Report

D6.7 Final project meeting with the SAB

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Executive Summary

The final OLISSIPO Meeting was held on 16 and 17 June 2024 to get together all project members from the four Twinning partners and Scientific Advisory Board members. The meeting was beneficial for reflecting on the activities carried out during these three and a half years and discussing relevant topics such as the closure of the project and actions to continue with the project objectives after its completion.

Table of Contents

1. Introduction

The OLISSIPO Final Annual Meeting was held at ETH Zurich, D-BSSE in Basel, on June 16 and 17, 2024. This deliverable shows the minutes of the OLISSIPO Final Meeting.

2. Minutes

2.1. Agenda - OLISSIPO Final Meeting

June 16, 2024

18:30 Welcome dinner at Restaurant Fischerstube

June 17, 2024

9:00 Welcome, Intro - Prof. Susana Vinga

9:30 ESR talks:

- Rita Baião, INESC-ID - *Statistical Learning for Multi-Omics Integration in Precision Cancer Medicine*
- Kevin Rupp, ETHZ - *Modeling metastatic progression from cross sectional data*

— 10:30 Coffee break —

11:00 ESR talks

- Anastasiia Horlova, EMBL - *Towards Understanding Stem Cell Proliferation in Intestinal Processes using Single-Cell in vivo CRISPR Perturbation Data*
- Lara Fuhrmann, ETHZ - *VILOCA: Sequencing quality aware haplotype reconstruction and mutation calling for short and long read data*
- Matthias Meyer-Bender, EMBL - *Analysis of highly multiplexed fluorescence images in the context of B-cell Non-Hodgkin lymphomas*

— 12:30 - 14:00 Lunch —

14:00 - 14:30 OLISSIPO main achievements

14:30 - 15:30 Future steps and discussion

— 15:30 - 16:00 Coffee break —

16:00 - 18:00 Dual seminars by the SAB members

A new parameter-free framework for sequence comparison

Pavel A. Pevzner, University of California San Diego

Uncovering how mRNA transcription and degradation shape embryonic development

Magnus Rattray, University of Manchester

18:00 - 18:50 Apero

19:30 - Dinner at Restaurant Rhywyera

Abstracts

A new parameter-free framework for sequence comparison

The recent advances in "complete genomics" revealed many previously inaccessible genomic regions and enabled analysis of their associations with diseases. However, analysis of variations in centromeres, immunoglobulin loci, and other biomedically important highly-repetitive regions (HRRs) faces an algorithmic challenge since there are currently no tools for aligning HRRs. Counterintuitively, the previously developed alignment approaches, such as the Smith-Waterman algorithm or minimap2, fail to construct biologically adequate alignments of HRRs. We present UniAligner, a fast parameter-free sequence alignment algorithm that prioritizes matches of rare substrings shared by two sequences. We applied UniAligner to human centromeres and primate immunoglobulin loci and quantified the extremely high rate of tandem duplications and deletions in centromeres, thus demonstrating that centromeres represent the most rapidly evolving regions of the human genome.

Uncovering how mRNA transcription and degradation shape embryonic development

We are using probabilistic time-series models to gain insights into transcription dynamics in the early drosophila embryo. We consider the very earliest stage of development, where maternal transcripts are progressively replaced by zygotic gene expression. We have used a combination of whole embryo RNA-Seq, live cell imaging and fixed single molecule imaging experiments to gain insights into the mechanisms regulating RNA levels in the cell. Using a total RNA-Seq time course that captures intronic and exonic reads, we can model the production and degradation of RNA by combining a differential equation model of degradation with a Gaussian process model of transcription. We infer half-lives for a large set of zygotic genes and show how degradation rate regulates the difference in timing of peak levels of nascent and mature transcripts. Short half-life mRNAs are more likely to be associated with P-bodies and we find evidence of 5' to 3' degradation occurring in P-bodies for a subset of mRNAs. We then consider whether mRNA degradation is regulated spatially in the case of stripe patterns formed by the pair-rule gene eve. By combining data from live-cell imaging of transcription with fixed imaging of mature transcripts, modelling suggests that mRNA degradation is increased outside of stripe regions, leading to sharper stripes. We find increased co-localisation of P-bodies with eve mRNA in spatial regions with higher inferred degradation, suggesting spatial regulation of mRNA degradation is also associated with P-bodies.

2.2. Participants List

The people who attend the meeting in the representation of each institution are shown in the following list:

Name	Entity
Anastasiia Horlova	EMBL
Harald Vohringer	EMBL
Matthias Meyer-Bender	EMBL
Petr Smirnov	EMBL
Anika John	ETHZ
Auguste Rimaite	ETHZ
Daniel Fridljand	ETHZ
Jack Kuipers	ETHZ
Johannes Gawron	ETHZ
Kevin Rupp	ETHZ
Lara Fuhrmann	ETHZ
Norio Zimmermann	ETHZ
Pawel Czyz	ETHZ
Rudolf Shill	ETHZ
Alexandre Francisco	INESC-ID/IST
Ana Rita Baião	INESC-ID/IST
Cátia Vaz	INESC-ID
Emanuel Gonçalves	INESC-ID/IST
Marschit Prajapati	FU Berlin
Marie-France Sargot	INRIA (online)
Niko Beerenwinkel	ETHZ
Susana Vinga	INESC-ID/IST
Magnus Rattray	University of Manchester
Pavel Pevzner	UCSD

