# Fabian J. Theis

## List of Publications by Year in Descending Order

**Source:** https://exaly.com/author-pdf/3553837/fabian-j-theis-publications-by-year.pdf
**Version:** 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

| | |
|---|---|
| 452 | papers |
| 24,212 | citations |
| 76 | h-index |
| 147 | g-index |
| 539 | ext. papers |
| 35,548 | ext. citations |
| 9.1 | avg, IF |
| 7.5 | L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 452 | Integration of single-cell transcriptomes and chromatin landscapes reveals regulatory programs driving pharyngeal organ development.. *Nature Communications*, **2022**, 13, 457 | 17.4 | 1 |
| 451 | Squidpy: a scalable framework for spatial omics analysis.. *Nature Methods*, **2022**, | 21.6 | 22 |
| 450 | CellRank for directed single-cell fate mapping.. *Nature Methods*, **2022**, | 21.6 | 12 |
| 449 | Effect of Atmospheric Aging on Soot Particle Toxicity in Lung Cell Models at the Air-Liquid Interface: Differential Toxicological Impacts of Biogenic and Anthropogenic Secondary Organic Aerosols (SOAs).. *Environmental Health Perspectives*, **2022**, 130, 27003 | 8.4 | 8 |
| 448 | Spatial components of molecular tissue biology.. *Nature Biotechnology*, **2022**, | 44.5 | 8 |
| 447 | A Python library for probabilistic analysis of single-cell omics data.. *Nature Biotechnology*, **2022**, 40, 163-166 | 44.5 | 9 |
| 446 | Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation.. *Molecular Systems Biology*, **2022**, 18, e10798 | 12.2 | 24 |
| 445 | Parkinson's disease motor symptoms rescue by CRISPRa-reprogramming astrocytes into GABAergic neurons.. *EMBO Molecular Medicine*, **2022**, e14797 | 12 | 0 |
| 444 | Ly6D+Siglec-H+ precursors contribute to conventional dendritic cells via a Zbtb46+Ly6D+ intermediary stage. *Nature Communications*, **2022**, 13, | 17.4 | 2 |
| 443 | Benchmarking atlas-level data integration in single-cell genomics.. *Nature Methods*, **2021**, | 21.6 | 35 |
| 442 | Toward modeling metabolic state from single-cell transcriptomics. *Molecular Metabolism*, **2021**, 57, 101398 | 8.6 | 2 |
| 441 | scCODA is a Bayesian model for compositional single-cell data analysis. *Nature Communications*, **2021**, 12, 6876 | 17.4 | 6 |
| 440 | SARS-CoV-2 infection triggers profibrotic macrophage responses and lung fibrosis.. *Cell*, **2021**, 184, 6243-6261.e27 | 56.2 | 22 |
| 439 | scPower accelerates and optimizes the design of multi-sample single cell transcriptomic studies. *Nature Communications*, **2021**, 12, 6625 | 17.4 | 7 |
| 438 | Identification and characterization of distinct brown adipocyte subtypes in C57BL/6J mice. *Life Science Alliance*, **2021**, 4, | 5.8 | 8 |
| 437 | A field guide to cultivating computational biology. *PLoS Biology*, **2021**, 19, e3001419 | 9.7 | 2 |
| 436 | Cell-Type-Specific Impact of Glucocorticoid Receptor Activation on the Developing Brain: A Cerebral Organoid Study. *American Journal of Psychiatry*, **2021**, appiajp202121010095 | 11.9 | 2 |

| | | | |
|---|---|---|---|
| 435 | Over 1000 tools reveal trends in the single-cell RNA-seq analysis landscape. *Genome Biology*, **2021**, 22, 301 | 18.3 | 15 |
| 434 | Asc-1 regulates white versus beige adipocyte fate in a subcutaneous stromal cell population. *Nature Communications*, **2021**, 12, 1588 | 17.4 | 7 |
| 433 | Posterior subcapsular cataracts are a late effect after acute exposure to 0.5 Gy ionizing radiation in mice. *International Journal of Radiation Biology*, **2021**, 97, 529-540 | 2.9 | 2 |
| 432 | Integrated intra- and intercellular signaling knowledge for multicellular omics analysis. *Molecular Systems Biology*, **2021**, 17, e9923 | 12.2 | 26 |
