Appendix: Model codes

Model m: Assessing coarticulatory patterns

> *m <- bam(peakX ~ te(time, VpeakX, k=c(4,10), by=cohort.consonant) + cohort.consonant +*
> *s(time, subject, by=consonant, bs='fs', m=1, k=4) +*
> *s(VpeakX, subject, by=consonant, bs='fs', m=1),*
> *data=datc, discrete=T, nthreads=32, rho=0.35, AR.start=datc$start.event)*

Model m tests whether the horizontal position of the highest point on the tongue dorsum (*peakX*) depends on the horizontal position of the tongue dorsum during V50 (*VpeakX*) at the four target time points V100, C50, C100, and ə50. Within the tensor product (te) term, both predictors *time* and *VpeakX* as well as their interaction is included. The k parameter specifies the maximal non-linearity by setting the size of basis dimensions for both predictors. It is limited to the number of the predictors' unique points and therefore set to four for *time* and to the default value of 10 for *VpeakX*. The following by-parameter specifies the levels the non-linear patterns are fit for: Here, all 15 possible combinations of *age cohort* and *consonant* (i.e. three-year-olds-/b/, three-year-olds-/d/, three-year-olds-/g/, …, adults-/g/). Possible constant differences in the horizontal position of *peakX* between the age cohorts and consonants were considered by including the nominal variable *cohort.consonant* (the interaction between cohort and consonant). The random effect structure of the model, defined in the two factor smooth terms (s), included potentially non-linear patterns over *time* and for V*peakX* for each participant and consonant. In the final row of the model specification, the data set is defined (datc), a faster fitting method is employed, the number of processors used to run the model is specified, and autocorrelation (here at a level of about 0.35) in the data is accounted for.

Model mb7: Assessing differences of coarticulatory patterns between age cohorts

> *mb7 <- bam(peakX ~ te(time, VpeakX, k=c(4,10), by=consonant) + consonant +*
> *te(time, VpeakX, k=c(4,10), by=IsC3b) +*
> *te(time, VpeakX, k=c(4,10), by=IsC4b) +*
> *te(time, VpeakX, k=c(4,10), by=IsC5b) +*
> *te(time, VpeakX, k=c(4,10), by=IsAb) +*
> *te(time, VpeakX, k=c(4,10), by=IsC3d) +*
> *te(time, VpeakX, k=c(4,10), by=IsC4d) +*
> *te(time, VpeakX, k=c(4,10), by=IsC5d) +*
> *te(time, VpeakX, k=c(4,10), by=IsAd) +*
> *te(time, VpeakX, k=c(4,10), by=IsC3g) +*
> *te(time, VpeakX, k=c(4,10), by=IsC4g) +*
> *te(time, VpeakX, k=c(4,10), by=IsC5g) +*
> *te(time, VpeakX, k=c(4,10), by=IsAg) +*

s(time, subject, by = consonant, bs = 'fs', m = 1, k = 4) +
s(VpeakX, subject, by = consonant, bs = 'fs', m = 1),
data = datc, discrete = T, nthreads = 32, rho = 0.35,
AR.start = datc$start.event))

In contrast to Model m, model mb7 includes binary difference tensors to compare age cohorts to each other. Here, the variable *IsC3b* for example refers to a previously specified difference smooth for cohort C3 when the consonant is /b/. Since no difference smooth for cohort C7 is included in the model, this cohort is taken as reference.