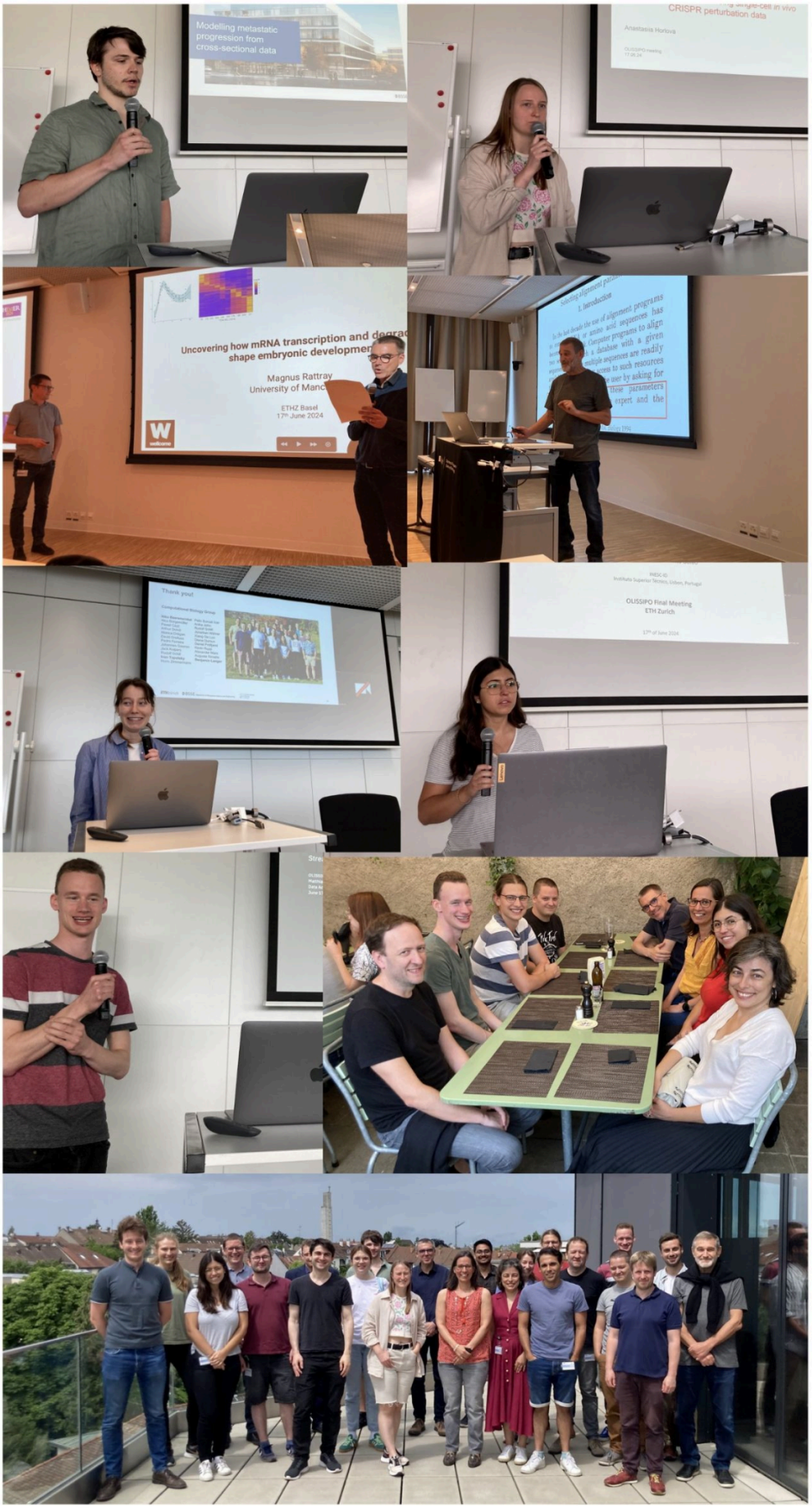

Figure 1. Photos in the OLISSIPO Final meeting.

2.3. Discussion Points

Topic	Responsible	Status
WP1. Scientific internships and staff exchanges	All	Completed. D1.3 to be submitted until the end of June 2024.
WP2. Organization of Schools and Training Workshops	All	Completed. Possibility of continuing online events among the Consortium, for example Twin Seminars and Thematic Workshops. Possibility of bidding for future international conferences (ECCB'2028 in Lisbon). D2.4 to be submitted until the end of June 2024.
WP3. Outreach activities: gathering other projects and institutions and relevant stakeholders	All	Final dissemination activities will be updated on the webpage.
WP4. Training activities for Early Stage Researchers (ESR)	All	Completed. Possibility of continuing online events among the Consortium, for example Twin Seminars and Thematic Workshops on cophylogeny. D4.3 to be submitted until the end of June 2024.
WP5. Management training of INESC-ID staff and PI	All	Completed.
WP6. Financial reporting (QMRs)	INESC-ID	Update on the Deliverables and Final Report deadlines.

Overall, there was an update of the final activities and an overview of the project OLISSIPO's major results and achievements.