

# BEZIER MODELLING AND HIGH ACCURACY CURVE FITTING TO CAPTURE HARD PALATE VARIATION

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## ABSTRACT

The human hard palate shows between-subject variation that is known to influence articulatory strategies. In order to link such variation to human speech, we are conducting a cross-sectional MRI study on multiple populations. A model based on Bezier curves using only three parameters was fitted to hard palate MRI tracings using evolutionary computation. The fits produced consistently yield high accuracies. For future research, this new method may be used to classify our MRI data on ethnic origins using e.g., cluster analyses. Furthermore, we may integrate our model into three-dimensional representations of the vocal tract in order to investigate its effect on acoustics and cultural transmission.

**Keywords:** Anatomical variation, hard palate, Bezier curve fitting, evolutionary computation.

## 1. BACKGROUND

Human physiology varies from individual to individual. Moreover, many anatomical properties are shared within and differ between populations, e.g., craniofacial morphology [13]. Our current line of research investigates one particularly interesting case of this anatomical variation in humans: vocal tract (VT) anatomy. More specifically, if variation with respect to VT morphology introduces different costs in producing different vocalizations, populations sharing such morphology might come to use different (between-population) phonetic distributions (cf. [10]). This can happen through a process known as (anatomically biased) cultural evolution (cf. [3, 5]).

While preliminary studies have shown that between-subject variation in VT morphology indeed exists and that it might subsequently lead to different articulatory strategies [2, 11], large-scale cross-sectional studies have so far not been conducted. In our research, we are working to collect these much needed data by MRI and intra-oral scanning on different populations. The data will then be used to investigate any correlations between VT morphology and phonetic and possibly phonological features used

in the populations' respective languages.

As a way of condensing the data we will collect, we developed a model of the hard palate (mid-sagittal plane) aimed to describe the variation observed with as little as three parameters (§2). Using a curve fitting procedure, we verified that our model indeed describes hard palate profiles with high accuracy and yields very low error rates to all cases fitted (§3). Furthermore, our optimization technique consistently converges on positions that are close to a one-to-one (isomorphic) mapping between hard palate profile and parameter values. This shows that our three-parameter model, in combination with our fitting procedure, may be used to accurately identify anatomical properties of the hard palate (as in e.g., [11]).

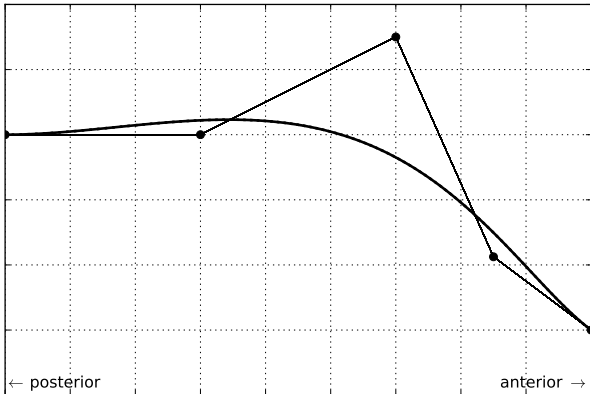
## 2. MODEL DESCRIPTION

### 2.1. Bezier curve

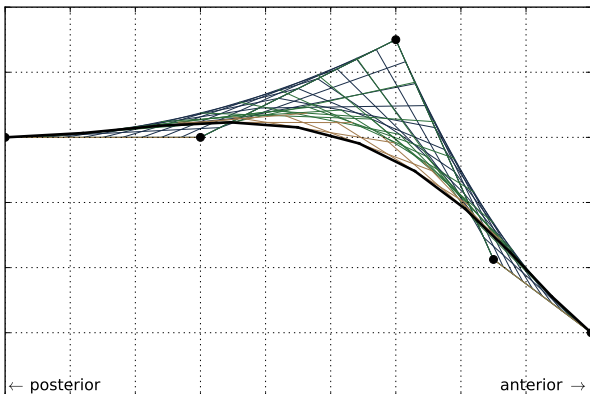
A Bezier curve is a mathematical model (parametric curve) that can be used to form higher-order splines. Bezier curves are shaped by defining a number of control points, which are (in sequence) connected by control vectors (Fig. 1). The control vectors are divided into equidistant segments, which are then each interconnected between-parent-vector. The segmenting and interconnecting procedure is repeated in recursive fashion until a sequence of singleton vectors (i.e., not further divisible by recursion) remains. This procedure is known as De Casteljaeu's algorithm (cf. Fig. 2). Effectively, one could imagine the control points pulling on different parts on the curve, each warping it with varying magnitudes and directions (cf. [7]). Finally, the sequence of singleton vectors is sampled and interpolated to yield the actual Bezier curve (Fig. 1).

