By dominating affixal alignment constraints, markedness constraints can compel infixation (McCarthy and Prince 1993; Prince and Smolensky 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, as Wilson observes. Its influence on affix placement is much like its influence on epenthesis. When the stem

contains a nasal consonant followed by a blocker like [r], then an oral affix can be forced out of suffixal position to improve alignment of [nasal] (20a). 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 is its wont (20b). The affix will also be suffixed if it is itself nasalizable and no blocker precedes it in the stem (20c). Nothing like this behavior has been observed among the known cases of phonologically-conditioned affix placement. It is presumably impossible.

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

a. Prefixation when inaccessible to harmony

/mar, o/	*NASLIQ	ALIGN-R ([nasal], word)	ALIGN-R (-o, word)
i. → omār		1	3
ii. mārō		2 W	L
iii. mārō̃	1 W	L	L

b. Suffixation with no nasal to harmonize

/par, o/	*NASLIQ	ALIGN-R ([nasal], word)	ALIGN-R (-o, word)
i. → paro			
ii. opar			3 W

c. Suffixation when accessible to harmony

/maw, o/	*NASLIQ	ALIGN-R ([nasal], word)	ALIGN-R (-o, word)
i. → mawō̃			
ii. omawō̃			3 W

We will now look at how cases like this play out in SH. We first need a theory of phonology-morphology interaction in HS to serve as the basis for analyzing affix displacement phenomena. To this end, I adopt the framework of Wolf (2008). Wolf proceeds from the assumption 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 an abstract morpheme is spelled out by some formative.

Affix displacement phenomena show that the location of spell-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, which favors candidates where the phonological spell-out of a feature matches its location in morphosyntactic structure. Affix displacement is violation of MIRROR to satisfy some higher-ranking constraint.

We now have the resources necessary to study the consequences of SH for our hypothetical example. Small capitals – MAS, PAR, MAW – will be used for the morphosyntactic representation of roots, and the [o] suffix will spell-out PLURAL. We begin with PAR. The input is the morphosyntactic structure [PAR PLURAL]. The first derivational step spells out the morphosyntactic representation PAR as the phonological string [par]. This change improves performance on the constraint MAX-M (see (21)), but because it introduces phonological structure where previously there was none, it brings violations of phonological markedness constraints, including SHARE([nasal]). (In subsequent examples, the root spell-out step will be omitted.)

(21) First step: [PAR PLURAL] → [par PLURAL]

[PAR PLURAL]	*NASLIQ	MAX-M	SHARE([nas])
a. → [p a r PLURAL]		1	2
b. [PAR 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:

(22) Second step: [par PLURAL] → [paro]

[par PLURAL]	*NASLIQ	MAX-M	SHARE([nas])	MIRROR
a. → [p a r o]			3	
b. [p a r PLURAL]		1 W	2 L	
c. [o p a r]			3	3 W
d. [p o a r]			3	2 W

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

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

(23) Second step: [mar PLURAL] → [maro]

[mar PLURAL]	*NASLIQ	MAX-M	SHARE([nas])	MIRROR
a. → [m a r o]			3	
b. [m a r PLURAL]		1 W	2 L	
c. [mã r PLURAL]		1 W	1 L	
d. [o m a r]			3	3 W
e. [m o a r]			3	2 W

This is the crucial tableau. It shows that SHARE([nasal]), unlike ALIGN in (20b), 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 [õm|a|r] or [mõ|a|r], 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. An 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 at the same time.

5.5. Allomorph selection

In phonologically conditioned allomorphy, 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 consonant-final stems and [ka] (voiced intervocalically to [ga]) follows vowel-final stems:

(24) 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 (e.g., Burzio 1994; Hargus 1995; Hargus and Tuttle 1997; Mascaró 1996, 2007; Mester 1994; Perlmutter 1998; Tranel 1996a, 1996b, 1998):

- (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] over [cip-ka] and [c^ha-i], respectively.