| 431 | Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. *EMBO Molecular Medicine*, **2021**, 13, e12871 | 12 | 8 |
| 430 | Comparison of genome-wide gene expression profiling by RNA Sequencing microarray in bronchial biopsies of COPD patients before and after inhaled corticosteroid treatment: does it provide new insights?. *ERJ Open Research*, **2021**, 7, | 3.5 | 1 |
| 429 | Graph representation learning for single-cell biology. *Current Opinion in Systems Biology*, **2021**, 28, 100347-100347 | 3.2 | 2 |
| 428 | Swarm Learning for decentralized and confidential clinical machine learning. *Nature*, **2021**, 594, 265-270 | 50.4 | 89 |
| 427 | Cellular connectomes as arbiters of local circuit models in the cerebral cortex. *Nature Communications*, **2021**, 12, 2785 | 17.4 | 1 |
| 426 | Epithelial cell plasticity drives endoderm formation during gastrulation. *Nature Cell Biology*, **2021**, 23, 692-703 | 23.4 | 8 |
| 425 | Machine learning for perturbational single-cell omics. *Cell Systems*, **2021**, 12, 522-537 | 10.6 | 8 |
| 424 | Single-cell RNA sequencing reveals ex vivo signatures of SARS-CoV-2-reactive T cells through 'reverse phenotyping'. *Nature Communications*, **2021**, 12, 4515 | 17.4 | 5 |
| 423 | AutoGeneS: Automatic gene selection using multi-objective optimization for RNA-seq deconvolution. *Cell Systems*, **2021**, 12, 706-715.e4 | 10.6 | 8 |
| 422 | Asthma in farm children is more determined by genetic polymorphisms and in non-farm children by environmental factors. *Pediatric Allergy and Immunology*, **2021**, 32, 295-304 | 4.2 | 8 |
| 421 | CD23 Levels on B Cells Determine Long-Term Therapeutic Response in Patients with Atopic Eczema Treated with Selective IgE Immune Apheresis. *Journal of Investigative Dermatology*, **2021**, 141, 681-685.e6 | 4.3 | |
| 420 | Non-canonical Wnt/PCP signalling regulates intestinal stem cell lineage priming towards enteroendocrine and Paneth cell fates. *Nature Cell Biology*, **2021**, 23, 23-31 | 23.4 | 9 |
| 419 | Single-cell molecular profiling of all three components of the HPA axis reveals adrenal ABCB1 as a regulator of stress adaptation. *Science Advances*, **2021**, 7, | 14.3 | 10 |
| 418 | Deep learning the collisional cross sections of the peptide universe from a million experimental values. *Nature Communications*, **2021**, 12, 1185 | 17.4 | 21 |

| | | | |
|---|---|---|---|
| 417 | Deep Learning-based Propensity Scores for Confounding Control in Comparative Effectiveness Research: A Large-scale, Real-world Data Study. *Epidemiology*, **2021**, 32, 378-388 | 3.1 | 1 |
| 416 | CD81 marks immature and dedifferentiated pancreatic β-cells. *Molecular Metabolism*, **2021**, 49, 101188 | 8.8 | 2 |
| 415 | Sfaira accelerates data and model reuse in single cell genomics. *Genome Biology*, **2021**, 22, 248 | 18.3 | 5 |
| 414 | Mapping single-cell data to reference atlases by transfer learning. *Nature Biotechnology*, **2021**, | 44.5 | 20 |
| 413 | Group Testing for SARS-CoV-2 Allows for Up to 10-Fold Efficiency Increase Across Realistic Scenarios and Testing Strategies. *Frontiers in Public Health*, **2021**, 9, 583377 | 6 | 9 |
| 412 | RNA velocity-current challenges and future perspectives. *Molecular Systems Biology*, **2021**, 17, e10282 | 12.2 | 11 |
| 411 | Early IFN-γ signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. *Immunity*, **2021**, 54, 2650-2669.e14 | 32.3 | 31 |
| 410 | EpiScanpy: integrated single-cell epigenomic analysis. *Nature Communications*, **2021**, 12, 5228 | 17.4 | 8 |
