Jonas Mandel
Senior Bioinformatics Scientist

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olished bioinformatics scientist with 14 years of experience in bioinformatics, omics data analysis, machine learning, and clinical istics. Expert omics data analyst for RNAseq, scRNAseq, long-read sequencing, biomarker data analysis, GWAS. Expert R nmer with working knowledge of Python and proficiency in various bioinformatics & biostatistics methods & tools. Strong nce in scientific writing & communication for a variety of audiences (researchers, clinicians, investors). Focus areas: immuno-y, cardiology, neurology, rare diseases.

Experience

Bioinformatics Scientist - Mnemo Therapeutics *2021 - 2025, Paris*

eveloped pipelines for detection of alternative splicing and cancer neoantigen prediction using RNAseq, scRNAseq, and long-read NAseq (PacBio).
ed integration of transcriptomics (>20K RNAseq samples) and immunopeptidomics databases (>1.5K samples) to generate target eptides libraries: >1.2K putative targets, leading to 8 validated peptide targets.
esigned statistical analysis of neoantigen recurrence and peptide prioritization, instrumental for target mining strategy for vaccine nd CAR-T development.
mplemented long-read RNAseq pipeline for alternative splicing discovery & quantification based on IsoSeq3 & SQANTI.
oordinated cross-team efforts as work package lead for immunopeptidomics target mining; prepared scientific deliverables and resentations.
articipated in the design & setup of the bioinformatics work environment from scratch: github, AWS, Trello, …
ompany-wide support to develop automated data analysis and reporting.

rker Biostatistician - Sanofi / Ividata *2018 - 2021, Paris*

ed biomarker analyses in phase 2/3 trials (Sarilumab, Dupilumab, SAR440340) using RNAseq, SNP microarray, and proteomics link): SAP authoring & implementation with R, oversight of CROs, preparation of deliverables.
iomarker biostatistician and machine learning advisor in several R&D projects in oncology, cardiology, multiple sclerosis.
eveloped a shiny app for interactive reporting of omics biomarker data analysis.
articipated in the development of R trainings "Introduction to R" and "Graphs in R" for Sanofi statisticians & programmers.

al Biostatistician - Sanofi / Ividata *2016 - 2018, Paris*

MA Study biostatistician for phase 3b clinical trial (Alirocumab, hypercholesterolemia): authoring SAP and TLFs specs, coordi-ation with CRO & clinical team to prepare of deliverables (KRM, CSR), supervision & QC of CRO's activities.
ed the biostatistics & data analysis strategy for the Alirocumab publication program, overseeing data mining and post-hoc analyses f 14 pooled clinical trials to generate scientific insights and support publications in peer-reviewed journals.

tistician & Computational Genomics Scientist - Pharnext *2012 - 2015, Paris*

ed design & implementation of a workflow for GWAS data imputation and analysis to discover disease-specific genomic alterations.
esigned & wrote SAP for Phase II/III clinical trials with adaptive designs, interim futility and power analysis, procedures for ultiple endpoints. Meta-analysis of clinical trials.
onducted biomarker statistical analysis for in-house clinical trials, including reportings and presentations for internal and external akeholders (scientific & business).

tistics & Bioinformatics research engineer - Institut Curie / IN-I U900 *2009 - 2012, Paris*

erformed omics statistical analyses (gene microarray, RNAseq, exome seq, SNP array) for various cancer research projects.
evelopment automated workflows for omics data analysis.
articipated to developing internal R programming training initiatives.

tistics & Data Science

tatistical modelling & inference: generalized linear model, mixed effects model, survival analysis, meta-analysis, PLS, prin-pal component regression, interim analysis for clinical trials, conditional power analysis.
Multivariate statistics: PCA, PLS, t-SNE, UMAP, multiple correspondence analysis, factor analysis.
Machine learning: supervised classification & regression (LDA, SVM, Lasso / Elastic Net, boosting, bagging, random forests, GBoost, …), unsupervised clustering (hierarchical clustering, k-means, DBSCAN, gaussian mixture models, …).

& Bioinformatics

Transcriptomics (RNAseq, scRNAseq): alignment, normalization, differential analysis, splicing detection & quantification.
ong-read sequencing (PacBio): transcript identification, isoform quantification, differential analysis.
Genomics (WGS/WES): variant calling, CNV analysis, fusion gene detection.
NP microarrays & GWAS: imputation, association testing.
athway enrichment: GSA/GSEA.