Positive Constraints and Finite Goodness in Harmonic Serialism

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1   Introduction

In Optimality Theory (OT) (Prince and Smolensky, 1993/2004), constraints have traditionally been negatively rather than positively defined; that is, they assign **violations** rather than **rewards**. Because OT's Gen can perform multiple operations (and multiple instances of a single operation) simultaneously, negative constraints have been necessary. A positive constraint suffers from the **Infinite Goodness** problem (Prince, 2007); for any structure favored by a positive constraint, an infinite number of instances of that structure can be epenthesized, and there ceases to be an optimum.

In Harmonic Serialism (HS) (McCarthy, 2000, 2002, 2007), however, Gen is restricted to performing one operation at a time. This means that infinitely epenthetic candidates can no longer be entertained, and positive constraints are a viable possibility. In this paper, I discuss the properties of HS that render positive constraints feasible, as well as possible limitations on the types of constraints that may be viably positive.

Furthermore, I argue that positive constraints have certain advantages over their negatively-defined counterparts. In particular, negative constraints driving autosegmental spreading processes produce a number of pathological predictions; because they assign violations for unassimilated segments, they interact in unattested ways with processes that affect the number of segments in a word. A positive spreading constraint, on the other hand, assigns rewards for assimilated segments; this, combined with the gradual harmonic improvement of HS, permits a superior account of harmony processes.

The paper is organized as follows. Section 2 discusses the infinite goodness problem and its resolution in HS, section 3 shows how a positive constraint provides a better account of harmony processes than its negative counterparts, and 4 discusses potential limitations on the formulation of positive constraints in HS.

2   The Infinite Goodness Problem

The Infinite Goodness problem arises because positive and negative constraints are not simply the mirror image of each other — they assign marks differently. Compare, for example, positive and negative formulations of a constraint like Onset.

(1)   a.   (−)Onset: Assign -1 for every syllable that does not have an onset.

    b.   (+)ONSET: Assign +1 for every syllable that has an onset.

Both versions of the constraint demand that syllables have onsets; both prefer a candidate with an epenthetic onset (2a) over a faithful, onsetless candidate (2b). However, a positively formulated ONSET constraint will prefer a candidate with both an epenthetic onset and an epenthetic CV syllable (2c) over a candidate with a single epenthetic onset (2b), while the negative version of the constraint exerts no such preference.

(2)

ap	(−)ONSET	(+)ONSET
a. .ap.	−1	
b. .ʔap.		+1
c. .ʔap.ʔə.		+2

In a language where ONSET dominates faithfulness, the negative version of the constraint will compel the insertion of an onset into the syllable in (2). A candidate like (2c) will be (correctly) harmonically bounded — it doesn't perform any better than its competitor on ONSET, and gratuitously violates faithfulness. However, if a positive version of ONSET dominates faithfulness, a candidate like (2c) will be chosen over a candidate like (2b).

The problem with this is immediately apparent: if (+)ONSET favors a candidate with an additional epenthetic syllable over a candidate with mere onset epenthesis, it will favor a candidate with two epenthetic syllables over a candidate with only one epenthetic syllable, a candidate with three epenthetic syllables over a candidate with two, and so on. Because GEN can provide an infinite set of candidates with increasingly many epenthetic syllables (3), there exists no optimal candidate (Prince, 2007).

(3)

ap	(−)ONSET	(+)ONSET
a. .ap.	−1	
b. .ʔap.		+1
c. .ʔap.ta.		+2
d. .ʔap.ta.ka.		+3
e. .ʔap.+$\aleph_0$		+∞

With parallel OT's unrestrained GEN, positive constraints are untenable. Any constraint satisfied by epenthesis necessarily encounters the infinite goodness problem — for any structure preferred by a positive constraint, infinitely many instances of that structure can be

inserted, and optimality becomes impossible. However, in Harmonic Serialism (HS), a derivational variant of OT with a number of independent typological advantages[1], a sufficiently restricted GEN allows positive constraints to avoid the problem of infinite goodness.

In HS, GEN is restricted to producing candidates that each differ from the input by at most a single application of a single change.[2] This finite candidate set is evaluated by EVAL, just like in parallel versions of OT, but instead of exiting the derivation as the surface form, the optimum is sent back to GEN to serve as the input to a new step in the derivation. Once again, candidates differing from this new input by at most a single instance of a single change are generated and evaluated. The GEN→EVAL loop continues until the changes made by GEN no longer increase harmony — the derivation **converges** when the faithful candidate at the current step is chosen as optimal.