| 409 | Diet-induced alteration of intestinal stem cell function underlies obesity and prediabetes in mice. *Nature Metabolism*, **2021**, 3, 1202-1216 | 14.6 | 2 |
| 408 | Current Smoking Alters Gene Expression and DNA Methylation in the Nasal Epithelium of Patients with Asthma. *American Journal of Respiratory Cell and Molecular Biology*, **2021**, 65, 366-377 | 5.7 | 0 |
| 407 | Vertical sleeve gastrectomy triggers fast β-cell recovery upon overt diabetes. *Molecular Metabolism* , **2021**, 54, 101330 | 8.8 | 2 |
| 406 | Self-supervised retinal thickness prediction enables deep learning from unlabelled data to boost classification of diabetic retinopathy. *Nature Machine Intelligence*, **2020**, 2, 719-726 | 22.5 | 12 |
| 405 | Predicting single-cell gene expression profiles of imaging flow cytometry data with machine learning. *Nucleic Acids Research*, **2020**, 48, 11335-11346 | 20.1 | 6 |
| 404 | Inhibition of LTβR signalling activates WNT-induced regeneration in lung. *Nature*, **2020**, 588, 151-156 | 50.4 | 26 |
| 403 | Post-surgical adhesions are triggered by calcium-dependent membrane bridges between mesothelial surfaces. *Nature Communications*, **2020**, 11, 3068 | 17.4 | 23 |
| 402 | The proteome landscape of the kingdoms of life. *Nature*, **2020**, 582, 592-596 | 50.4 | 64 |
| 401 | Automatic identification of relevant genes from low-dimensional embeddings of single-cell RNA-seq data. *Bioinformatics*, **2020**, 36, 4291-4295 | 7.2 | 2 |
| 400 | Model-based analysis of response and resistance factors of cetuximab treatment in gastric cancer cell lines. *PLoS Computational Biology*, **2020**, 16, e1007147 | 5 | 2 |

| | | | |
|---|---|---|---|
| 399 | Protocol of a population-based prospective COVID-19 cohort study Munich, Germany (KoCo19). *BMC Public Health*, **2020**, 20, 1036 | 4.1 | 26 |
| 398 | DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. *PLoS Computational Biology*, **2020**, 16, e1007616 | 5 | 14 |
| 397 | Eleven grand challenges in single-cell data science. *Genome Biology*, **2020**, 21, 31 | 18.3 | 274 |
| 396 | Targeted pharmacological therapy restores βcell function for diabetes remission. *Nature Metabolism*, **2020**, 2, 192-209 | 14.6 | 44 |
| 395 | Epithelial Planar Bipolarity Emerges from Notch-Mediated Asymmetric Inhibition of Emx2. *Current Biology*, **2020**, 30, 1142-1151.e6 | 6.3 | 9 |
| 394 | SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. *Cell*, **2020**, 181, 1016-1035.e19 | 56.2 | 1326 |
| 393 | Predicting antigen specificity of single T cells based on TCR CDR3 regions. *Molecular Systems Biology*, **2020**, 16, e9416 | 12.2 | 24 |
| 392 | The single-cell eQTLGen consortium. *ELife*, **2020**, 9, | 8.9 | 68 |
| 391 | A sparse deep learning approach for automatic segmentation of human vasculature in multispectral optoacoustic tomography. *Photoacoustics*, **2020**, 20, 100203 | 9 | 14 |
| 390 | Conditional out-of-distribution generation for unpaired data using transfer VAE. *Bioinformatics*, **2020**, 36, i610-i617 | 7.2 | 18 |
| 389 | Determinants of SARS-CoV-2 receptor gene expression in upper and lower airways **2020**, | | 8 |
| 388 | Munich School for Data Science (MUDS) – Eine Graduiertenschule für Data Science in München. *Informatik-Spektrum*, **2020**, 42, 429-431 | 0.3 | |
| 387 | IL-17C amplifies epithelial inflammation in human psoriasis and atopic eczema. *Journal of the European Academy of Dermatology and Venereology*, **2020**, 34, 800-809 | 4.6 | 10 |
| 386 | Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. *Nature Communications*, **2020**, 11, 3559 | 17.4 | 106 |
