Curriculum Vitae

Andreas HEINZEL, M.S.c

Date of Birth	August 6th, 1985
Place of Birth	Salzburg
Citizenship	Austrian

EDUCATION

- 2010 – ongoing
  University of Vienna
  Informatics (Dr.) program
- 2008 – 2010
  Upper Austria University of Applied Sciences, Hagenberg:
  Bioinformatics (M.S.c) program
- 2005 – 2008
  Upper Austria University of Applied Sciences, Hagenberg:
  Bioinformatics (B.S.c) program
- 2000 – 2004
  BORG & Sport-RG Salzburg (school with a focus on science)
  A-levels (June 16th, 2004)

LANGUAGE SKILLS

- German - written and spoken
- English - written and spoken

WORK EXPERIENCE

- January 2017 - ongoing:
  Medical University of Vienna – Department for Nephrology and Dialysis, Vienna
- H, Vienna
- June 2008 – January 2017:
  emergentec biodevelopment GmbH, Vienna
- February – June 2008:
  Research Institute for Genetics and Selection of Industrial Microorganisms, Genetika, Moscow
  Internship
- August – September 2007:
  Tecan Austria GmbH - Analysegeräte, Meßgeräte, Salzburg
  Internship
- Summer 2005 / 2006:
  Mobil-Tec Elektronik GmbH, Salzburg
  internship
- November 2002 – April 2004:
  Netronics Netzwerktechnik-GmbH, Salzburg:
  spare-time work

Key Data

- Hands-on translational research expertise
- Hands-on software development expertise
- Author of research publications / book contributions in the field of translational research and bioinformatics
- Contributions to publicly available research tools

TUTORING AND TEACHING

- October 2011 – ongoing:
  Upper Austria University of Applied Sciences, Hagenberg:
  Course – Relational Databases and SQL / Extensible Markup Language

- October 2009 – February 2014:
  Upper Austria University of Applied Sciences, Hagenberg:
  Course - Full cycle project
- February 2013 – July 2013:
  University of Applied Sciences Technikum Wien:
  Course - Object oriented methods
- October 2012 – February 2013:
  University of Applied Sciences Technikum Wien:
  Course - Programming, algorithms and data structures
- September 2009, 2010, …, 2015:
  University of Applied Sciences Technikum Wien:
  Course - Required Elective Module 1 - Introduction to Programming
- March - July 2010:
  University of Applied Sciences Technikum Wien:
  Tutor - Programming, Algorithms and Data Structures
- June 2009:
  University of Applied Sciences Technikum Wien:
  Tutor - Programming, Algorithms and Data Structures
- November 2008 – January 2009:
  University of Applied Sciences Technikum Wien:
  Tutor - Programming, Algorithms and Data Structures
- October 2007 – July 2010:
  Upper Austria University of Applied Sciences, Hagenberg:
  Tutor - Relational Databases, SQL and XML

PUBLICATIONS

- Mayer et al. Systems biology derived biomarkers to predict progression of renal function decline in type 2 diabetes mellitus. Diabetes Care, 2017
- Gogalic et al. Validation of a protein panel for the non-invasive detection of recurrent non-muscle invasive bladder cancer. BIOMARKERS, 2017
- Marhold et al. Synthetic lethal combinations of low-toxicity drugs for breast cancer identified in silico by genetic screens in yeast. (submitted 2017)
- Heinzel et al. Validation of systems biology derived molecular markers of donor organ status associated with long term allograft function. (submitted 2016)
- Heinzel et al. Synthetic lethality guiding selection of drug combinations in ovarian cancer. (submitted 2016)
- Mayer et al. Predictive biomarkers for linking disease pathology and drug effect. Curr Pharm Des., 2016
- Pena et al. Serum metabolites predict response to angiotensin II receptor blockers in patients with diabetes mellitus. J Transl Med. 2016
- Andorfer et al. Vascular endothelial growth factor A as predictive marker for mTOR inhibition in relapsing high-grade serous ovarian cancer. BMC Syst Biol., 2016
- Rudnicki et al. Renal microRNA- and RNA-profiles in progressive chronic kidney disease. Eur J Clin Invest., 2016
- Pena et al. Plasma proteomics classifiers improve risk prediction for renal disease in patients with hypertension or type 2 diabetes. J Hypertens., 2015
- Heinzel et al. Molecular disease presentation in diabetic nephropathy. Nephrol Dial Transplant., 2015
- Lambers et al. Drugs meeting the molecular basis of diabetic kidney disease: bridging from molecular mechanism to personalized medicine. Nephrol Dial Transplant., 2015

