

Jesper L.V. Maag

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SUMMARY

I am a highly motivated and productive bioinformatician experienced in next generation sequencing analysis. Through my Ph.D. and postdoc, I have developed data analysis pipelines, conducted data and statistical analysis of complex genomic datasets, visualized and successfully communicated the results in multiple peer-reviewed publications and presentations at both national and international conferences. I have effectively and successfully led, managed, and worked in collaborative, multi-national, research teams. I am highly adaptable, a quick learner, and a self-taught coder — all of which has made me successful in analysing the complexity of the genome.

EDUCATION

2017 Ph.D. Candidate in Medicine (Computational biology), Garvan Institute of Medical Research, UNSW, Sydney, Australia.

My doctoral research utilised computational means to discover and implicate the function of previously overlooked genomic elements e.g. noncoding RNAs and repeat elements, in cancer and memory formation.

2012 M.S., Pharmaceutical Science, Uppsala University, Uppsala, Sweden.

Focusing on Alzheimer's Disease, I learned the investigatory skills required to conduct molecular biology research.

2010 Exchange studies, Flinders University, Adelaide, Australia.

EXPERIENCE

2018-Present Senior Computational Biologist. Center for Epigenetics Research. Memorial Sloan Kettering Cancer Center, New York, USA.

2016-2018 Postdoctoral Fellow, Genomics/Bioinformatics, Institute for Systems Genetics, New York University, New York, USA.

2016 Supervisor of second-year intern (Computer Science; Pre-Health track, New York University), Genomics, Garvan Institute of Medical Research.

2012-2013 Research Intern, Genomics/Bioinformatics, Garvan Institute of Medical Research, Sydney, Australia.

2009 Supervisor of third-year Laboratory class, Pharmacognosy, Uppsala University, Uppsala, Sweden.

2006 Group leader in the Swedish Army (compulsory military service)

COMPUTER SKILLS

- R
- Bash
- Unix
- ggplot2
- Github
- HPC
- Bioconductor
- Python
- Machine Learning

GENOMIC SKILLS

- RNA-seq
- Methylation
- ChIP-seq
- Noncoding RNA
- DHS
- Enhancers
- Cancer genomics
- DNase/ATAC Seq
- Whole-genome Seq

- GENERAL SKILLS**
- Analysis of large complex datasets
 - Pipeline creation
 - Broad scientific communication
 - Cross-functional teamwork
 - Independent research
 - Statistics
 - Visualisations
 - Problem solving
- CERTIFIED COURSEWORK**
- 2018** Bayesian Statistics: Techniques and Models by University of California, Santa Cruz on Coursera.
- 2018** Bayesian Statistics: From Concept to Data Analysis by University of California, Santa Cruz on Coursera.
- 2017** Machine Learning by Stanford University on Coursera.
- 2017** The Business of Science for Scientists, New York University.
- 2017** Science Diplomacy, New York University.
- LANGUAGES**
- English:** Fluent
- Swedish:** Native
- HONORS AND AWARDS**
- 2015** Second Poster Prize, COMBINE Symposium.
- 2013** Student Poster Presentation Prize, Australasian Microarray Associated Technologies Association Conference.
- 2013** First Prize, The Art of Personal Genomics' design in the Science as Art competition, Garvan Institute of Medical Research, Sydney, Australia.
- GRANTS**
- 2016** The Postgraduate Research Student Support (PRSS) grant from UNSW to travel to Keystone ncRNA in health & disease in USA.
- 2014** European Molecular Biology Laboratory (EMBL) Australia PhD Student Travel Grant to attend the 16th EMBL PhD symposium in Heidelberg, Germany.
- 2014** Okinawa Institute of Science and Technology (OIST) Travel Grant to participate in OIST workshop in high-throughput sequencing data analysis in Okinawa, Japan.
- 2014** Travel grant to present at the Australian High Content Screening and RNAi meeting.
- 2014** Travel grant to enrol in the 2014 Winter School in Mathematical & Computational Biology in Brisbane, Australia.
- 2013** Tuition and fee scholarship from the University of New South Wales (UNSW), including living entitlements.
- 2011** Leffmans, CR Travel Stipend from Uppsala University, Sweden to conduct master's research in Scott Smid's lab at University of Adelaide, Australia.

PUBLICATIONS Published

Suan D, Krutler S, **Maag JLV**, Butt D, Bourne K, Hermes JR, Avery DT, Young C, Statham A, Elliott M, Dinger ME, Basten A, Tangye SG, Brink R (2017). CCR6 Defines Memory B Cell Precursors in Mouse and Human Germinal Centers, Revealing Light-Zone Location and Predominant Low Antigen Affinity. *Immunity*, 47:1142.

Bartonicek N[†], Clark MB[†], Quek XC, Torpy J, Pritchard A, **Maag JLV**, Gloss BS, Crawford J, Taft RJ, Hayward N, Montgomery G, Mattick J.S, Mercer TR, Dinger ME (2017). Intergenic Disease-associated Regions are Abundant in Novel Regulatory Transcripts. *Genome Biology*, 18: 241.