| 385 | LifeTime and improving European healthcare through cell-based interceptive medicine. *Nature*, **2020**, 587, 377-386 | 50.4 | 56 |
| 384 | Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. *Cell*, **2020**, 182, 1419-1440.e23 | 36.2 | 558 |
| 383 | Generalizing RNA velocity to transient cell states through dynamical modeling. *Nature Biotechnology*, **2020**, 38, 1408-1414 | 44.5 | 383 |
| 382 | identification of apoptotic and extracellular vesicle-bound live cells using image-based deep learning. *Journal of Extracellular Vesicles*, **2020**, 9, 1792683 | 16.4 | 6 |

| | | | |
|---|---|---|---|
| 381 | Impact of Brain Fatty Acid Signaling on Peripheral Insulin Action in Mice. *Experimental and Clinical Endocrinology and Diabetes*, **2020**, 128, 20-29 | 2.3 | 1 |
| 380 | Altered relaxation times in MRI indicate bronchopulmonary dysplasia. *Thorax*, **2020**, 75, 184-187 | 7.3 | 8 |
| 379 | Pheno-seq - linking visual features and gene expression in 3D cell culture systems. *Scientific Reports* , **2019**, 9, 12367 | 4.9 | 10 |
| 378 | Current best practices in single-cell RNA-seq analysis: a tutorial. *Molecular Systems Biology*, **2019**, 15, e8746 | 12.2 | 574 |
| 377 | MPRAnalyze: statistical framework for massively parallel reporter assays. *Genome Biology*, **2019**, 20, 183 | 18.3 | 27 |
| 376 | Establishment of a high-resolution 3D modeling system for studying pancreatic epithelial cell biology in vitro. *Molecular Metabolism*, **2019**, 30, 16-29 | 8.8 | 15 |
| 375 | Aldh1b1 expression defines progenitor cells in the adult pancreas and is required for Kras-induced pancreatic cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 20679-20688 | 11.5 | 25 |
| 374 | Single-cell RNA-seq denoising using a deep count autoencoder. *Nature Communications*, **2019**, 10, 390 | 17.4 | 314 |
| 373 | IRE1□XBP1s pathway promotes prostate cancer by activating c-MYC signaling. *Nature Communications*, **2019**, 10, 323 | 17.4 | 93 |
| 372 | Dynamic modelling of an ACADS genotype in fatty acid oxidation - Application of cellular models for the analysis of common genetic variants. *PLoS ONE*, **2019**, 14, e0216110 | 3.7 | 0 |
| 371 | A cellular census of human lungs identifies novel cell states in health and in asthma. *Nature Medicine*, **2019**, 25, 1153-1163 | 50.5 | 334 |
| 370 | Inferring Interaction Networks From Multi-Omics Data. *Frontiers in Genetics*, **2019**, 10, 535 | 4.5 | 52 |
| 369 | Comprehensive single cell mRNA profiling reveals a detailed roadmap for pancreatic endocrinogenesis. *Development (Cambridge)*, **2019**, 146, | 6.6 | 50 |
| 368 | Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. *Nature Communications*, **2019**, 10, 2548 | 17.4 | 54 |
| 367 | PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. *Genome Biology*, **2019**, 20, 59 | 18.3 | 369 |
| 366 | Common patterns of gene regulation associated with Cesarean section and the development of islet autoimmunity - indications of immune cell activation. *Scientific Reports*, **2019**, 9, 6250 | 4.9 | 4 |
| 365 | The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. *American Journal of Respiratory Cell and Molecular Biology*, **2019**, 61, 31-41 | 5.7 | 98 |
| 364 | Deep learning: new computational modelling techniques for genomics. *Nature Reviews Genetics*, **2019**, 20, 389-403 | 30.1 | 367 |

| | | | |
|---|---|---|---|
| 363 | Inferring population dynamics from single-cell RNA-sequencing time series data. *Nature Biotechnology*, **2019**, 37, 461-468 | 44.5 | 46 |
