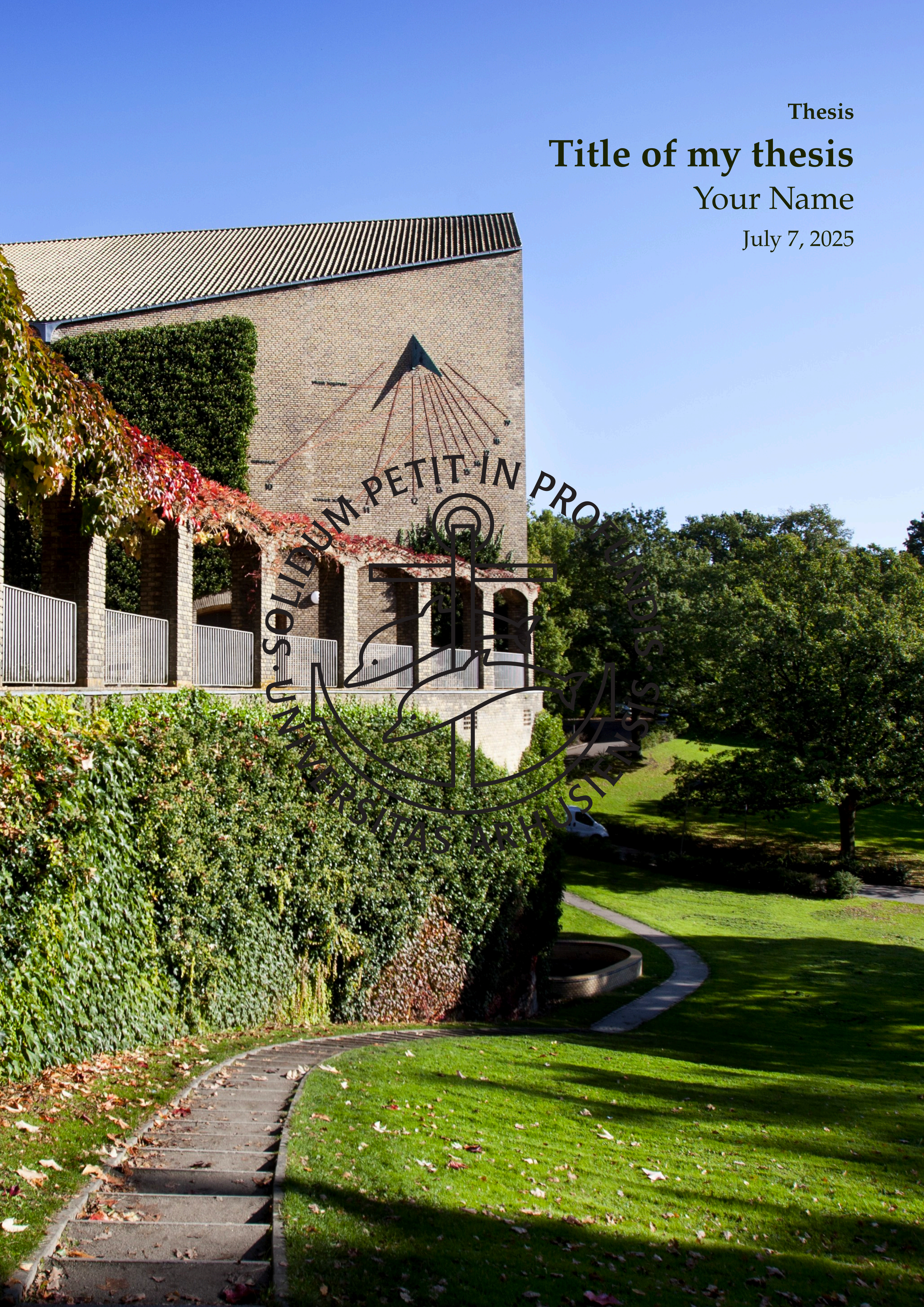

Thesis

Title of my thesis

Your Name

July 7, 2025

SOLIDUM PETIT IN PROFUNDIS · UNIVERSITAS ARHUSIENSIS

Title of my thesis

Some subtitle for my thesis

Your Name
Aarhus University

Master of Science in Bioinformatics

July 7, 2025

Submitted in fulfillment of the requirements of the degree of Master of Science in Bioinformatics

> “In plain language, the thesis describes an analysis of something. Somethings was not previously know. I found something and was able to conclude something. The perspectives of this result is something.
>
> - Your Name”

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1 Introduction

Chromatin architecture is of high interest in molecular biology, and increasingly so in molecular evolution. A high-throughput method for mapping the 3D organization of the genome was proposed by Lieberman-Aiden et al. (2009). Here, chromatin interactions from Hi-C sequencing is used to generate an interaction matrix of valid Hi-C contacts, and PCA is performed on the covariance matrix of the observed and expected matrix. The following rationale is proposed and experimentally supported; if clustering into 2 types (A/B compartments), genomic positions that interact will have a positive value in the covariance matrix, and vice versa for positions that do not interact. Then, when PCA is performed, the first principal component captures the variance that arise from being in different compart by its sign. The direction of the eigenvector (the sign) is then phased with a biologically relevant measure (such as GC content) to establish that the A compartment is largely the *active* chromatin and B is largely *inactive*.

2 Methods

Here are methods

2.1 Method 1

The first method with a code block

```
# Python code
e = mc**2

print(e)
```

3 Results

Results are written here

4 Discussion

The discussion

5 Conclusion

I am concluding this analysis

6 Bon mot

> “Nothing in Biology Makes Sense except in the Light of Evolution
> - Theodosius Dobzhansky”

7 References

Lieberman-Aiden, Erez, Nynke L. Van Berkum, Louise Williams, Maxim Imakaev, Tobias Ragoczy, Agnes Telling, Ido Amit, et al. 2009. "Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome." *Science* 326 (5950): 289–93. https://doi.org/10.1126/science.1181369.

Bioinformatics Research Centre
Department of Molecular Biology and Genetics
Aarhus University
Universitetsbyen 81
8000 Aarhus C
Denmark