Our Bezier model was designed to approximate the human hard palate on the mid-sagittal plane. In Fig. 1, one can imagine the curve following the contour of the lingual surface terminating at the central maxillary incisors on the right, and transitioning posteriorly into the velum on the left. The curve shown in Figs. 1 and 2 has all its parameters set to a neutral position. By varying these parameters, we can

**Figure 1:** The Bezier curve used to model the mid-sagittal hard palate profile. Shown are the control points (solid dots), top-level control vectors (between control points) and the resulting Bezier curve itself (smooth black line). Segmenting resolution is set to 100 segments per vector.



**Figure 2:** The same Bezier curve as shown in Fig. 1, but now with intermediate-level control vectors displayed. For illustrative purposes, segmenting resolution was decreased to 10 segments per vector.



generate a wide variety of palate profiles (cf. §2.2).

## 2.2. Parameters

Our model is controlled with five parameters  $p$  (where  $0 \leq p \leq 1$ ), each intended to capture one particular palate feature:

**Alveolar angle** controls the angle of inclination of the alveolar ridge from  $180^\circ$  (approximating a sigmoidal profile) to  $90^\circ$  (approximating a parabolic profile).

**Alveolar weight** modifies the ‘magnitude’ of alveolar angle. For example, with a sigmoidal profile, the onset of the upward inflection coming from the incisors gets shifted more posteriorly for higher values. With a parabolic pro-

file, the vertical onset (coming from the incisors) gets amplified and in effect becomes steeper. If set to 0, alveolar angle gets neutralized.

**Palatal concavity** increases the vertical displacement between velar transition and palatal roof. In effect, larger values increase the doming of the hard palate. A value of 0 means the palate can only decline moving towards the incisors.

**Palatal fronting** shifts the palatal roof more anteriorly for higher values. Depending on the other parameter values, this generally results in steeper inflections.

**Rotation** rotates the curve with a particular angle.

While the parameters are designed to have an intuitive interpretation, their effects on the Bezier curve can still be complex. The parameters are abstract entities that are meant to provide a less component-driven (but more interaction-driven) formalization of the hard palate. In doing so, we aim to increase the model’s accuracy at a possible loss of comprehensibility (but also avoiding over-simplification).

## 3. VALIDATION

### 3.1. Preliminary curve fit

#### 3.1.1. Procedure

In order to validate our Bezier model (§2), we fitted it to a sample of 28 MRI (from [14]) tracings of the hard palate on the mid-sagittal plane.

Because our model is an instance of a 4<sup>th</sup>-order Bezier curve, it cannot be considered a well-founded relation (i.e., it cannot be represented as a mathematical function) and as such cannot be used in classical (including non-linear) regression. Fitting our Bezier curve is thus an optimization problem.

Previous research has shown that the application of genetic algorithms (GAs) shows promising results in fitting Bezier surfaces to three-dimensional point-clouds [8]. Since our model is already constrained by the parameters we laid out (§2.2), has some top-down, informed dispositions, and is only two-dimensional, we deemed GA application to be feasible.

The algorithm we implemented is a straightforward GA (Table 1). Solutions (individuals) are ‘genetically’ encoded by five genes: one for each parameter. These genes encode the shape of the Bezier curve (the ‘phenotype’). The mean squared error between phenotype and palate tracing determines the ‘fitness’ of each individual. This fitness measure is then used for selection: only the fittest individuals are able to survive and ‘reproduce’. Reproduction

works by mutating genes following a Gaussian distribution (viz. asexual reproduction). A new generation (the union of parents and offspring) is then evaluated, selected for and mutated again, etc. As such, the Darwinian principles of variation, selection and reproduction are hereby simulated and exploited to find a close-to-optimal fit.

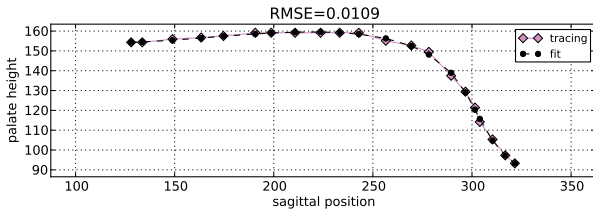
**Table 1:** GA parameters (cf. [6]).

