# Chapter 1

# Introduction

## 1.1 Overview

The comparison of geometric shapes is a task which naturally arises in many applications, such as in computer vision, computer aided design, robotics, medical imaging, etc. Usually geometric shapes are represented by a number of simple objects (*sites*) that either describe the boundary of the shape, or the whole shape itself. Sites are often chosen to be linear objects, such as line segments, triangles, or simplices in general, since linear objects are easier to handle in algorithms. But sometimes also patches of algebraic curves or surfaces, such as circular arcs or portions of spheres or cylinders are of interest. In order to compare two shapes we need to have a notion of similarity or dissimilarity, which arises from the desired application. There is a large variety of different similarity measures, see [15, 71] for surveys of distance measures for shapes. Popular similarity notions are, for example, the Hausdorff distance, the area of symmetric difference, or especially for curves the turn-angle distance, or the Fréchet distance. The application usually supplies a distance measure, and furthermore a set of allowed transformations, and the task is to find a transformation that, when applied to the first object, minimizes the distance to the second one. Typical transformation classes are translations, rotations, combinations of translations and rotations (called *rigid motions* or *Euclidean transformations*), combinations of translations and scalings (called *homotheties*), combinations of rigid motions and scalings (called *similarities*), or arbitrary *affine transformations* in general. See [15] for an overview of matching algorithms for various types of shapes, distance measures, and transformation classes.

In the literature most matching algorithms either attack two-dimensional problems, or consider finite point sets in higher dimensions. However, there have been very few results on comparing shapes more complicated than finite point sets in dimensions larger than 2. The only result about higher-dimensional objects in higher-dimensional space of which we are aware is an algorithm for computing the Hausdorff distance between two sets of $k$-dimensional simplices in arbitrary fixed dimension $d$, which was presented in [45, 13]. This is however not a matching algorithm since it computes the distance, but does not allow to search for a transformation optimizing the distance between the two objects.

The contribution of this thesis consists of several algorithms for matching simplicial objects or polygonal curves in two, three, and higher dimensions, under different transformation classes. In Chapter 3 we consider the Hausdorff distance for simplicial objects in arbitrary dimension under translations. Faster variants for special shape classes, such as terrains and convex polyhedra, are considered in Chapter 4. We furthermore investigate a distance measure which is natural to choose for terrains. Whereas Chapter 3 and Chapter 4 are mainly concerned with variants of the Hausdorff distance under translations, we investigate in Chapter 5 and Chapter 6 the Fréchet distance for curves. The Fréchet distance is a natural distance measure for curves, but has not been investigated much in the literature. In Chapter 5 we present the first algorithms to optimize the Fréchet distance under various transformation classes for curves in higher dimensions. In Chapter 6 we consider a partial matching variant with a different flavor: In a given geometric graph we show how to find a polygonal path which resembles another input curve as close as possible in the Fréchet distance.

## 1.2 Credits

There are so many people who have supported me in writing this dissertation in so many different ways. I thank Helmut Alt for introducing me to the subject of geometric shape matching which turned out to be right in the center of my interests. I am not sure if I should thank him for letting me organize the famous noon seminar of the work group, but I thank him for many ideas and discussions, for being very understanding and supporting, for reading this thesis, for his delicious cakes, not for the bell-peppers, but for letting Laura and me share an office. I thank Frank Hoffmann and Lorenz Wernisch for the great seminar on DNA sequence comparison which initiated my interest in the work group. Many thanks go to my co-authors for sharing their knowledge and experience with me, and for many fruitful and interesting discussions: Helmut Alt, Peter Braß, Alon Efrat, Michael Godau, Frank Hoffmann, Christian Knauer, Stephen Kobourov, Klaus Kriegel, Klaus-Peter Pleißner, Günter Rote, Sven Schönherr, Christof Schultz. I thank Peter Braß and Günter Rote for proof-reading preliminary parts of this thesis. I am very grateful to Helmut Alt and Alon Efrat for supporting my career in many different ways. Of course I thank all members of the work group "Theoretical Computer Science" at Freie Universität Berlin for their generous help and support, for many many fruitful discussions, for the toy pets, just for being friends, and of course for the great coffee rounds. Many thanks go to Boris Aronov for devoting the time to read this thesis and for many useful comments. And finally I thank my family and all my friends for their friendship and their support and for having so much good time together.