

Dr. Asis Hallab

Curriculum Vitae

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Summary

Science	14 years experience in Bioinformatics : developing and programming new methods, with application in genome projects, comparative genomics, and agricultural sciences. Design of software tools for the management and processing of big data in the life sciences.
Business Enterprises	24 years experience in agile software development and project management of web-based tailored software solutions.
Management responsibility	Head of software development and scientific management of distributed and international teams developing programs for data science and carrying out bioinformatics research in English, Spanish, and German. Director of the “applied bioinformatics” study-program at the university for applied sciences in Bingen.
Education	PhD in Bioinformatics , Diploma in Biology, with background in zoology, botany, ecology, population genetics, (theoretical) informatics, mathematics, statistics, and agricultural science.

IT-Skills

Programming languages	R, Javascript and Node.js, Rust, Java, Python, Ruby, Shell-Script, C/C++, Fortran, Perl, PHP, objective C, Matlab / Scilab, Julia, and PL/SQL.
Frameworks	GraphQL, React.js, Vue.js, Express, Bioconductor, BioJava, BioRuby, BioPerl, Ruby-OnRails, jQuery, Spring, JEE-Stack (Hibernate ORM, JBoss AS, JBoss Seam, JSTL, Apache Struts, Apache Tomcat, JSP, JSF).
Versioning systems	git, Subversion, CVS
Databases	Postgresql, MySQL, SqlLite, Oracle, ANSI SQL 2000, Redis, Cassandra, Mongo-DB, Neo4J, HBase, Apache Hive, Presto, Amazon's Simple Storage Service (S3), and Couch-DB.
Operating Systems	Linux, Mac OS X, Windows (Server and Workstation). Containerization with Docker, Kubernetes, and Pachyderm.

Professional Experience

- 2022 – now **Professor for Applied Bioinformatics**, *University of applied sciences Bingen*, Fachbereich 2
Director of the “applied bioinformatics” study-program. Teaching of applied bioinformatics to bachelor and master students. This involves courses on elementary algorithms, data structures, genome and transcriptome sequencing, genome assembly, quantification, transcriptomics, system’s biology, data analysis and visualization, data management, the scientific method, and basic biology.
- 2016 – now **Senior Postdoctoral Fellow**, *Forschungszentrum Jülich*, Institute for Bio- and Geosciences Plant Sciences (IBG-4), Prof. Björn Usadel
Comparative genomics of Solanaceae and wild maize relatives, development and evaluation of protein function prediction tools, transcriptome analyses, administration and management of big data in life sciences. Software development project leader (Node.js and React, big data storages). Coordinator of several joint international research projects, including partners from industry and publicly funded institutes. Supervision of doctoral students, postdoctoral fellows, remote supervision of an international distributed team of software developers.
- 2013 – 2016 **Postdoctoral Fellow**, *Max Planck Institute for Plant Breeding Research*, department of Comparative Development and Genetics, Prof. Miltos Tsiantis
Sequencing and comparative genomics of the genome of *Cardamine hirsuta*. Development of new gene family analysis methods, implemented in R/C++, and aimed at the detection of species specific evolutionary trends.
- 2009 – 2015 **Doctoral Student**, *University of Bonn and Max Planck Institute for Plant Breeding Research*, group Plant Computational Biology, Prof. Heiko Schoof
Development of new machine learned methods to predict protein function. The programs, written in Java and R, were applied in the genome projects of Tomato, barrelclover, watermelon, wheat, and rye among others:
github.com/groupschoof/AHRD#7-references,
github.com/groupschoof/AHRD_on_gene_clusters
- 2003 – 2013 **Software Architect and Project Manager**, *InterTech / Fischer Hard- & Software*, Managing owner Frank Fischer
Development and project management of tailored software solutions for medium sized companies. Following the technological evolution most frequently applied languages and Frameworks were Ruby, RubyOnRails, Javascript, JQuery, Java, JSP, JSF, Struts, PHP, and relational and document-based databases.
- 1999 – 2001 **Software Developer**, *Oneview — a daughter of Denkwerk*
Development and architecture of the social bookmark service Oneview in Java (WebObjects), objective C, PHP, and PL/SQL.
- 1996 – 1999 **Disabled Person Nurse**, *German Red Cross*
Part time individual care of severely disabled people.