Representation	Floating-point valued vector $V$ ( $ V  = 5, \{v \in V : 0 \leq v \leq 1\}$ )
Population size	100, initialized with 1000
Recombination	None
Mutation	Gaussian ( $\mu = 0, \sigma = 0.01$ )
Parent selection	Stochastic universal sampling ( $s = 1.25$ )
Survivor selection	$\mu + \lambda$ (with elitism)
$N^\circ$ replications	10

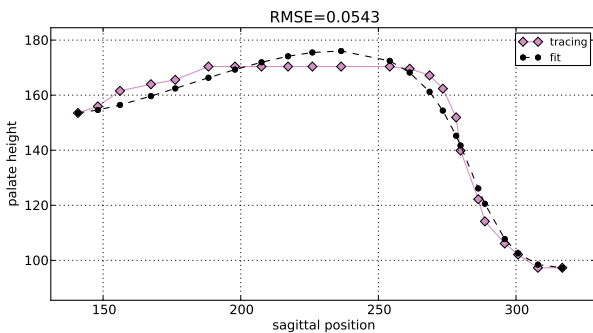
### 3.1.2. Results

Initial results when fitting our Bezier curve (§2) appear promising (Root Mean Squared Error (RMSE):  $\mu = 0.02, \sigma = 0.01$ , where  $0 \leq RMSE \leq 1$ ). The most accurate fit obtained is shown in Fig. 3, the least in Fig. 4.

**Figure 3:** The most accurate fit ( $0 \leq RMSE \leq 1$ ).



**Figure 4:** The least accurate fit ( $0 \leq RMSE \leq 1$ ).



To check for parameter-profile isomorphism, for each case we checked the dispersion (i.e., standard deviation) of the parameters associated with the elites (the best-fitted individual of an entire replication)

obtained during 10 replications of the GA. As can be seen in Fig. 5, all parameters except rotation converge on widely-dispersed values, averaging to a dispersion-rate of  $\sim 0.077$  (for comparison's sake, a run with no selective pressure averages to  $\sim 0.252$ ).

**Figure 5:** Elite parameter values (vertical axes) obtained from 10 replications (different shades) of the GA. Horizontal axes denote the MRI case fitted to. Weight parameter not shown. Note the stability of rotation.

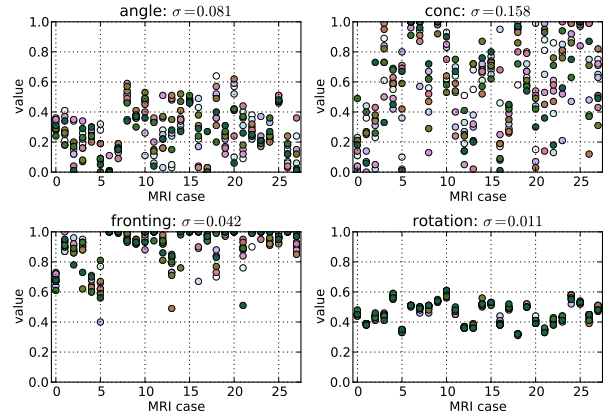
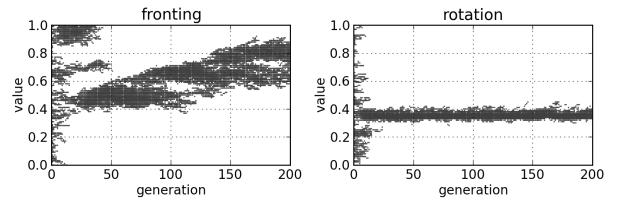


Figure 6 shows the convergence of two parameters in one illustrative case. Note the difference from fronting with rotation: With fronting (and the other parameters not shown here), there is a continuous tendency for branching and drift, indicating a well-tuned algorithm that avoids local optima. Despite this, rotation behaves much more rigidly. Together with the unusually low dispersion values, this suggests it being a disproportionately large factor in the appearance of the hard palate profile (cf. §4).

