CV

Johan Hallin

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

contact

johan.h.hallin@gmail.com

j-hallin.github.io

+33 6 84 91 74 19

12 rue Paul Reboux
06300 Nice, France

Skills

- R programming
- Unix bash
- Python
- HTML / CSS
- Writing
- Presenting
- Supervising
- Design
- English
- Swedish
- Spanish

Education

Bachelor of Science
Biology
University of Gothenburg
2010 - 2013

Master or Science
Molecular biology
University of Gothenburg
2013 - 2014

PhD
University of Nice, Sophia Antipolis
2014 - 2018

Experience

For my Bachelor's and Master's thesis I was working with Jonas Warringer. I was in charge of a large experimental evolution project for my Bachelor's thesis which was taken over by a PhD student as I started my Master's thesis. This thesis was also 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.
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 initiated by a postdoc in the lab by constructing a large phenotyping experiment.
I enrolled in the competitive LabEx Signalife PhD program and joined Dr. Liti's team as a PhD student. It resulted in two successfull papers stemming from a large scale experiment I performed. 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, handling large amounts of data. My next step is to improve my practical genomics skills by working with big NGS datasets to elucidate the nature of meiotic recombination.

Papers

K. Martens, **J. Hallin**, *et al*. Predicting quantitative traits from genome and phenome with near perfect accuracy. *Nature Communications*, 2016

J. Hallin, K. Martens, *et al*. Powerful decomposition of complex traits in a diploid model. *Nature Communications*, 2016

M. Zackrisson, **J. Hallin**, *et al*. Scan-o-matic: High-resolution microbial phenomics at a massive scale. *G3*, 2016

J. Yue, [...], **J. Hallin**, *et al*. Contrasting genome dynamics between domesticated and wild yeasts. *bioRxiv*, 2016

I. Vazques-Garcia, Francisco Salinas, [...], **J. Hallin**, *et al.* Background-dependent effects of selection in subclonal heterogeneity. *bioRxiv*, 2016

Awards & Scholarships

2016 Oral Presentation Prize
Signalife Student Conference

2016 Visiting researcher Sanger institute, U.K.
Doctoral school ED85

2014 Erasmus Placement program

2013 Educational Stipend
University of Gothenburg

Referee

Nature Ecology and Evolution