- Bosse et al. Interaction networks for identifying coupled molecular processes in microbial communities. BioData Min., 2015
- Pena et al. A panel of novel biomarkers representing different disease pathways improves prediction of renal function decline in type 2 diabetes. PLoS One, 2015
- Bhat et al. Protein interactome of muscle invasive bladder cancer. PLoS One, 2015
- Wilflingseder et al. MicroRNAs in kidney transplantation. Nephrol Dial Transplant., 2015
- Wilflingseder et al. Molecular pathogenesis of post-transplant acute kidney injury: assessment of whole-genome mRNA and miRNA profiles. PLoS One, 2014
- Heinzel et al. From molecular signatures to predictive biomarkers: modeling disease pathophysiology and drug mechanism of action. Front Cell Dev Biol., 2014
- Heinzel et al. Functional molecular units for guiding biomarker panel design. Methods Mol Biol., 2014
- Heinzel et al. Data integration for DN-specific molecular process, biomarker and drug candidate selection. Poster presented at the 4th SysKid annual meeting, 2014, Berlin, Germany
- Heinzel. Biomarker panel selection from Omics profiles. Talk given at the 1st Meeting on OMICS towards the systems biology approach in renal disease and transplantation (ERA-EDTA), 2013, Bari, Italy
- Fritz et al. CRIME – Cross Reference Information Mapping Engine. Poster presented at the 5th OEGMBT annual meeting, 2013, Innsbruck, Austria
- Stütz et al. miRway – miRNA pathway tool. Poster presented at the 5th OEGMBT annual meeting, 2013, Innsbruck, Austria
- Borckholder et al. A generic, service-based data integration framework applied to linking drugs & clinical trials. Procedia Computer Science, 2013
- Fechete et al. Procedural and functional relations in expanded gene / protein interaction networks. Journal of Computer Science & Systems Biology, 2013
- Heinzel et al. Molecular models of the cardiorenal syndrome. Electrophoresis, 2013
- Heinzel et al. UNITS showcase, integration concept. Short talk given at the 3rd SysKid annual meeting, 2013, Vienna, Austria
- Heinzel et al. Pathways and processes in the context of molecular UNITS. Short talk given at the 3rd SysKid annual meeting, 2013, Vienna, Austria
- Heinzel et al. A molecular model of diabetic nephropathy as basis for marker and target selection. Poster presented at the 3rd SysKid annual meeting, 2013, Vienna, Austria
- Rudnicki et al. A Bioinformatics Analysis of Renal miRNA – and mRNA expression signatures in progressive chronic kidney disease. Poster presented at the 50th ERA-EDTA Congress, 2013, Istanbul, Turkey
- Wilfingseder et al. Molecular Model of Acute Kidney Injury from integrating ‘Omics’ Data and Literature Mining. Poster presented at the 50th ERA-EDTA Congress, 2013, Istanbul, Turkey
- Söllner et al. Synthetic lethality for linking Mycophenolate Mofetil mode of action with molecular disease and drug profiles. Molecular BioSystems, 2012
- Ivcevic et al. Identification of miRNA pathways discriminating acute cellular and humoral renal allograft rejection by using a newly developed miRNA pathway tool. Poster presented at the ASN Kidney Week, 2012, San Diego, California

- Wilfingseder et al. Systems Biology Analysis of Acute Kidney Injury. Poster presented at the ASN Kidney Week, 2012, San Diego, California
- Gottwald et al. Synlet – Utilizing data from yeast for identifying the Achilles' heel of cancer. Poster presented at the 4th OEGMBT annual meeting, 2012, Graz, Austria
- Heinzel et al. A concept for identifying molecular subtypes of a common clinical phenotype. Poster presented at the 2nd SysKid annual meeting, 2012, Bergamo, Italy
- Fechete et al. Integration towards a SysKid biomarker panel. Poster presented at the 2nd SysKid annual meeting, 2012, Bergamo, Italy
- Heinzel et al. Data graphs for linking clinical phenotype and molecular feature space. International Journal of Systems Biology and Biomedical Technologies, 2011
- Fechete et al. Mapping of molecular pathways, biomarkers and drug targets for diabetic nephropathy. Proteomics Clinical applications, 2011
- Söllner et al. Computational Vaccinology: Concept and application of a computational vaccinology workflow. Immunome Research, 2010
- Heinzel et al. Application of Systems Biology for understanding of Disease and selection of Molecular Targets for Therapy. Poster presented at the ACM International Conference on Bioinformatics and Computational Biology, 2010, Niagara Falls, USA
- Heinzel et al. A look at the Herpesviridae family in the context of molecular disease-drug-target networks. Poster presented at the 1st Annual World Congress of Immunodiseases and Therapy, 2010, Beijing, China
- Medvedeva et al. Intergenic, gene terminal, and intragenic CpG islands in the human genome. BMC Genomics (2010) vol. 11 pp. 48
- Jurczak et al. RNAStructVis - A RNA structure visualizer. Poster presented at the 16th Annual International Conference Intelligent Systems for Molecular Biology, 2008, Toronto, Canada
- Polishchuk et al. A comparative analysis of the binding sites of proteins regulating the transcription in the early development of Drosophila melanogaster, determined by the ChIP-chip method and the theoretically predicted clusters of the binding sites of these proteins. Biofizika (2008) vol. 53 (5) pp. 754-7
- Heinzel et al. Comparison of ChIP-chip SP1 Binding Location Data for Human Chromosome 21, 22 with PWM Hits. Poster presented at the Sixth International Conference on Bioinformatics of Genome Regulation and Structure, 2008 Novosibirsk, Russia

CONTRIBUTIONS TO FREE SOFTWARE

- Id Mapper: http://www.idmapper.com/
- miRway: http://mirway.nephrogene.at