As a consequence, HS derivations must be **gradual** and **harmonically improving**. Because GEN is restricted, each step in the derivation can advance by at most a single change. Because each step involves choosing an optimum at EVAL, and the derivation converges if the faithful candidate is chosen, each step must improve performance with respect to the constraint hierarchy.

The gradual harmonic improvement involved in HS derivations means that positive constraints can avoid the infinite goodness problem. Compare, for example, the candidates generated as a result of epenthesis by parallel OT's unrestrained GEN, which can perform an unbounded number of epenthesis operations, to those created by HS's restricted GEN, which can perform at most one instnace of epenthesis (4).

(4)   *Possible candidates in OT and HS*

	OT	**HS**
Input	/ap/	.ap.
a.	.ap.	.ap.
b.	.ʔap.	.ʔap.
c.	.ʔap.ta.	—
d.	.ʔap.ta.ka.	—
e.	.ʔap.$+\aleph_0$	—

Candidate (4a), the faithful candidate, and candidate (4b), which has a single epenthetic segment, are possible candidates in both parallel OT and in HS. The problematic candidates (4c-e), on the other hand, are not possible members of this candidate set in HS. Because they involve multiple applications of a single operation (epenthesis) and simultaneous application of multiple operations (epenthesis and syllabification), they cannot be produced by a restricted HS GEN. This result depends, of course, on the nature of the epenthesis operation

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[1]See e.g. Elfner (2009); Kimper (to appear); Jesney (2009); McCarthy (2008b,a, to appear); Pruitt (2008); Wolf (2008) and other papers in this volume.

[2]What constitutes a single change is a matter of ongoing research; see for example McCarthy (2010) for a discussion of the kinds of evidence brought to bear on this question.

— here I make the assumption that at most a single segment can be inserted at once, but any definition of epenthesis which is restricted to the insertion of a bounded number of segments will produce a similar result.

If (+)ONSET dominates DEP, a HS derivation proceeds as follows. At the first step[3] in (5), epenthesizing an onset garners a reward on (+)ONSET and wins over the faithful candidate. At Step 2, epenthesizing does not improve performance on (+)ONSET, so the faithful candidate is chosen as optimal, and the the derivation converges.

(5) **Step 1**

.ap.	(+)ONSET	DEP
a. .ap.	W	L+1
b. ☞ .ʔap.	+1	

Step 2: *Convergence*

.ʔap.	(+)ONSET	DEP
a. ☞ .ʔap.	+1	+1
b. .ʔap.ʔ	+1	W

At any given step of the derivation, the candidate set produced by HS's restrained GEN is finite — this means that the potential for infinite goodness can't interfere with the ability to find an optimum at EVAL. Because there are not infinitely many candidates with increasing numbers of epenthesized onsets, there will in fact exist a candidate that garners the most rewards on a positive constraint. This means that at least some constraints in HS can be positive without running afoul of infinite goodness, but it does not necessarily mean that any constraint can be positive. See Section 4 for a discussion of the restrictions on the formulation of positive constraints.

3 Wherefore positive constraints: Harmony

The previous section established that positive constraints are viable in HS; this section argues that, in at least some contexts, they are not only viable but also desirable. Autosegmental spreading has proven challenging to account for with a negative spreading constraint — Wilson (2004, 2006) identifies a number of pathological predictions made by common harmony constraints. In particular, commonly-used constraints make problematic predictions

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[3]Following initial syllabification steps, not shown; for a concrete proposal regarding syllabification in HS, see Elfner (2009).

in systems where spreading is blocked. For example, in Malay, nasal harmony is blocked by obstruents (Onn, 1980; Walker, 2000):

(6) *Nasal harmony in Malay*

   a. Unbounded rightward spreading
       mĩnõm   'to drink'
       bãŋõn   'to rise'
       mãĵãn   'stalk (palm)'
       pəŋɔ̃ŋãh̃ãn   'central focus'
       mɔ̃nãw̃ãn   'to capture'
   b. Blocked by obstruents
       mãkan   'to eat'
       pəŋãw̃ãsan   'supervision'

One common approach to spreading is AGREE, which assigns violations to a sequence of [αF][–αF] (Bakovic, 2000; Eisner, 1999; Lombardi, 1999, 2001; Pulleyblank, 2004). This constraint suffers from the **Sour Grapes** problem — if complete harmony is impossible, no spreading is predicited. Take, for example, an input like /pəŋawasan/ — a constraint like AGREE(NAS) will assign a violation for the [+NAS][–NAS] sequence [ŋa]. However, the attested output form [pəŋãw̃ãsan], where nasality has spread several segments to the right, performs no better — AGREE(NAS) will assign a violation to the [ãs] sequence. Harmony has not improved performance on AGREE(NAS), and has gratuitously violated faithfulness, so is predicted to be harmonically bounded. Nevertheless, languages like Malay, rather than giving up whenever total agreement is impossible, spread as far as is possible. See Wilson (2004); McCarthy (2004, to appear) for further discussion of this pathology.

