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Introduction

To provide a comprehensive background for the following chapters that focus on the interaction of human mesenchymal stromal cells (hMSCs) with multiple myeloma (MM) cells, this

Aims

This project defines these aims:

- Characterize the interaction between myeloma cells and mesenchymal stromal cells
- Develop methods
- Face the challenge of time-dependent cell adhesion through
- Provide tools to analyze multidimensional cell adhesion data

Summarising Discussion

Time Lapse

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Myeloma

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Semi-Automated Analysis Improves Agility During Establishing new *in vitro* Methods

Was plotastic useful for me? - Yes incredibly. I was able to perform the statistical tests and visualize the data in a fraction of the time that I would have needed manually. This allowed me to focus on the interpretation of the results and the writing of the manuscript. There was one particular example where my analysis was so fast, that I fed raw datatables during microscopy into python scripts and was able to adapt the experimental technique during the experiment. This allows for an agile and adaptive work environment that is not possible with manual analysis and proved invaluable during development of *in vitro* methods. - These experiments benefited from the use of plotastic, as the

Further research is needed to assess the true impact of semi-automated analysis on the agility of establishing new *in vitro* methods.

Plotastic and Jupyter Notebooks as a Standard for Research Documentation

How Biosciences can Benefit from Standards of Software Development

chapter 2 has laid down the benefits of using plotastic in combination with jupyter notebooks

It is important to note that GitHub are not reserved for software development. Bioscientists are encouraged to use these tools as well which are available with free, robust well-designed and intuitive graphical user interfaces developed by the distinguished experts of the open source community. Its robustness is unparalleled and have withstood the test of time.

It is a database that documents every minor change thoroughly, noting every little change in text, providing unmatched flexibility but also replicability. Researchers can

GitHub encourages the use by Scientists.

In conclusion, as bioscience continues to generate increasingly complex datasets, the distinction between biologists and bioinformaticians blurs, emphasizing the need for all researchers to adopt computational tools. The development of new software to handle semi-big data effectively is not just an enhancement but a necessity to ensure the future reliability and efficiency of scientific research. This thesis proposes a framework for understanding and addressing the semi-big data challenges, setting the stage for a discussion on innovative solutions like the software tools described in subsequent chapters.

In conclusion, the integration of coding in bioscience research is not just a trend but a necessity. As the field continues to evolve, the demarcation between biologists and computational scientists blurs, underscoring the importance of coding skills for the next generation of researchers. The ability to code is fast becoming an indispensable asset, as integral to bioscience as traditional laboratory skills.

The reproducibility of qPCR has been a long-standing issue in the field⁵.

⁵Bustin (2014): “ *By 2009 it was pretty obvious that many publications using PCR based methods were seriously flawed* ”

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Appendices

A Supplementary Data & Methods

A.1 Figures

A.2 Tables

A.3 Materials & Methods

B Documentation of `plotastic`