| 362 | A strategy for high-dimensional multivariable analysis classifies childhood asthma phenotypes from genetic, immunological, and environmental factors. *Allergy: European Journal of Allergy and Clinical Immunology*, **2019**, 74, 1364-1373 | 9.3 | 16 |
| 361 | Is the humoral immunity dispensable for the pathogenesis of psoriasis?. *Journal of the European Academy of Dermatology and Venereology*, **2019**, 33, 115-122 | 4.6 | 8 |
| 360 | BART-Seq: cost-effective massively parallelized targeted sequencing for genomics, transcriptomics, and single-cell analysis. *Genome Biology*, **2019**, 20, 155 | 18.3 | 12 |
| 359 | scGen predicts single-cell perturbation responses. *Nature Methods*, **2019**, 16, 715-721 | 21.6 | 89 |
| 358 | Evaluation of Deep Learning Strategies for Nucleus Segmentation in Fluorescence Images. *Cytometry Part A: the Journal of the International Society for Analytical Cytology*, **2019**, 95, 952-965 | 4.6 | 106 |
| 357 | scSLAM-seq reveals core features of transcription dynamics in single cells. *Nature*, **2019**, 571, 419-423 | 50.4 | 77 |
| 356 | Meeting the Challenges of High-Dimensional Single-Cell Data Analysis in Immunology. *Frontiers in Immunology*, **2019**, 10, 1515 | 8.4 | 34 |
| 355 | Concepts and limitations for learning developmental trajectories from single cell genomics. *Development (Cambridge)*, **2019**, 146, | 6.6 | 89 |
| 354 | An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. *Nature Communications*, **2019**, 10, 963 | 17.4 | 186 |
| 353 | A test metric for assessing single-cell RNA-seq batch correction. *Nature Methods*, **2019**, 16, 43-49 | 21.6 | 140 |
| 352 | Metabolic regulation of pluripotency and germ cell fate through ▯ketoglutarate. *EMBO Journal*, **2019**, 38, | 13 | 41 |
| 351 | Multi-experiment nonlinear mixed effect modeling of single-cell translation kinetics after transfection. *Npj Systems Biology and Applications*, **2019**, 5, 1 | 5 | 23 |
| 350 | Whither systems medicine?. *Experimental and Molecular Medicine*, **2018**, 50, e453 | 12.8 | 37 |
| 349 | Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. *Science*, **2018**, 360, | 33.3 | 233 |
| 348 | netReg: network-regularized linear models for biological association studies. *Bioinformatics*, **2018**, 34, 896-898 | 7.2 | 5 |
| 347 | Maternal whole blood cell miRNA-340 is elevated in gestational diabetes and inversely regulated by glucose and insulin. *Scientific Reports*, **2018**, 8, 1366 | 4.9 | 20 |
| 346 | Epigenetically Regulated Chromosome 14q32 miRNA Cluster Induces Metastasis and Predicts Poor Prognosis in Lung Adenocarcinoma Patients. *Molecular Cancer Research*, **2018**, 16, 390-402 | 6.6 | 27 |

| | | | |
|---|---|---|---|
| 345 | Lifetime study in mice after acute low-dose ionizing radiation: a multifactorial study with special focus on cataract risk. *Radiation and Environmental Biophysics*, **2018**, 57, 99-113 | 2 | 23 |
| 344 | Type I Immune Response Induces Keratinocyte Necroptosis and Is Associated with Interface Dermatitis. *Journal of Investigative Dermatology*, **2018**, 138, 1785-1794 | 4.3 | 23 |
| 343 | Dynamic landscape of pancreatic carcinogenesis reveals early molecular networks of malignancy. *Gut*, **2018**, 67, 146-156 | 19.2 | 30 |
| 342 | Prediction of type 1 diabetes using a genetic risk model in the Diabetes Autoimmunity Study in the Young. *Pediatric Diabetes*, **2018**, 19, 277-283 | 3.6 | 16 |
| 341 | Early Identification of Bronchopulmonary Dysplasia Using Novel Biomarkers by Proteomic Screening. *American Journal of Respiratory and Critical Care Medicine*, **2018**, 197, 1076-1080 | 10.2 | 14 |