Education

- 2009–2015 **Doctoral Studies**, *University of Bonn and Max Planck Institute for Plant Breeding Research*, group Crop Bioinformatics, Prof. Heiko Schoof
1 Semester introduction to statistics for mathematicians.
Final degree: 1.1 “magna cum laude”.
- 2014 **Population Genetics**, *University of Lausanne*, Swiss Institute in Statistical Genetics, Prof. Jerome Goudet and Prof. Bruce Weir
Population Genetic Data Analysis.
- 2008 **Diploma Studies**, *University of Cologne*, Botanical Institute, Prof. Michael Melkonian
Diploma thesis about the phylogeny of Cyanobacteria (algae) collected during my ecological research in the Mexican rain forests. Work involved isolation and characterization of strains, Sanger sequencing, assembly, and phylogenetic analysis.
- 2002 – 2007 **Study of Biology**, *University of Cologne*
Major subjects: Botany, Zoology, and theoretical informatics.
Final degree: 1.0 “sehr gut”.
- 2005 – 2006 **German Academic Exchange Service Fellowship**, *Universidad Nacional y Autonoma de México*, Department of Ecology, Prof. Juan Nuñez
Ecology and population genetics within a conservational project investigating human influences on the Mexican rainforest. Theory, field work, and wet lab.
Final degree: 9.5.
- 2001 – 2002 **Travels through Southeast Asia, Oceania, the Caribbean, Mexico, and Central America**
Studies of foreign languages: English and Spanish.
- 1996 – 1999 **Basic studies of informatics and mathematics**, *University of Bonn*
Courses in mathematics, informatics, statistics, and agricultural sciences.
- 1986 – 1995 **High School**, *Dreikönigsgymnasium Köln*
Final degree (“Abitur”): 1.5.

Languages

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| German | Mother tongue |
| English | Professional level |
| Spanish | Professional level |
| French | Basic skills |
| Latin | Proficiency certificate (“Großes Latinum”) |