Another common approach to spreading, which does not suffer from the Sour Grapes problem, is to use gradient alignment constraints on feature domains (Archangeli and Pulleyblank, 2002; Cole and Kisseberth, 1994, 1995; Kirchner, 1993; Pulleyblank, 1996; Smolensky, 1993). Constraints like ALIGN assign violations to segments that intervene between the edge of the feature domain and the edge of the bounding domain.

However, in words where harmony is blocked, a sufficiently highly ranked ALIGN can block epenthesis. Consider Malay′, where ALIGN dominates a constraint against word-final consonant clusters (which in turn dominates DEP). When harmony is blocked, an epenthesized segment increases the distance between the edge of the feature domain and the word edge — ALIGN will prefer a candidate with no epenthesis (7a) over a candidate with an epenthetic segment (7b).

(7)

nawakast	ALIGN-R(NAS,PWD)	*CC#	DEP
a. ☞ nãw̃ãkast	–4	–1	
b. nãw̃ãkasət	W–5	L	W–1

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In Malay′, final clusters are normally resolved by epenthesis (8a). However, in words where spreading is blocked, no epenthesis occurs (8b). More broadly, a constraint like ALIGN-R can produce a language where harmony does not occur, but epenthesis is still blocked to the right of a nasal segment. These patterns are unattested, in Malay or elsewhere (Wilson, 2004, 2006).

(8)

	ALIGN-R(NAS,PWD)	*CC#	DEP
a. tawakasət ∼ tawakast		W	L
b. nãw̃ãkast ∼ nãw̃ãkasət	W	L	W

ALIGN blocks epenthesis because it assigns a violation to each segment intervening between the edge of the feature domain and the edge of the word; epenthesizing a segment, then, adds to the number of violations assigned by ALIGN. Broadly speaking, the problem is that ALIGN is sensitive to the number of non-harmonized segments in a word; a number of the other pathologies identified by Wilson (2004) (including those related to deletion, allomorph selection, and reduplication) also arise because of this kind of segment-counting.

McCarthy (to appear) notes that serial evaluation plays a role in resolving some of the problematic predictions of ALIGN and other harmony constraints (including, to some extent, the Sour Grapes problem). However, sensitivity to the number of non-harmonized segments in a word remains — segment-counting pathologies like harmony-dependent epenthesis blocking are still predicted with ALIGN in HS. The competitors at the nth step of a HS derivation in (9) are exactly the same as those in the OT derivation in (7).

(9) **Step n**

nãw̃ãkast	ALIGN-R(NAS,PWD)	*CC#	DEP
a. ☞ nãw̃ãkast	−4	−1	
b. nãw̃ãkasət	W−5	L	W−1

Because a positively-defined spreading constraint assigns rewards for autosegmental associations rather than assigning violations for failure to assimilate, it will not be sensitive to the number of non-harmonized segments present. Unlike ALIGN, a positive spreading constraint (10) will not suffer from segment-counting pathologies.[4]

(10) (+)SPREAD(F): Assign +1 for each segment linked to F as a dependent.[5]

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[4]Wilson solves these problems by using Targeted Constraints, which contain a reward-assigning component. See McCarthy to appear for another kind of proposal to address this class of pathologies.

[5]I assume that each feature domain has one and only one head; at present, it does not matter which segment serves as head, as long as there can be only one. For discussion of headed domains in autosegmental spreading, see Cole and Kisseberth (1994); McCarthy (2004); Smolensky (2006) and others.

In this case the relevant single change performed by GEN is the creation of a single autosegmental link (or, more generally, spreading the relevant feature to a single segment). Harmony thus proceeds one segment a time, as in the derivation in (11). At the first step, the candidate with nasal spreading wins over the faithful candidate. This is again the case at the second and third steps; spreading will continue to iterate, segment by segment, until there are no more segments left unassociated or until spreading is blocked. The latter is true in (11); at the fourth step, spreading conflicts with (+)OBSORAL. The faithful candidate is chosen as optimal, and the derivation converges.

