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# Incongruencies between phonological theory and phonetic measurement

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### Supplementary materials

#### Appendix: Model details and optimisation

Model optimisations were conducted in Matlab with a multiple starting point global optimisation procedure. The cost function was the total root mean square error (RMSE) in LE and RE. The oscillator equation is shown in (7a) below. For the oscillator equation in (7a), the indices i/j = 1, 2, 3of the coupling matrix  $\Phi$  correspond to C<sub>1</sub>, C<sub>2</sub> and V planning oscillators respectively. The coupling matrix  $\Phi$  has the structure in (7b), where *b* is the strength of anti-phase coupling,  $a_1$  is the strength of in-phase C<sub>1</sub>-V coupling and  $a_2$  is the strength of in-phase C<sub>2</sub>-V coupling. The relative phase  $\varphi_{ij}$  is defined as in (7c). The model-predicted RE and LE shifts are calculated as in (7d), where  $\beta$  is the biomechanical correction parameter.

(7) a. 
$$x_i = 2\pi f + \sum_j - \Phi_{ij} \sin(\varphi_{ij})$$
  
b.  $\Phi = \begin{bmatrix} b & a_1 \\ b & a_2 \\ a_1 & a_2 \end{bmatrix}$   
c.  $\varphi_{ij} = \theta_i - \theta_j$   
d.  $RE = \frac{\varphi_{23}}{2\pi f} + \beta, LE = \frac{\varphi_{13}}{2\pi f}$ 

#### 2 Doris Mücke, Anne Hermes and Sam Tilsen

In all cases, the frequencies (f) of the oscillators, coupling parameters  $(b, a_1, a_2)$ , and biomechanical correction  $(\beta)$  were optimised separately for each subject, condition and target. Because a very small temporal difference between LE and RE leads to a large frequency, the oscillator frequency was limited to a maximum of 10 Hz, in order to maintain a behaviourally plausible value. For all models, the mean value of  $a_1$  and  $a_2$ ,  $(\hat{a})$ , was fixed at 5, and the ratio of the anti-phase force to average in-phase force  $(b/\hat{a})$  was allowed to vary from 0 to 2.

The simple, complex balanced and complex imbalanced models correspond to different constraints on the coupling matrix  $\Phi$ . In all models, the in-phase coupling parameters are positive (a > 0) and the anti-phase coupling parameter is negative (b < 0). In the simple model,  $a_1 = 0$  and  $b = -a_2$ . Note that it is not necessary to allow b and  $a_2$  to vary independently in a simple model, because the system will always evolve toward a state in which C<sub>1</sub> and  $C_2$  have maximal relative phase ( $\pi$ ) and in which  $C_2$  and V have minimal relative phase (0), regardless of the relative strength of b and  $a_2$ . There is also no sense in which the simplex model can be imbalanced, because there is only one in-phase coupling parameter and because the in-phase and antiphase parameters do not interact with respect to the stable equilibrium of the system. In the complex balanced model,  $b = -a_1 = a_2$ . In the complex imbalanced model, there are no equality constraints on the parameters. In this case, the parameter  $a^*$  was optimised, representing the difference between  $a_1$  and  $a_2$ ; hence  $a_1 = \hat{a} + a^*/2$  and  $a_2 = \hat{a} - a^*/2$ . A negative value of  $a^*$  represents stronger in-phase coupling of  $C_1$  to V than that of  $C_2$  to V. The structurally heterogeneous model was constructed by selecting either the simple balanced or the complex balanced model on a by-subject/ by-target/by-condition basis, according to which of these two models had a lower RMSE. For models with a biomechanical correction parameter, the RE generated by the coupling models was adjusted by a free parameter constrained in the range [0, 40 ms], as shown in (7d).

Each optimisation run used a 4th order Runge-Kutta algorithm to numerically simulate the evolution of CCV phases starting from an initial condition of  $\theta_i = (0.1, -0.1, 0)$ . The numeric simulation was conducted for a simulation period of 2 seconds, which is sufficient for stabilisation. The tables in §3.1.2 and §3.2.2 provide the sum of the RMSE of the models for each subject, condition and target.