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
Université de Côte, d'Azur
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 evolutionary genome dynamics between domesticated and wild yeasts. *Nature Genetics*, 2017

I. Vazques-Garcia, […], **J. Hallin**, *et al.* Background-dependent effects of selection in subclonal heterogeneity. Cell Reports, 2017

AWARDS & SCHOLARSHIPS 🏅

2017	Poster Prize *28th ICYGMB*
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

Yeast