

# JOHAN HALLIN

## EDUCATION

Bachelor of Science  
Biology  
University of Gothenburg  
2010 - 2013

Master of Science  
Molecular biology  
University of Gothenburg  
2013 - 2014

PhD  
Université Côte d'Azur  
2014 - 2018

## EXPERIENCE

For my Bachelor's and Master's thesis I was working in the lab of Jonas Warringer. During my Bachelor I was in charge of a large experimental evolution project which was later taken over by a PhD student. My Master's was also focused on experimental evolution, looking into the different evolutionary trajectories of clonal colonies and colonies with standing genetic variation. During my time in Gothenburg I supervised master students and the occasional postdoc and also helped set up the novel phenotyping methodology Scan-o-matic<sup>3</sup>.

After my Master's I was granted an Erasmus Placement Program scholarship to go to Gianni Liti's lab at the institute for research on cancer and aging, Nice (IRCAN). During this period I enhanced my molecular biology skills and was key in finalizing a project in the lab by constructing a large phenotyping experiment<sup>5</sup>.

I enrolled in the competitive LabEx Signallife PhD program and joined Dr. Liti's team as a PhD student. It resulted in two successful papers stemming from a large scale experiment I performed<sup>1,2</sup>. The two papers were highly collaborative with close collaborations between labs in France, Sweden and the U.K. During this period I further advanced my programming and analytical skills by handling large amounts of data and by spending two weeks as a visiting researcher in Leopold Parts lab at the Sanger Institute. I am continuing my work with Gianni by working with big NGS datasets to elucidate the nature of meiotic recombination.

I recently started my first post doc position with Christian Landry. Here I hope to further improve my molecular biology and bioinformatics skills while studying the exciting phenomenon of de novo gene emergence

## PAPERS

- ① K. Märtens\*, J. Hallin\*, *et al.* Predicting quantitative traits from genome and phenome with near perfect accuracy. *Nature Communications*, 2016
- ② J. Hallin\*, K. Märtens\*, *et al.* Powerful decomposition of complex traits in a diploid model. *Nature Communications*, 2016
- ③ M. Zackrisson, J. Hallin, *et al.* Scan-o-matic: High-resolution microbial phenomics at a massive scale. *G3*, 2016
- ④ J. Yue, [..2..], J. Hallin, *et al.* Contrasting evolutionary genome dynamics between domesticated and wild yeasts. *Nature Genetics*, 2017
- ⑤ I. Vazques-Garcia, [..4..], J. Hallin, *et al.* Background-dependent effects of selection in subclonal heterogeneity. *Cell Reports*, 2017

## AWARDS & SCHOLARSHIPS


- |      |  |
|------|--|
| 2017 | Poster Prize<br>28 <sup>th</sup> ICYGMB                            |
| 2016 | Oral Presentation Prize<br>Signalife Student Conference            |
| 2016 | Visiting researcher Sanger Institute, U.K.<br>Doctoral school ED85 |
| 2014 | Erasmus Placement Program  |
| 2013 | Educational Stipend<br>University of Gothenburg                    |

## REFeree


Nature Ecology and Evolution  
Yeast

I am a dedicated scientist with an eye for details. I have managed large projects with close collaborators and have positioned myself at the intersection of computational and molecular biology

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 scholar.google.com/citations?user=rtnFHLUAAAAJ&hl

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## Skills

R programming



Unix bash



Python



Yeast genetics



Writing



Presenting



Supervising



Design



English



Swedish



Spanish

