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Incongruencies between phonological theory and phonetic measurement

Doris Mücke
University of Cologne

Anne Hermes
Laboratoire de Phonétique et Phonologie, UMR 7018 (CNRS/Sorbonne Nouvelle)

Sam Tilsen
Cornell University

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 $i/j = 1, 2, 3$ of the coupling matrix Φ correspond to C_1, C_2 and V planning oscillators respectively. The coupling matrix Φ has the structure in (7b), where b is the strength of anti-phase coupling, a_1 is the strength of in-phase C_1-V coupling and a_2 is the strength of in-phase C_2-V coupling. The relative phase φ_{ij} is defined as in (7c). The model-predicted RE and LE shifts are calculated as in (7d), where β 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. $RE = \frac{\varphi_{23}}{2\pi f} + \beta,\ LE = \frac{\varphi_{13}}{2\pi f}$

In all cases, the frequencies (f) of the oscillators, coupling parameters (b, a_1, a_2), and biomechanical correction (β) 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 Φ. 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_1 and C_2 have maximal relative phase (π) 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 anti-phase 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.