

Voronoi diagrams (VD) describe spatial relationships among a given set of input sites. The family of VD for a set of points is a well-explored domain and effective algorithms for their construction exist. Although the family of VD for a set of spheres has been known for many years, properties of these diagrams and algorithms for their construction are a relatively new thing. Their importance grows with the development in the area of molecular biology. The goal of this work is to survey the theory behind VD of spheres, implement one of the existing algorithms for their construction as a library and use the library on a real data, such as proteins.