(11) **Step 1**

nawakast	(+)OBSORAL	(+)SPREAD(NAS)	(+)IDENT(NAS)
a. nawakast	+2	W	L+8
b. ☞ nãwakast	+2	+1	+7

Step 2

nãwakast	(+)OBSORAL	(+)SPREAD(NAS)	(+)IDENT(NAS)
a. nãwakast	+2	W+1	L+8
b. ☞ nãw̃akast	+2	+2	+7

Step 3

nãw̃akast	(+)OBSORAL	(+)SPREAD(NAS)	(+)IDENT(NAS)
a. nãw̃akast	+2	W+2	L+8
b. ☞ nãw̃ãkast	+2	+3	+7

Step 4: *Convergence*

nãw̃ãkast	(+)OBSORAL	(+)SPREAD(NAS)	(+)IDENT(NAS)
a. ☞ nãw̃ãkast	+2	+3	+8
b. nãw̃ãk̃ast	W+1	L+4	W+7

Because it assigns rewards for harmony rather than violations for failure to harmonize, (+)SPREAD(NAS) will not be sensitive to the number of segments to the right of the blocking obstruent in [nãw̃ãkast]. Consider a candidate with epenthesis to break up the final cluster — both the faithful candidate (12a) and the candidate with epenthesis (12b) perform equally well on (+)SPREAD(NAS).

(12) **Step 4**

nã̃w̃ãkast	(+)SPREAD(NAS)	(+)CV
a. nã̃w̃ãkast	+3	W+3
b. ☞ nã̃w̃ãkasət	+3	+4

A positive spreading constraint, therefore, cannot block epenthesis. Furthermore, a constraint like (+)SPREAD(NAS) is prevented from *inducing* epenthesis by the restricted GEN in HS. As we saw in the discussion above, a positive constraint like (+)SPREAD(F) in parallel OT would suffer from the infinite goodness problem. In this case, it would cause infinite harmony by epenthesis — inserting and harmonizing a segment would earn a reward, so infinitely many epenthesized segments would be preferred.

In HS, however, epenthesis and harmony cannot occur concurrently. (+)SPREAD(F), therefore, can't induce epenthesis on its own — the intermediate step necessary will not constitute an improvement. An epenthetic candidate (13b) performs no better on (+)SPREAD(F) than the faithful candidate (13a). Because there is no possible candidate at this step with both epenthesis and harmony, the faithful candidate is chosen and the derivation converges.

(13) **Step 4**: *Convergence*

nã̃w̃ãkast	(+)SPREAD(NAS)	(+)DEP
a. ☞ nã̃w̃ãkast	+3	+1
b. nã̃w̃ãʔkast	+3	L

The solution presented here has centered around pathologies involving epenthesis, but is general to the set of pathologies involving the number of non-harmonized segments in a word. A positive spreading constraint exerts no preference against non-harmonized segments, and because a HS GEN is restricted to making gradual changes, a positive constraint cannot itself induce processes that increase the number of segments available to harmony. This section has presented a brief discussion of the advantages of using positive constraints to drive autosegmental spreading, but is not a fully developed theory; for a more detailed proposal, see Kimper (2011).

4   The scope of the solution

Because HS derivations are gradual and harmonically improving, they provide a possible way out of the infinite goodness problem suffered by positive constraints in parallel versions of OT. The previous section showed how a positive constraint — with the restricted GEN of

HS — proves desirable in the realm of autosegmental spreading. However, it is important to note that the solution to infinite goodness presented by HS is not universal; that is, it is not true that any and all constraints can necessarily be positively defined, even when GEN is restricted to producing a limited candidate set.[6]

This is because a finite candidate set is not in and of itself sufficient to prevent infinite goodness — HS derivations only converge when the single changes produced by GEN fail to produce harmonic improvement. This means that in order to avoid infinite goodness, a derivation must be sufficiently gradual to prevent a positive constraint from inducing an infinite loop of instant satisfaction.

With a positive version of ONSET, the derivation in (5) converges at the second step — it's not possible to both epenthesize a segment and create the supporting structure that would make it an onset; epenthesis and syllable creation constitute separate steps. This is also true for the positive spreading constraint in the previous section; because it is not possible to simultaneously insert a segment and create and autosegmental link, any further satisfaction requires a two-step process, and the first of those steps (epenthesis) must be *independently* harmonically improving in order to take place.