The following tableaux illustrate:

(25) 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	

Wilson shows that a pathology emerges when $\text{ALIGN-R}([\text{nasal}], \text{word})$ is allowed to participate in allomorph selection. This constraint will prefer the shorter suffix allomorph when the stem contains a $[\text{nasal}]$ feature that cannot spread onto the suffix. Furthermore, it can 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 (26) illustrates. Although ONSET favors the allomorph $[-\text{ga}]$ after vowel-final stems, its effect is overridden by $\text{ALIGN-R}([\text{nasal}], \text{word})$ when the stem contains a nasal consonant. But with roots that do not contain a nasal, $\text{ALIGN-R}([\text{nasal}], \text{word})$ is vacuously satisfied by both candidates, and ONSET favors $[-\text{ga}]$.

(26) 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 (26), the choice between $[i]$ and $[ka]$ will be determined by ONSET except when the stem contains a nasal consonant at any distance, 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.

SHARE([nasal]) does not make these predictions. It simply favors the shorter allomorph, [i], since this allomorph introduces one SHARE([nasal]) violation while the longer allomorph [k|a] introduces two. SHARE([nasal]) has this effect regardless of whether the stem contains a nasal consonant:

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

a. No nasal in stem

/t a- {i, k a}/	SHARE([nas])	ONSET
i. → t a i	2	1
ii. t a g a	3 W	L

b. Nasal in stem

/n a m i- {i, k a}/	SHARE([nas])	ONSET
a. → n a m i i	4	1
b. n a m i g a	5 W	L

This effect of SHARE([nasal]) in systems of allomorphy might seem a bit odd, but it is not pathological. As in the case of epenthesis (section 5.3), SHARE([nasal]) predicts a system that we already predict in another, more obvious way. The language in (27) is simply one where ONSET does not choose among allomorphs; 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 (27). But a language without allomorphy is a possible human language, so there is no pathological prediction being made.

Although (27) is a language without nasal harmony, the result is the same in a language with harmony. The reason is the same as in section 5.4: 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.⁶

5.6. Summary

When SHARE and its associated representational assumptions are combined with HS, 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 metathesis pathologies, and it also explains why inserting [nasal] is not a legitimate way of improving performance on SHARE([nasal]). Furthermore, HS denies SHARE the power to have even local effects on epenthesis or allomorph selection.

6. Conclusion

Harmonic Serialism has OT's core 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 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 chapter is an exploration of that question and those constraints in the domain of autosegmental spreading 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.

Notes

¹ This work is much the better for the feedback I received from the participants in the UMass Phonology Grant Group in Fall, 2008: Diana Apoussidou, Emily Elfner, Karen Jesney, Peter Jurgec, Kevin Mullin, Kathryn Pruitt, Brian Smith, Wendell Kimper, and especially Joe Pater. Grace Delmolino provided welcome stylistic support. This research was funded by grant BCS-0813829 from the National Science Foundation to the University of Massachusetts Amherst.

²In the earliest literature on autosegmental phonology such as Goldsmith (1976a, 1976b) or Clements and Ford (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 (1975).

³The definition of SHARE in (9) is intended to allow some leeway depending on how phenomena like neutral segments or problems like locality are handled. Thus, the “adjacent elements” referred to in the definition of SHARE could be feature-geometric V-Place nodes (Clements and Hume 1995), segments, moras, syllables, or other “P-bearing units” (Clements 1980, 1981). Adjacency is also an abstraction, as the adjacency parameters in Archangeli and Pulleyblank (1987, 1994) make clear.

⁴Under the assumptions about GEN in (12), 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.

⁵Wilson cites one more pathological prediction of ALIGN. In a language with positional faithfulness to [nasal] in stressed syllables, such as Guaraní (Beckman 1998), stress could be shifted to minimize ALIGN([nasal]) violations. I do not address this here because it is one of many pathologies associated with positional faithfulness — pathologies that are eliminated in HS, as Jesney (to appear) demonstrates.

⁶Wilson also points out a related prediction. If it dominates MAX-BR, ALIGN-R([nasal], word) can cause a reduplicative suffix to copy fewer segments when the stem contains a nasal consonant: /pataka-RED/ → [pataka-taka] versus /makasa-RED/ → [makasa-sa] (if other constraints favor a disyllabic reduplicant that can shrink to monosyllabic under duress). This behavior is also unattested, and cannot arise in SH. The reasoning is similar to the allomorphy case.

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