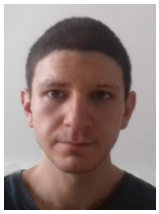

Mehmet Tekman

Staufen
Breisgau-
Hochschwarzwald
Baden-Württemberg
Deutschland
+49 1523 802 5117

email: mtekman89@gmail.com
langs: English,Türkçe,Deutsch
nationality: British
github: mtekman

Post-Doc Bioinformatician / Software Developer with experience in single-cell RNA clusteral analysis, DNA variant and haplotype analysis, and open-source automation pipelines developed in rapport with scientists and clinicians alike

Education, Qualifications, and Work Experience

London, UK	Whitgift School	09.2000 - 10.2007	*Private school, top 10 in UK*	4 As
	University College London (UCL)	09.2007 - 08.2011	*MSci Astrophysics*	Grade - 2:1 Honours
		09.2011 - 08.2012	*MSc Computer Science*	Distinction
	Royal Free Hospital (UCL)	09.2012 - 10.2016	*PhD Biomedical Science*	(No corrections)
		10.2016 - 09.2017	*Post-Doc Biomedical Scientist*	DNA Variant Analysis Linkage and Haplotypes Teaching Assistant
Freiburg, DE	Galaxy Team (Backofen Group)	09.2017 - (current)	*Post-Doc Bioinformatician*	Galaxy Tool Development Galaxy Training Workshops scRNA Analysis Teaching / Mentoring
	Max-Planck Institute (Grün Lab)	10.2018 - (current)	*Guest Scientist*	scRNA Analysis

Notable Works

High-Throughput Linkage Analysis Pipeline Performs comprehensive quality linkage analysis through a series of curated collection of quality checking utilities modified accordingly to handle large-data. (Github)

High-Throughput Sequence Analysis Pipeline VCF variant annotation and filtering utility that makes additional use of family data and penetrance models, and multiple annotation sources to produce an interactive web-report. (Bitbucket)

Haplotype Visualization and Pedigree Tool Web-based pedigree creation application, with haplotype visualization and partial reconstruction for genotype analysis and comparison. (Github)

Single Cell Training Materials on Galaxy Collection of trainings and wrappers for scRNA-seq analysis, incorporated into the Galaxy Training Network for both 10x and custom protocols, from pre-processing to downstream analysis. (GTN)

Publications

2014

- S. Drury, C. Boustred, M. Tekman, H. Stanescu, R. Kleta, N. Lench, L. S. Chitty, and R. H. Scott. A novel homozygous ERCC5 truncating mutation in a family with prenatal arthrogryposis–further evidence of genotype-phenotype correlation. *Am. J. Med. Genet. A*, 164A(7):1777–1783, Jul 2014

2015

- N. E. Mencacci, I. Rubio-Agusti, A. Zdebik, F. Asmus, M. H. Ludtmann, M. Ryten, V. Plagnol, A. K. Hauser, S. Bandres-Ciga, C. Bettencourt, P. Forabosco, D. Hughes, M. M. Soutar, K. Peall, H. R. Morris, D. Trabzuni, M. Tekman, H. C. Stanescu, R. Kleta, M. Carecchio, G. Zorzi, N. Nardocci, B. Garavaglia, E. Lohmann, A. Weissbach, C. Klein, J. Hardy, A. M. Pittman, T. Foltynie, A. Y. Abramov, T. Gasser, K. P. Bhatia, and N. W. Wood. A missense mutation in KCTD17 causes autosomal dominant myoclonus-dystonia. *Am. J. Hum. Genet.*, 96(6):938–947, Jun 2015
- P. Le Quesne Stabej, H. J. Williams, C. James, M. Tekman, H. C. Stanescu, R. Kleta, L. Ocaka, F. Lescai, H. L. Storr, M. Bitner-Glindzicz, C. Bacchelli, G. S. Conway, G. E. Moore, B. G. Gaspar, M. Hubank, R. H. Scott, E. Chanudet, and E. Stupka. STAG3 truncating variant as the cause of primary ovarian insufficiency. *Eur. J. Hum. Genet.*, 24(1):135–138, Jun 2015

2016

- D. M. Rowczenio, D. S. Iancu, H. Trojer, J. A. Gilbertson, J. D. Gillmore, A. D. Wechalekar, M. Tekman, H. C. Stanescu, R. Kleta, T. Lane, P. N. Hawkins, and H. J. Lachmann. Autosomal dominant familial Mediterranean fever in Northern European Caucasians associated with deletion of p.M694 residue-a case series and genetic exploration. *Rheumatology (Oxford)*, May 2016
- O. Abdelhadi, D. Iancu, M. Tekman, H. Stanescu, D. Bockenhauer, and R. Kleta. Founder mutation in KCNJ10 in Pakistani patients with EAST syndrome. *Mol Genet Genomic Med*, 4(5):521–526, Jun 2016

2017

- P. Stabej, C. James, L. Ocaka, M. Tekman, S. Grunewald, E. Clement, H. Stanescu, R. Kleta, D. Morrogh, A. Calder, et al. An example of the utility of genomic analysis for fast and accurate clinical diagnosis of complex rare phenotypes. *Orphanet Journal of Rare Diseases*, 12(1):24, 2017
- O. Cabezas, S. Flanagan, H. Stanescu, E. Garcia-Martinez, R. Caswell, H. Lango-Allen, M. Anton-Gamero, J. Argente, A. Bussell, A. Brandli, et al. Polycystic kidney disease with hyperinsulinemic hypoglycemia caused by a promoter mutation in pmm2. *Journal of the American Society of Nephrology*, 2017
- M. Tekman, A. Medlar, M. Mozere, R. Kleta, and H. Stanescu. Haploforge: a comprehensive pedigree drawing and haplotype visualization web application. *Bioinformatics*, 33(24):3871–3877, 2017

2018

- M. Tekman, M. Mozere, J. Kari, D. Bockenhauer, R. Kleta, and H. Stanescu. Ovas: an open-source variant analysis suite with inheritance modelling. *BMC bioinformatics*, 19(1):46, 2018
- M. Reichold, E. Klootwijk, J. Reinders, E. Otto, M. Milani, C. Broeker, C. Laing, J. Wiesner, S. Devi, W. Zhou, et al. Glycine amidinotransferase (gatm), renal fanconi syndrome, and kidney failure. *Journal of the American Society of Nephrology*, 29(7):1849–1858, 2018

2019

- Danit Oz-Levi, Tsviya Olender, Ifat Bar-Joseph, Yiwen Zhu, Dina Marek-Yagel, Iros Barozzi, Marco Osterwalder, Anna Alkelai, Elizabeth K Ruzzo, Yujun Han, et al. Noncoding deletions reveal a gene that is critical for intestinal function. *Nature*, 571(7763):107–111, 2019