This means that the degree to which infinite goodness can be avoided will depend crucially on the degree to which GEN is restricted. Consider, for example, a context-free markedness constraint like (+)OBSORAL, which assigns a reward to every oral obstruent. Whether a constraint of this type is viable as a positive constraint depends on the nature of the epenthesis operation itself.

If a segment and its features can be inserted simultaneously, a constraint like (+)OBSORAL can be instantly satisfied by epenthesis. At each successive step in the derivation, yet another oral obstruent can be epenthesized; because (+)OBSORAL will continue assigning rewards to non-faithful candidates, the derivation will never converge. In other words, a positive constraint may be infinitely satisfied if the structure it prefers can be created with a single step of a single operation, where that operation is not limited by existing structure. Relevant operations include segment epenthesis, epenthesis of floating features, and prosodic parsing.

This can be seen in the derivation in (14). (+)OBSORAL dominates faithfulness, and as a result the nasal obstruent in the input denasalizes — precisely the effect we would expect from the constraint's negatively defined counterpart. However, at the second step, a candidate with a fully-specified epenthetic segment is entertained; in particular, a fully specified oral obstruent. This candidate is chosen as the winner, because it performs better on (+)OBSORAL. At the third step, yet another fully specified oral obstruent can be inserted, again performing better on the positive constraint. The derivation will continue thus indefinitely, never converging, and falling victim once again to the infinite goodness

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[6]Flemming (2001) uses a positively defined contrast maximization constraint; because this constraint evaluates inventories rather than derivations, the distinction between parallel and serial versions of OT is not relevant, and the present solution to the infinite goodness problem does not extend to that case.

problem.

(14)   *Infinite derivation with fully-specified epenthesis*

Step 1

tap̃	(+)OBSORAL	FAITH
a. tap̃	W+1	L+1
b. ☞ tap	+2	

Step 2

tap	(+)OBSORAL	FAITH
a. tap	+2	+1
b. ☞ tapt	+3	W

Step 3

tapt	(+)OBSORAL	FAITH
a. tapt	+3	+1
b. ☞ taptt	+4	W

Step ∞ …

The situation is improved considerably with a more gradual epenthesis operation. McCarthy (2008a) presents evidence from cluster simplication suggesting that deletion of segments and deletion of features constitute separate operations. Maintaining a separation of operations on features and operations on segments in GEN for insertion as well as deletion means that derivations can be sufficiently gradual to prevent constraints like (+)OBSORAL from triggering infinitely long derivations.

The derivation above now follows a rather different course. At the first step in (15), denasalizing that obstruent earns a reward on (+)OBSORAL, at the expense of faithfulness. In order for (+)OBSORAL to earn further rewards at the second step, GEN would need to provide a candidate with epenthesis of a fully-specified oral obstruent. However, with separate insertion operations for segments and features, such a candidate is not a possible member of the candidate set. The best that GEN can do is to epenthesize a featureless default segment; this is not sufficient to earn a reward from (+)OBSORAL, and gratuitously violates faithfulness. The faithful candidate is the winner, and the derivation converges.

(15)   *Finite derivation with restricted epenthesis*

Step 1

10

tap̃	(+)ObsOral	Faith
a. tap̃	W+1	L+1
b. ☞ tap	+2	

Step 2: *Convergence*

tap	(+)ObsOral	Faith
a. ☞ tap	+2	+1
b. tapʔ	+2	W

It is not possible to satisfy a constraint like (+)ObsOral through gradual epenthesis; the conditions necessary to earn rewards on even a context-free markedness constraint cannot be created wholesale in one step. At the second step in (15), there is no access to the information that the epenthesized default segment could subsequently become specified as oral and earn a reward on (+)ObsOral. Because each step in a HS derivation must be harmonically improving to prevent immediate convergence, a two-step progression towards further satisfying a constraint is impossible.

Even with a restricted Gen, it is still not true that any possible constraint formulation will be viable as a positive constraint. For example, a constraint like (+)Seg (assign +1 for every segment) would be obviously problematic, as would a constraint like (+)High (assign +1 for every high tone, whether or not it's associated with a TBU). The epenthesis operation simply cannot be sufficiently restricted to prevent indefinite satisfaction without disastrous consequences elsewhere. However, there appears to be no evidence in favor of the existence of constraints like this, which are in many ways the positive counterparts to constraints like *Seg (see e.g. Gouskova 2003 for arguments against *Seg and constraints like it).