Publications

- [1] Murukarthick Jayakodi, Agnieszka A. Golicz, Jonathan Kreplak, Lavinia I. Fechete, Deepti Angra, Petr Bednář, Elesandro Bornhofen, Hailin Zhang, Raphaël Boussageon, Sukhjiwan Kaur, Kwok Cheung, Jana Čížková, Heidrun Gundlach, Hallab, Asis, Baptiste Imbert, Gabriel Keeble-Gagnère, Andrea Koblížková, Lucie Kobrlová, Petra Krejčí, Troels W. Mouritzen, Pavel Neumann, Marcin Nadzieja, Linda Kærgaard Nielsen, Petr Novák, Jihad Orabi, Sudharsan Padmarasu, Tom Robertson-Shersby-Harvie, Laura Ávila Robledillo, Andrea Schiemann, Jaakko Tanskanen, Petri Törönen, Ahmed O. Warsame, Alexander H. J. Wittenberg, Axel Himmelbach, Grégoire Aubert, Pierre-Emmanuel Courty, Jaroslav Doležel, Liisa U. Holm, Luc L. Janss, Hamid Khazaei, Jiří Macas, Martin Mascher, Petr Smýkal, Rod J. Snowdon, Nils Stein, Frederick L. Stoddard, Jens Stougaard, Nadim Tayeh, Ana M. Torres, Björn Usadel, Ingo Schubert, Donal Martin O'Sullivan, Alan H. Schulman, and Stig Uggerhøj Andersen. "The giant diploid faba genome unlocks variation in a global protein crop". In: **Nature** 615.7953 (2023), pp. 652–659. DOI: 10.1038/s41586-023-05791-5.
- [2] Constantin Eiteneuer, David Velasco, Joseph Atemia, Dan Wang, Rainer Schwacke, Vanessa Wahl, Andrea Schrader, Julia J. Reimer, Sven Fahrner, Roland Pieruschka, Ulrich Schurr, Björn Usadel, and Hallab, Asis. "GXP: Analyze and Plot Plant Omics Data in Web Browsers". In: **Plants** 11.6 (2022), p. 745. DOI: 10.3390/plants11060745.
- [3] Mohsen Hajheidari, Nina Gerlach, Kristof Dorau, M Amin Omidbakhshfard, Lina Pesch, Jörg Hofmann, Hallab, Asis, Gabriel Y Ponce-Soto, Anastasiya Kuhalskaya, David B Medeiros, Amélia Bourceret, the RECONSTRUCT Consortium, Björn Usadel, Jochen Mayer, Alisdair Fernie, Tim Mansfeldt, Uwe Sonnewald, and Marcel Bucher. "Crop genetic diversity uncovers metabolites, elements, and gene networks predicted to be associated with high plant biomass yields in maize". In: **PNAS Nexus** 1.3 (2022), pgac068. DOI: 10.1093/pnasnexus/pgac068.
- [4] Adrian F. Powell, Ari Feder, Jie Li, Maximilian H.-W. Schmidt, Lance Courtney, Saleh Alseekh, Emma M. Jobson, Alexander Vogel, Yimin Xu, David Lyon, Kathryn Dumschott, Marcus McHale, Ronan Sulpice, Kan Bao, Rohit Lal, Asha Duhan, Hallab, Asis, Alisandra K. Denton, Marie E. Bolger, Alisdair R. Fernie, Sarah R. Hind, Lukas A. Mueller, Gregory B. Martin, Zhangjun Fei, Cathie Martin, James J. Giovannoni, Susan R. Strickler, and Björn Usadel. "A *Solanum lycopersicoides* reference genome facilitates insights into tomato specialized metabolism and immunity". In: **The Plant Journal** 110.6 (2022), pp. 1791–1810. DOI: 10.1111/tpj.15770.
- [5] I. M. De-la Cruz, Hallab, A., U. Olivares-Pinto, R. Tapia-López, S. Velázquez-Márquez, D. Piñero, K. Oyama, B. Usadel, and J. Núñez-Farfán. "Genomic signatures of the evolution of defence against its natural enemies in the poisonous and medicinal plant *Datura stramonium* (Solanaceae)". In: **Scientific Reports** 1 (Jan. 13, 2021), p. 882.
- [6] Ali Hadizadeh Esfahani, Janina Maß, Hallab, Asis, Bernhard M Schuldt, David Nevarez, Björn Usadel, Mark-Christoph Ott, Benjamin Buer, and Andreas Schuppert. "Plant PhysioSpace: a robust tool to compare stress response across plant species". In: **Plant Physiology** (July 17, 2021).
- [7] Qingwen Chen, Ting Jiang, Yong-Xin Liu, Haili Liu, Tao Zhao, Zhixi Liu, Xiangchao Gan, Hallab, Asis, Xuemei Wang, Juan He, Yihua Ma, Fengxia Zhang, Tao Jin, M. Eric Schranz, Yong Wang, Yang Bai, and Guodong Wang. "Recently duplicated sesterterpene (C25) gene clusters in *Arabidopsis thaliana* modulate root microbiota". In: **SCIENCE CHINA Life Sciences** 62.7 (May 10, 2019), pp. 947–958.