| 340 | Toll-like receptor 7/8 agonists stimulate plasmacytoid dendritic cells to initiate T17-deviated acute contact dermatitis in human subjects. *Journal of Allergy and Clinical Immunology*, **2018**, 141, 1320-1333.e11 | 11.5 | 27 |
| 339 | Lineage marker synchrony in hematopoietic genealogies refutes the PU.1/GATA1 toggle switch paradigm. *Nature Communications*, **2018**, 9, 2697 | 17.4 | 15 |
| 338 | SCANPY: large-scale single-cell gene expression data analysis. *Genome Biology*, **2018**, 19, 15 | 18.3 | 1418 |
| 337 | Impulse model-based differential expression analysis of time course sequencing data. *Nucleic Acids Research*, **2018**, 46, e119 | 20.1 | 38 |
| 336 | MetaMap: an atlas of metatranscriptomic reads in human disease-related RNA-seq data. *GigaScience*, **2018**, 7, | 7.6 | 12 |
| 335 | Data Driven Computational Modeling of Hematopoiesis in Myelodysplastic Syndromes Unveils Differences in Hematopoietic Stem Cell Kinetics Compared to Age-Matched Healthy Controls. *Blood*, **2018**, 132, 4354-4354 | 2.2 | |
| 334 | MicroRNA as an Integral Part of Cell Communication: Regularized Target Prediction and Network Prediction. *Lecture Notes in Bioengineering*, **2018**, 85-100 | 0.8 | |
| 333 | Information Theoretic Concepts to Unravel Cell-Cell Communication. *Lecture Notes in Bioengineering*, **2018**, 115-136 | 0.8 | |
| 332 | Mechanistic description of spatial processes using integrative modelling of noise-corrupted imaging data. *Journal of the Royal Society Interface*, **2018**, 15, 20180600 | 4.1 | 1 |
| 331 | Efficient Parameter Estimation Enables the Prediction of Drug Response Using a Mechanistic Pan-Cancer Pathway Model. *Cell Systems*, **2018**, 7, 567-579.e6 | 10.6 | 56 |
| 330 | Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. *Metabolomics*, **2018**, 14, 128 | 4.7 | 63 |
| 329 | Increasing Neural Stem Cell Division Asymmetry and Quiescence Are Predicted to Contribute to the Age-Related Decline in Neurogenesis. *Cell Reports*, **2018**, 25, 3231-3240.e8 | 10.6 | 19 |
| 328 | Copy number aberrations from Affymetrix SNP 6.0 genotyping data-how accurate are commonly used prediction approaches?. *Briefings in Bioinformatics*, **2018**, | 13.4 | 1 |

| | | | |
|---|---|---|---|
| 327 | Bayesian parameter estimation for biochemical reaction networks using region-based adaptive parallel tempering. *Bioinformatics*, **2018**, 34, i494-i501 | 7.2 | 8 |
| 326 | LNA++: Linear Noise Approximation with First and Second Order Sensitivities. *Lecture Notes in Computer Science*, **2018**, 300-306 | 0.9 | |
| 325 | Inductive and Selective Effects of GSK3 and MEK Inhibition on Nanog Heterogeneity in Embryonic Stem Cells. *Stem Cell Reports*, **2018**, 11, 58-69 | 8 | 8 |
| 324 | Inhibition of fat cell differentiation in 3T3-L1 pre-adipocytes by all-trans retinoic acid: Integrative analysis of transcriptomic and phenotypic data. *Biomolecular Detection and Quantification*, **2017**, 11, 31-44 | 12 | 7 |
| 323 | Parallelization and High-Performance Computing Enables Automated Statistical Inference of Multi-scale Models. *Cell Systems*, **2017**, 4, 194-206.e9 | 10.6 | 36 |
| 322 | AURKA, DLGAP5, TPX2, KIF11 and CKAP5: Five specific mitosis-associated genes correlate with poor prognosis for non-small cell lung cancer patients. *International Journal of Oncology*, **2017**, 50, 365-372 | 4.4 | 73 |
| 321 | cgCorrect: a method to correct for confounding cell-cell variation due to cell growth in single-cell transcriptomics. *Physical Biology*, **2017**, 14, 036001 | 3 | 9 |
| 320 | Prospective identification of hematopoietic lineage choice by deep learning. *Nature Methods*, **2017**, 14, 403-406 | 21.6 | 102 |