Potentially more difficult to contend with are prosodic alignment constraints. A constraint like (+)Align-R(Ft,Wd), for example, would assign a reward for each foot that is aligned to the right edge of some word. The problem with a constraint like this is that it can be infinitely satisfied by building vacuously recursive prosodic structure; consider the derivation in (16).[7] At the first step, (+)Align prefers a candidate with a foot parsed at the right edge of the word over an unparsed candidate or a candidate with a foot at the left edge. At the second step, however, we see that additional satisfaction of (+)Align is possible with parsing an additional recursive foot; now there are two feet whose right edges align with the right edge of the prosodic word, and hence to rewards. Because this was accomplished in a single step, it will continue indefinitely, and the derivation will not converge.[8]

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[7]Curly braces here represent prosodic words, while parentheses denote feet.

[8]Reversing the roles of word and foot in the constraint will be of no help; it will just cause prosodic words, rather than feet, to be infinitely recursively built.

(16) **Step 1**

{ka.ta.pa}	(+)Align(Ft,Wd)	Faith
a. {ka.ta.pa}	W	L+1
b. ☞ {ka.(ta.pa)}	+1	
c. {(ka.ta).pa}	W	

Step 2

{ka.(ta.pa)}	(+)Align(Ft,Wd)	Faith
a. {ka.(ta.pa)}	W+1	L+1
b. ☞ {ka.((ta.pa))}	+2	

Step ∞ ...

Even if it is possible to avoid this problem — for example, by restricting the foot-building operation so that vacuously recursive structure does not result — there are other issues with positive alignment constraints. In particular, the gradient evaluation of alignment over varying distances from the desired edge is lost; a positive constraint can reward satisfaction, but not varying degrees of failure to satisfy.[9] The alignment constraint schema, then, translates poorly into a system of positive constraints.

It would likely be technically possible to devise a set of positively-defined constraints which mimic the effects of the Align schema. But this raises the question of whether or not such a move would be desirable. While one of the benefits of positive constraints is that they can help to alleviate some instances of the **too many repairs** problem (as was the case in the spreading example in the previous section), one side effect is losing the ability to cohesively handle certain conspiracies.

A constraint like *NC̬ (Pater, 1999), for example, crucially relies on its negative definition to produce the attested range of effects. Capturing the same set of effects would require a range of distinct positive constraints, one for each attested repair. This loses the generalization that this set of alternations are all seeking to solve the same problem, and the constraints needed would likely introduce problems of their own. For example, post-nasal voicing is an attested repair for *NC̬ violations; a positive constraint producing this result would need to assign rewards to sequences of a nasal followed by a voiced stop. However, this such a constraint would be predicted to induce alternations of its own — it could not only induce post-nasal voicing, but also pre-voiced nasalization.

None of these problems seem to be technically insurmountable; nonetheless, it does not

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[9]Though see McCarthy (2003) for arguments in favor of restricting constraints to categorical evaluation, which would likely resolve this issue.

appear as though a CON consisting of all and only positive constraints is the way forward. While we saw in Section 3 above that a positively-defined constraint produces superior results for autosegmental spreading, some generalizations, like *NÇ, are better suited to negative definition. For most constraints, though, a sufficiently restricted GEN in HS will mean that positive and negative versions have the same practical effect (as we saw with ONSET in Section 2 above) — further research is needed to identify points of departure, and which of those constraints are better suited to positive definition and which are better suited to negative definition.

5   Conclusion

In this paper, I have shown that positively-defined constraints, which suffered from the Infinite Goodness problem in parallel versions of OT, are a viable option in HS. Because GEN is restricted to performing at most a single instance of a single operation, the candidate set does not contain candidates with infinitely many epenthesized instances of the structure preferred by a positive constraint. With a sufficiently restricted GEN, most kinds of OT constraint can be implemented positively without running afoul of infinite goodness. Some constraints remain better suited to negative definitions, so a CON which may admit both positive and negative constraints is proposed.

   Furthermore, I have argued that there is at least one domain where positive constraints produce a better result than their negative counterparts; namely, autosegmental spreading. Negatively defined harmony constraints penalize unassimilated segments, and therefore are able to influence processes like epenthesis which increase the number of segments in a word. A positively defined harmony constraint, on the other hand, avoids a number of the pathological predictions of its negative predecessors — because it assigns rewards to assimilated segments, it is not sensitive to the number of segments which have failed to harmonize, and therefore exerts no undue segment-counting influence, and is appropriately limited to merely inducing assimilation.

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