- [8] Maria Jose Molina-Contreras, Sandi Paulišić, Christiane Then, Jordi Moreno-Romero, Pedro Pastor-Andreu, Luca Morelli, Irma Roig-Villanova, Huw Jenkins, Hallab, Asis, Xiangchao Gan, Aurelio Gomez-Cadenas, Miltos Tsiantis, Manuel Rodríguez-Concepción, and Jaime F. Martínez-García. "Photoreceptor Activity Contributes to Contrasting Responses to Shade in Cardamine and Arabidopsis Seedlings". In: **The Plant Cell** 31.11 (Nov. 1, 2019).
- [9] Rainer Schwacke, Gabriel Y. Ponce-Soto, Kirsten Krause, Anthony M. Bolger, Borjana Arsova, Hallab, Asis, Kristina Gruden, Mark Stitt, Marie E. Bolger, and Björn Usadel. "MapMan4: a refined protein classification and annotation framework applicable to multi-omics data analysis". In: **Molecular Plant** (Jan. 9, 2019).
- [10] Mitzi Villajuana-Bonequi, Alexandra Matei, Corinna Ernst, Hallab, Asis, Björn Usadel, and Gunther Doehlemann. "Cell type specific transcriptional reprogramming of maize leaves during Ustilago maydis induced tumor formation". In: **Scientific Reports** 9.1 (July 15, 2019), p. 10227.
- [11] Max Crüsemann, Raphael Reher, Isabella Schamari, Alexander O. Brachmann, Tsubasa Ohbayashi, Markus Kuschak, Davide Malfacini, Alexander Seidinger, Marta Pinto-Carbó, René Richarz, Tatjana Reuter, Stefan Kehraus, Hallab, Asis, Misty Attwood, Helgi B. Schiöth, Peter Mergaert, Yoshitomo Kikuchi, Till F. Schäberle, Evi Kostenis, Daniela Wenzel, Christa E. Müller, Jörn Piel, Aurélien Carlier, Leo Eberl, and Gabriele M. König. "Heterologous Expression, Biosynthetic Studies, and Ecological Function of the Selective Gq-Signaling Inhibitor FR900359". In: **Angewandte Chemie (International Ed. in English)** 57.3 (Jan. 15, 2018), pp. 836–840.
- [13] Xiangchao Gan, Angela Hay, Michiel Kwantes, Georg Haberer, Hallab, Asis, Raffaele Dello Iorio, Hugo Hofhuis, Bjorn Pieper, Maria Cartolano, Ulla Neumann, Lachezar A. Nikolov, Baoxing Song, Mohsen Hajheidari, Roman Briskine, Evangelia Kougioumoutzi, Daniela Vlad, Suvi Broholm, Jotun Hein, Khalid Meksem, David Lightfoot, Kentaro K. Shimizu, Rie Shimizu-Inatsugi, Martha Imprialou, David Kudrna, Rod Wing, Shusei Sato, Peter Huijser, Dmitry Filatov, Klaus F. X. Mayer, Richard Mott, and Miltos Tsiantis. "The *Cardamine hirsuta* genome offers insight into the evolution of morphological diversity". In: **Nature Plants** 2 (Oct. 2016), p. 16167.
- [14] Georg Zocher, Joachim Vilstrup, Daniel Heine, Hallab, Asis, Emilie Goralski, Christian Hertweck, Mark Stahl, Till F. Schäberle, and Thilo Stehle. "Structural basis of head to head polyketide fusion by CorB". In: **Chemical Science** 6.11 (Oct. 13, 2015), pp. 6525–6536.
- [15] The Tomato Genome Consortium. "The tomato genome sequence provides insights into fleshy fruit evolution". In: **Nature** 485.7400 (May 31, 2012), pp. 635–641.
- [16] Nevin D. Young, Frédéric Debellé, Giles E. D. Oldroyd, Rene Geurts, Steven B. Cannon, Michael K. Udvardi, Vagner A. Bedito, Klaus F. X. Mayer, Jérôme Gouzy, Heiko Schoof, Yves Van de Peer, Sebastian Proost, Douglas R. Cook, Blake C. Meyers, Manuel Spannagl, Foo Cheung, Stéphane De Mita, Vivek Krishnakumar, Heidrun Gundlach, Shiguo Zhou, Joann Mudge, Arvind K. Bharti, Jeremy D. Murray, Marina A. Naoumkina, Benjamin Rosen, Kevin A. T. Silverstein, Haibao Tang, Stéphane Rombauts, Patrick X. Zhao, Peng Zhou, Valérie Barbe, Philippe Bardou, Michael Bechner, Arnaud Bellec, Anne Berger, Hélène Bergès, Shelby Bidwell, Ton Bisseling, Nathalie Choisne, Arnaud Couloux, Roxanne Denny, Shweta Deshpande, Xinbin Dai, Jeff J. Doyle, Anne-Marie Dutez, Andrew D. Farmer, Stéphanie Fouteau, Carolien Franken, Chrystel Gibelin, John Gish, Steven Goldstein, Alvaro J. González, Pamela J. Green, Hallab, Asis, Marijke Hartog, Axin Hua, Sean J. Humphray, Dong-Hoon Jeong, Yi Jing, Anika Jöcker, Steve M. Kenton, Dong-Jin Kim, Kathrin Klee, Hongshing Lai, Chunting Lang, Shaoping Lin, Simone L. Macmil, Ghislaine Magdelenat, Lucy Matthews, Jamison McCarrison, Erin L. Monaghan, Jeong-Hwan Mun, Fares Z. Najjar, Christine Nicholson, Céline Noirot, Majesta O'Bleness,