| 319 | Pulmonary microRNA profiles identify involvement of Creb1 and Sec14l3 in bronchial epithelial changes in allergic asthma. *Scientific Reports*, **2017**, 7, 46026 | 4.9 | 19 |
| 318 | fastER: a user-friendly tool for ultrafast and robust cell segmentation in large-scale microscopy. *Bioinformatics*, **2017**, 33, 2020-2028 | 7.2 | 43 |
| 317 | Identification of a plasma miRNA biomarker signature for allergic asthma: A translational approach. *Allergy: European Journal of Allergy and Clinical Immunology*, **2017**, 72, 1962-1971 | 9.3 | 34 |
| 316 | Model-based branching point detection in single-cell data by K-branches clustering. *Bioinformatics*, **2017**, 33, 3211-3219 | 7.2 | 7 |
| 315 | A BaSiC tool for background and shading correction of optical microscopy images. *Nature Communications*, **2017**, 8, 14836 | 17.4 | 99 |
| 314 | GATA2/3-TFAP2A/C transcription factor network couples human pluripotent stem cell differentiation to trophectoderm with repression of pluripotency. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E9579-E9588 | 11.5 | 56 |
| 313 | Reconstructing cell cycle and disease progression using deep learning. *Nature Communications*, **2017**, 8, 463 | 17.4 | 136 |
| 312 | Single cells make big data: New challenges and opportunities in transcriptomics. *Current Opinion in Systems Biology*, **2017**, 4, 85-91 | 3.2 | 96 |
| 311 | Systematic single-cell analysis provides new insights into heterogeneity and plasticity of the pancreas. *Molecular Metabolism*, **2017**, 6, 974-990 | 8.8 | 59 |
| 310 | Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. *Nature Communications*, **2017**, 8, 1483 | 17.4 | 26 |

| | | | |
|---|---|---|---|
| 309 | Comprehensive benchmarking of Markov chain Monte Carlo methods for dynamical systems. *BMC Systems Biology*, **2017**, 11, 63 | 3.5 | 22 |
| 308 | Peptide serum markers in islet autoantibody-positive children. *Diabetologia*, **2017**, 60, 287-295 | 10.3 | 13 |
| 307 | TALEN/CRISPR-mediated engineering of a promoterless anti-viral RNAi hairpin into an endogenous miRNA locus. *Nucleic Acids Research*, **2017**, 45, e3 | 20.1 | 6 |
| 306 | pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. *BMC Bioinformatics*, **2017**, 18, 429 | 3.6 | 0 |
| 305 | A scalable moment-closure approximation for large-scale biochemical reaction networks. *Bioinformatics*, **2017**, 33, i293-i300 | 7.2 | 0 |
| 304 | Model Based Targeting of IL-6-Induced Inflammatory Responses in Cultured Primary Hepatocytes to Improve Application of the JAK Inhibitor Ruxolitinib. *Frontiers in Physiology*, **2017**, 8, 775 | 4.6 | 11 |
| 303 | The Human Cell Atlas. *ELife*, **2017**, 6, | 8.9 | 937 |
| 302 | Correcting Classifiers for Sample Selection Bias in Two-Phase Case-Control Studies. *Computational and Mathematical Methods in Medicine*, **2017**, 2017, 7847531 | 2.8 | 6 |
| 301 | Scalable Parameter Estimation for Genome-Scale Biochemical Reaction Networks. *PLoS Computational Biology*, **2017**, 13, e1005331 | 5 | 87 |
| 300 | Calcium-regulatory proteins as modulators of chemotherapy in human neuroblastoma. *Oncotarget*, **2017**, 8, 22876-22893 | 3.3 | 23 |
| 299 | Parameter estimation for dynamical systems with discrete events and logical operations. *Bioinformatics*, **2017**, 33, 1049-1056 | 7.2 | 12 |
| 298 | An adaptive scheduling scheme for calculating Bayes factors with thermodynamic integration using Simpson's rule. *Statistics and Computing*, **2016**, 26, 663-677 | 1.8 | 13 |
