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Chair: Prof. Dr. Taejun Han

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This bachelor's project was conducted at the

Center for Biosystems and Biotech Data Science

Center for
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Here goes the acknowledgment.

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SUMMARY

Here comes the summary (about 15 to 20 lines, using multiple paragraphs), as shown below. The text of the summary makes use of 1.5 line spacing.

Deoxyribonucleic acid is a molecule that carries the genetic instructions used in the growth, development, functioning and reproduction of all known living organisms and many viruses. DNA and ribonucleic acid (RNA) are nucleic acids; alongside proteins, lipids and complex carbohydrates (polysaccharides), they are one of the four major types of macromolecules that are essential for all known forms of life. Most DNA molecules consist of two biopolymer strands coiled around each other to form a double helix.

The two DNA strands are called polynucleotides since they are composed of simpler monomer units called nucleotides. Each nucleotide is composed of one of four nitrogen-containing nucleobases (cytosine [C], guanine [G], adenine [A] or thymine [T]), a sugar called deoxyribose, and a phosphate group. The nucleotides are joined to one another in a chain by covalent bonds between the sugar of one nucleotide and the phosphate of the next, resulting in an alternating sugar-phosphate backbone. The nitrogenous bases of the two separate polynucleotide strands are bound together, according to base pairing rules (A with T and C with G), with hydrogen bonds to make double-stranded DNA.

Keywords

Here come the comma-separated keywords (3 to 5 capitalized keywords in alphabetical order), as shown below.

DNA, Double Helix, Genetic Information, Macromolecules, Nucleic Acids

ABBREVIATIONS

A	Adenine
C	Cytosine
DNA	Deoxyribonucleic acid
G	Guanine
RNA	Ribonucleic acid
T	Thymine

CONTENTS

1 INTRODUCTION

Here comes some text. This text makes use of 1.5 line spacing. For the references use [1].

For the tables use the format "Table 1" (see the folder "Tables").

Table 1: Leave-one-out cross-validation training errors for the considered mathematical model corresponding to the Bézier and the Lagrande approximations, respectively.

	Bézier approximation	**Lagrange approximation**
Training error	0.8233	0.6977

For the figures use the format "Fig. 1" (see the folder "Figures").

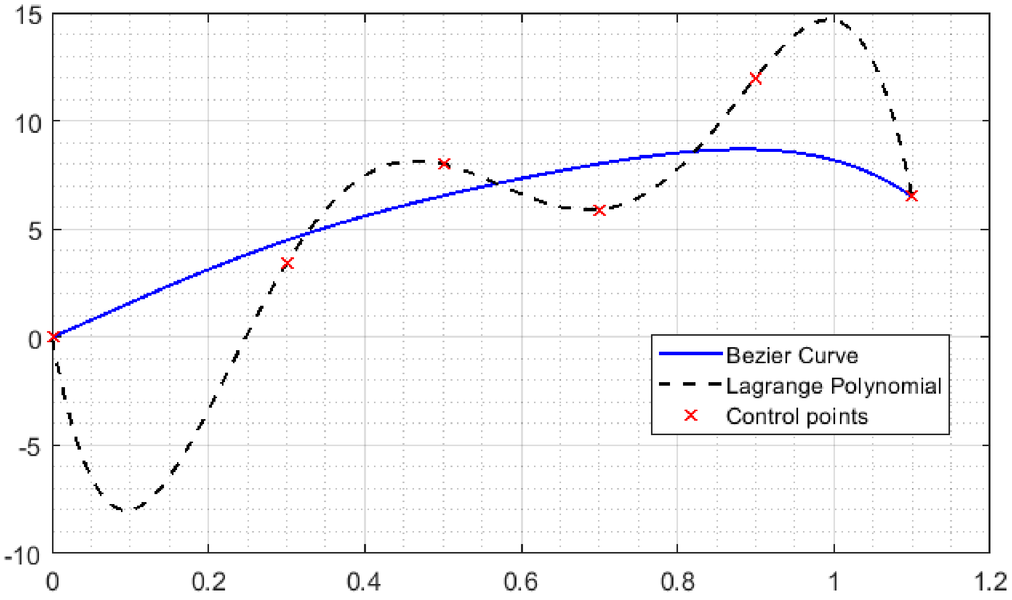

Figure 1: Comparison of the Bézier curve (highlighted in blue) and the Lagrange interpolating polynomial (highlighted in dashed black) defined by the same set of data points (highlighted in red) over the interval [0,1.1].

1.1 CONTEXT

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6 CONCLUSIONS AND FUTURE WORK

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APPENDIX A

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APPENDIX B

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APPENDIX C

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References

[1] Manvel Gasparyan, Arnout Van Messem, and Shodhan Rao. An automated model reduction method for biochemical reaction networks. *Symmetry*, 12(8):1321, 2020.