Charles R. Paule, Julie Poulain, Florent Prion, Baifang Qin, Chunmei Qu, Ernest F. Retzel, Claire Riddle, Erika Sallet, Sylvie Samain, Nicolas Samson, Iryna Sanders, Olivier Saurat, Claude Scarpelli, Thomas Schiex, Béatrice Segurens, Andrew J. Severin, D. Janine Sherrier, Ruihua Shi, Sarah Sims, Susan R. Singer, Senjuti Sinharoy, Lieven Sterck, Agnès Viollet, Bing-Bing Wang, Keqin Wang, Mingyi Wang, Xiaohong Wang, Jens Warfsmann, Jean Weissenbach, Doug D. White, Jim D. White, Graham B. Wiley, Patrick Wincker, Yanbo Xing, Limei Yang, Ziyun Yao, Fu Ying, Jixian Zhai, Liping Zhou, Antoine Zuber, Jean Dénarié, Richard A. Dixon, Gregory D. May, David C. Schwartz, Jane Rogers, Francis Quétier, Christopher D. Town, and Bruce A. Roe. "The Medicago genome provides insight into the evolution of rhizobial symbioses". In: **Nature** 480.7378 (Dec. 22, 2011), pp. 520–524.

Pre-Print

- [12] Bjoern Usadel, Takayuki Tohge, Federico Scossa, Nicolas Sierro, Maximilian Schmidt, Alexander Vogel, Anthony Bolger, Amanda Kozlo, Eugenia MA Enfissi, Kris Morreel, Manuel Regenauer, Hallab, Asis, Colin Ruprecht, Heidrun Gundlach, Manuel Spannagl, Yaw Koram, Klaus FX Mayer, Wout Boerjan, Paul D. Fraser, Staffan Persson, Nikolai V. Ivanov, and Alisdair R. Fernie. "The genome and metabolome of the tobacco tree, *Nicotiana glauca*: a potential renewable feedstock for the bioeconomy". **bioRxiv**: <https://www.biorxiv.org/content/10.1101/351429v1>. June 20, 2018.

Teaching Experience

- current Teaching of applied bioninformatics at the university of applied sciences in Bingen; modules comprise: Algorithmic Bioinformatics, Bioinformatics Data Analysis, Current Bioinformatics, Scientific Research, Data-Warehouse and Full Stack Web-Development, Comparative Genomics, Systems Biology, and the supervision of various Bachelor thesis projects.
- current Supervision of a PhD student in comparative genomics and population genetics of maize wild crop relatives (Teosinte).
- 2019 Joined supervision of a doctoral thesis with Prof. Juan Núñez-Farfán (UNAM).
- 2018 1 week intensive seminar “Advanced Comparative Genomics” at the institute for ecology (UNAM)
- 2015 – 2016 Joined supervision of a doctoral thesis with Prof. Miltos Tsiantis and Dr. Xiangchao Gan.
- 2011 – 2013 Joined supervision of two master theses with Prof. Heiko Schoof.

Oral Presentations

- 2012 **20th Plant And Animal Genome Conference, San Diego**
Genome-scale Protein Function Prediction using Phylogenomics, Data Integration and Lexical Scoring, applied on the genomes of tomato (*Solanum lycopersicum*) and the leguminous plant *Medicago truncatula* (pag.confex.com/pag/xx/webprogram/Paper2326.html).
- 2012 **Invited Speaker — Fraunhofer Institute for Algorithms and Scientific Computing SCAI, Sankt Augustin**
Automated Assignment of Human Readable Descriptions (AHRD).
- 2011 **PhD day — Max Planck Institute for Plant Breeding Research, Cologne**
Protein Function Prediction.
- 2009 **4th EUSOL meeting, Toledo**
Protein function prediction with Bayesian Phylogenomics.

Personal Interests

- Sports Karate (1st Dan / black belt), boxing, yoga, biking, hiking, and dancing.
- Inventing Board Games My game “Amino” is currently being evaluated by two publishers. See github.com/asishallab/Amino
- Cultures Languages, travelling, and cooking.

References

Dr. Alicia Mastretta Yanes

Comisión Nacional para el
Conocimiento y Uso de la Biodi-
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