Maag JLV[†] and Fisher OM[†], Levert-Mignon A, Kaczorowski DC, Thomas ML,

[†]Shared first author

Hussey DJ, Watson DI, Wettstein A, Bobryshev YV, Edwards M, Dinger ME and Lord RV (2017). Novel Aberrations Uncovered in Barrett's Esophagus and Esophageal Adenocarcinoma Using Whole Transcriptome Sequencing. *Molecular Cancer Research*, Epub.

Maag JLV, Kaczorowski DC, Panja D, Peters T, Bramham CR, Wibrand K. and Dinger, M.E (2017). Widespread promoter methylation of synaptic plasticity genes in long-term potentiation in the adult brain in vivo. *BMC Genomics*, 18:250.

Maag JLV, Panja D, Sporild I, Patil S, Kaczorowski DC, Bramham CR, Dinger ME, Wibrand K (2015). Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. *Front Neurosci*, 9:351.

Bartonicek N[†] and **Maag JLV**[†], Dinger ME (2016). Long noncoding RNAs in cancer: mechanisms of action and technological advancements. *Molecular Cancer*, 15:43.

Everaert C, Luypaert M, **Maag JLV**, Quek XC, Dinger ME, Hellemans J, Mestdagh P (2017). Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. *Scientific Reports*, 7:1559.

Barry G, Briggs JA, Hwang DW, Nayler SP, Fortuna PRJ, Jonkhout N, Dacht F, **Maag JLV**, Mestdagh P, Singh EM, Avesson L, Kaczorowski DC, Ozturk E, Jones NC, Vetter I, Arriola-Martinez L, Hu J, Franco GR, Warn VM, Gon, A, Dinger ME, Rigo F, Lipovich L, Morris MJ, OBrien TJ, Lee DS, Loeb JA, Blackshaw S, Mattick JS and Wolvetang EJ (2017). The long non-coding RNA NEAT1 modulates neuronal excitability. *Scientific Reports*, 7:40127.

Quek XC, Thomson DW, **Maag JLV**, Bartonicek N, Signal B, Clark MB, Gloss BS, Dinger ME (2015) lncRNADB v2.0: expanding the reference database for functional long noncoding RNAs. *Nucleic Acids Res*, 43:D168-173.

Janefjord E, **Maag JLV**, Harvey BS, Smid SD (2014). Cannabinoid effects on beta amyloid fibril and aggregate formation, neuronal and microglial-activated neurotoxicity in vitro. *Cell Mol Neurobiol*, 34:31-42.

Smid SD, **Maag JLV**, Musgrave IF (2012). Dietary polyphenol-derived protection against neurotoxic beta-amyloid protein: from molecular to clinical. *Food Funct*, 3:1242-1250.

Harvey BS, Ohlsson KS, **Maag JLV**, Musgrave IF, Smid SD (2012). Contrasting protective effects of cannabinoids against oxidative stress and amyloid-beta evoked neurotoxicity in vitro. *Neurotoxicology*, 33:138-146.

PRESENTATIONS

Conferences

2015 Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. Australian Genomics Technologies Association (AGTA) Conference.

2014 High throughput functional screening of long noncoding RNAs in Breast cancer. Australian High Content Screening and RNAi meeting.

2013 Candidate selection of differentially expressed long noncoding RNAs in a diversity of breast cancer cell lines for high throughput functional screening. Australian

High Content Screening and RNAi meeting.

Invited Presentations

2016 Transcriptomic investigation of esophageal adenocarcinoma development. Center for RNA system biology seminar hosted by Dr Mitchell O'Connell. University of California Berkeley.

2016 Transcriptomic investigation of esophageal adenocarcinoma development. Cancer Bioinformatics seminar hosted by Dr Marcin Imielinski. New York Genome Center.

2016 Transcriptomic investigation of esophageal adenocarcinoma development. Hosted by Dr Olivier Elemento. Institute for Computational Biomedicine, Weill Cornell Medical School.

2016 Transcriptomic investigation of noncoding elements in memory formation and cancer development. Hosted by Dr John Rinn. Department of Stem Cell and Regenerative Biology, Harvard University.

Posters

2016 Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. Keystone ncRNA in health & disease. Santa Fe, USA.

2016 Novel aberrations in Barrett's esophagus and esophageal adenocarcinoma identified through whole transcriptome sequencing. Keystone Cancer Genome. Banff, Canada.

2015 Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. The Australian Bioinformatics and Computational Biology Society (ABACBS) Conference.

2015 Dynamic expression of long noncoding RNAs and repeat elements in synaptic plasticity. COMBINE Symposium.

2014 High throughput functional screening of long noncoding RNAs in Breast cancer. 16th EMBL PhD Symposium in Heidelberg.

2014 High throughput functional screening of long noncoding RNAs in Breast cancer. High-throughput Sequencing Data Analysis workshop. Okinawa Institute of Science and Technology.

2014 High throughput functional screening of long noncoding RNAs in Breast cancer. Australian Society for Medical Research (ASMR) NSW Meeting. Melbourne, Australia.

2014 High throughput functional screening in differentially expressed long noncoding RNAs in breast cancer. Lorne Genome Conference. Lorne, Australia.

2013 Long noncoding RNAs in formation of memory through long-term potentiation. Australasian Microarray Associated Technologies Association (AMATA) Conference. Surfer's Paradise, Australia.