Tobias Rausch – Senior Bioinformatician (EMBL)

Brief biography

I have a background in computer science and in my PhD (2006-2009) I worked on the SeqAn library for sequence analysis. Since 2009 I have been working at the European Molecular Biology Laboratory (EMBL) as Senior Bioinformatician at the interface of omics data production (EMBL GeneCore) and its use in research (Korbel group).

Research Interests

Cancer Genomics	Somatic tumor rearrangements
Population Genomics	Germline genome variation
Rare diseases	Identification of causative mutations for rare disorders
Algorithm Engineering	Structural variant discovery in short- and long-reads

Selected software tools (https://github.com/tobiasrausch)

Delly	Structural variant discovery
Alfred	NGS alignment statistics
Wally	Short-read and long-read visualizations
Gear-Genomics	Web applications for molecular biologists https://www.gear-genomics.com

Selected publications (ORCID: 0000-0001-5773-5620)

Google Scholar: https://scholar.google.de/citations?user=fQ1VoZEAAAAJ

1. **Rausch, T.** et al. Long-read sequencing of diagnosis and post-therapy medulloblastoma reveals complex rearrangement patterns and epigenetic signatures. Cell Genom. 2023 Mar 22;3(4):100281.
2. **Rausch, T.** et al. Tracy: basecalling, alignment, assembly and deconvolution of sanger chromatogram trace files. BMC genomics 21 (1), 1-9 (2020).
3. **PCAWG Consortium**. Pan-cancer analysis of whole genomes. Nature 578 (7793), 82–93 (2020).
4. **Rausch, T.** et al. Alfred: interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing. Bioinformatics 35 (14), 2489-2491 (2019)
5. Sudmant, P. H., **Rausch, T.** et al. An integrated map of structural variation in 2,504 human genomes. Nature 526, 75–81 (2015).
6. Greil, J., **Rausch, T.** et al. Whole-exome sequencing links caspase recruitment domain 11 (CARD11) inactivation to severe combined immunodeficiency. J. Allergy Clin. Immunol. 131, 1376–1383.e3 (2013).
7. **Rausch, T.** et al. Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. Cell 148, 59–71 (2012).
8. **Rausch, T.** et al. DELLY: structural variant discovery by integrated paired-end and split-read analysis. Bioinforma. Oxf. Engl. 28, i333–i339 (2012).