# Why Polynomials Accurately Describe the Shape of a Girus

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**Giruses: a brief introduction.** While most viruses are small, there are viruses whose size – 300-500 nanometers – is larger than typical bacteria. They are called *giant viruses*, or *giruses*, for short. It is important to study giruses because, due to their relatively large size – comparable to the size of bacteria – they play an important role in ecology. It is also important to study them since they are, in many aspects, similar to usual viruses, but, because of their much larger size, it is easier to study their geometric shape.

**What is known about their geometry.** Similar to many other viruses, the surface of a girus consists of several faces. So, to describe this surface, it is sufficient to describe the shape of these faces. In general, the shape of a surface can be described as $f(x) = 0$ for some function $f(x)$, where $x = (x_1, x_2, x_3)$. So, to describe a surface, it is sufficient to describe the corresponding function.

A usual way to describe a general function is to select a basis $e_1(x)$, $e_2(x)$, ..., $e_n(x)$, and to try functions of the type $c_1 \cdot e_1(x) + \ldots + c_n \cdot e_n(x)$. In principle, there can be many different bases; it is desirable to select the one for which we can fit the data with the smallest number of parameters $c_i$. It turns out that for many marine giruses, a good description of the shape of their faces is provided by cubic polynomials [1].

**A natural question.** A natural question is: why polynomials – and not any other functions – provide a good basis for this problem?

**A possible explanation of why polynomials are a good approximation.** The surface of each face is smooth, so it is reasonable to consider smooth basic functions. Every sufficiently smooth function can be extended in Taylor series: $e_i(x) = e_{i,0}(x) + e_{i,1}(x) + \ldots$, where each $e_{i,k}(x)$ is a linear combination of monomials of order $k$, for which $e_{i,k}(\lambda \cdot x) = \lambda^k \cdot e_{i,k}(x)$ for each $\lambda > 0$.

Giruses vary in size. So, to find a basis that fits the shape of several of them, it is reasonable to select the basis for which the resulting family $F$ of approximating functions $\sum c_i \cdot e_i(x)$ should not change if we re-scale the girus. In precise terms, for each $\lambda$ and for each $i$, the re-scaled function $e_i(\lambda \cdot x)$ should also belong to $F$. If $e_{i,k}(x)$ is the first non-zero term in the Taylor expansion, then the function $\lambda^{-k} \cdot e_i(\lambda \cdot x) = e_{i,k}(x) + \lambda \cdot e_{i,k+1}(x) + \ldots$ should also be in $F$ for every $\lambda$. For $\lambda \to 0$, we conclude that $e_{i,k}(x)$ is in $F$.

Thus, the difference $e_i(x) - e_{i,k}(x)$ is also in $F$. Similar argument shows that the first term in the Taylor expansion of this difference – which is the second non-zero term in the expansion of $e_i(x)$ – should also be in $F$. Similarly, we can prove that each non-zero term $e_{i,j}(x)$ should be in $F$. In $F$ we have only $n$ linearly independent functions. Polynomials of different order are linearly independent, so we can have only a finite number of different non-zero terms $e_{i,j}(x)$. This means that each $e_i(x)$ is a sum of finitely many polynomials – and thus, itself a polynomial. This is exactly what we wanted to explain.

[1] M. Mackay, S.-Y. Yi, A. Duval, and C. Xiao, "Geometric modeling of girus trisymmetron", *Abstracts of the 17th Joint UTEP/NMSU Workshop on Mathematics, Computer Science, and Computational Science*, El Paso, Texas, November 7, 2015.