**Figure 6:** The difference in convergence of the fronting and rotation parameters.



## 3.2. Parameter constraining

### 3.2.1. Procedure

The Bezier model was designed to describe anatomical variation with a small number of parameters (§2). As we saw in §3.1.2, with five parameters the error is low indeed. However, the mapping between parameters and the Bezier curve's profile appears far from isomorphic, as indicated by relative high parameter

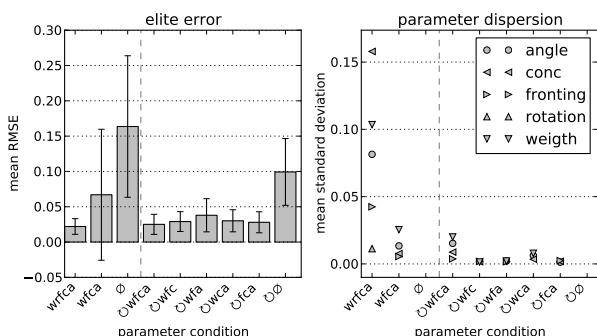
dispersion rates (Fig. 5). Furthermore, some parameters (e.g., rotation) might be too large a factor in the curve’s appearance for their use to be justified. Others might be simply redundant.

To investigate these matters, all our tracings were pre-aligned so that the angle of declination between the most posterior and anterior point equalled  $\sim 4.88^\circ$  (the sample average). Following this, we did a pairwise comparison where we fixed the remaining parameters to the sample averages obtained while fitting the five-parameter model. Thus, in total, we compared 64 conditions, i.e., the powersets of the five parameters for both the default and pre-aligned conditions.

### 3.2.2. Results

The error bars in Fig. 7 show that in the default condition, fixing rotation markedly increases the error rate (compare *wrfca* with *wfca*), and would account for almost half of the error in the condition in which all parameters were fixed to the five-parameter averages (condition  $\emptyset$ ). However, when we first pre-align the MRI tracings, fixing the rotation parameter has an almost negligible effect (compare *wrfca* with  $\circ$ *wfca*). Furthermore, we see that fixing one more parameter (besides rotation, i.e., conditions  $\circ$ *wfc*,  $\circ$ *wfa*,  $\circ$ *wca* and  $\circ$ *fca*) does not increase the error rates greatly as well.

**Figure 7:** Error rates (left) and parameter dispersion values (right) for selected conditions. Characters on horizontal axes denote which parameters were subject to optimization: a = angle, c = concavity, f = fronting, r = rotation, w = weight.  $\emptyset$  marks all parameters were fixed to the five-parameter averages.  $\circ$  marks the MRI images were pre-aligned. The dashed vertical line marks the distinction between default and pre-aligned conditions.



When we inspect the parameter dispersion values, we observe a general trend that fixing more parameters lowers dispersion. The decrease is especially pronounced when comparing the five-parameter con-

dition (*wrfca*) with the four-parameter conditions (*wfca* and  $\circ$ *wfca*). Going to the three-parameter conditions ( $\circ$ *wfc*,  $\circ$ *wfa*,  $\circ$ *wca* and  $\circ$ *fca*) further lowers dispersion to close-to-null values.

Altogether, these results indicate that we can trim the five-parameter model to a three-parameter iteration without increasing error-rates while simultaneously neutralizing parameter dispersion.

## 4. DISCUSSION

Our study has proposed using a Bezier curve to model the contour of the lingual surface of the hard palate on the mid-sagittal plane (§2.1). A genetic algorithm was used to yield high accuracies in fitting the Bezier curve to palate MRI tracings (§3.1.1).

The Bezier curve can be adjusted using five intuitive, anatomical parameters (§2.2). Anomalous behaviour was shown with the rotation parameter: Convergence stability was greater and elite dispersion was smaller compared to the other parameters (§3.1.2). We could, retrospectively, claim that rotating the Bezier curve does not describe a true anatomical property. Instead, it might e.g., reflect uncontrolled alignment of a subject’s cranium.

To resolve this, we demonstrated that the rotation parameter can be ‘dropped’, together with another parameter, by fixing them to the sample averages obtained from the five-parameter fit (§3.2). As such, this trimmed model increases the isomorphism (or one-to-one mapping) between parameters and hard palate profile. This is an effect of further constraining the model, resulting in increased convergence precision. Furthermore, trimming parameters does not necessarily lead to a corresponding increase in error rates. This is not to say the fixed parameters are not important: They are ‘pre-optimized’ to the sample-wide average, allowing the remaining parameters to differentiate between individual cases. Moreover, this reduction effectively deflates the search-space the GA has to traverse, without giving up on generality/accuracy.

Overall, our study shows that our model can be used to identify hard palate profiles and thus may be used to differentiate between populations using e.g., cluster analyses. For future studies, our formalization can be used in automated insertion of palate tracings into geometric (e.g., [1]) or finite-element (e.g., [12]) models of the vocal tract which we can then use to investigate the effects on acoustics. Finally, agent models based on these empirically grounded representations can be used to investigate anatomical biases in cultural transmission (e.g., [9, 4]).

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