| 297 | Diffusion pseudotime robustly reconstructs lineage branching. *Nature Methods*, **2016**, 13, 845-8 | 21.6 | 566 |
| 296 | Analysis of Cell Lineage Trees by Exact Bayesian Inference Identifies Negative Autoregulation of Nanog in Mouse Embryonic Stem Cells. *Cell Systems*, **2016**, 3, 480-490.e13 | 10.6 | 20 |
| 295 | Lactation is associated with altered metabolomic signatures in women with gestational diabetes. *Diabetologia*, **2016**, 59, 2193-202 | 10.3 | 17 |
| 294 | Early myeloid lineage choice is not initiated by random PU.1 to GATA1 protein ratios. *Nature*, **2016**, 535, 299-302 | 50.4 | 138 |
| 293 | Tailored parameter optimization methods for ordinary differential equation models with steady-state constraints. *BMC Systems Biology*, **2016**, 10, 80 | 3.5 | 15 |
| 292 | MEMO: multi-experiment mixture model analysis of censored data. *Bioinformatics*, **2016**, 32, 2464-72 | 7.2 | 4 |

| | | | |
|---|---|---|---|
| 291 | A computational model to predict severity of atopic eczema from 30 serum proteins. *Journal of Allergy and Clinical Immunology*, **2016**, 138, 1207-1210.e2 | 11.5 | 8 |
| 290 | A subset of metastatic pancreatic ductal adenocarcinomas depends quantitatively on oncogenic Kras/Mek/Erk-induced hyperactive mTOR signalling. *Gut*, **2016**, 65, 647-57 | 19.2 | 40 |
| 289 | The global gene expression profile of the secondary transition during pancreatic development. *Mechanisms of Development*, **2016**, 139, 51-64 | 1.7 | 19 |
| 288 | Bayesian Model Selection Methods and Their Application to Biological ODE Systems. *Studies in Mechanobiology, Tissue Engineering and Biomaterials*, **2016**, 243-268 | 0.5 | 8 |
| 287 | destiny: diffusion maps for large-scale single-cell data in R. *Bioinformatics*, **2016**, 32, 1241-3 | 7.2 | 301 |
| 286 | Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. *Cell Systems*, **2016**, 2, 49-58 | 10.6 | 11 |
| 285 | Unbiased Prediction and Feature Selection in High-Dimensional Survival Regression. *Journal of Computational Biology*, **2016**, 23, 279-90 | 1.7 | 16 |
| 284 | Epigenetic germline inheritance of diet-induced obesity and insulin resistance. *Nature Genetics*, **2016**, 48, 497-9 | 36.3 | 211 |
| 283 | Label-free cell cycle analysis for high-throughput imaging flow cytometry. *Nature Communications*, **2016**, 7, 10256 | 17.4 | 156 |
| 282 | Interleukin-4 and interferon-□orchestrate an epithelial polarization in the airways. *Mucosal Immunology*, **2016**, 9, 917-26 | 9.2 | 44 |
| 281 | Inference for Stochastic Chemical Kinetics Using Moment Equations and System Size Expansion. *PLoS Computational Biology*, **2016**, 12, e1005030 | 5 | 51 |
| 280 | Pitchfork and Gprasp2 Target Smoothened to the Primary Cilium for Hedgehog Pathway Activation. *PLoS ONE*, **2016**, 11, e0149477 | 3.7 | 18 |
| 279 | miTALOS v2: Analyzing Tissue Specific microRNA Function. *PLoS ONE*, **2016**, 11, e0151771 | 3.7 | 47 |
| 278 | MicroRNA-138 promotes acquired alkylator resistance in glioblastoma by targeting the Bcl-2-interacting mediator BIM. *Oncotarget*, **2016**, 7, 12937-50 | 3.3 | 47 |
| 277 | Inferring catalysis in biological systems. *IET Systems Biology*, **2016**, 10, 210-218 | 1.4 | 1 |
| 276 | Mitosis Detection in Intestinal Crypt Images with Hough Forest and Conditional Random Fields. *Lecture Notes in Computer Science*, **2016**, 287-295 | 0.9 | |
| 275 | CERENA: ChEmical REaction Network Analyzer--A Toolbox for the Simulation and Analysis of Stochastic Chemical Kinetics. *PLoS ONE*, **2016**, 11, e0146732 | 3.7 | 28 |
| 274 | A novel molecular disease classifier for psoriasis and eczema. *Experimental Dermatology*, **2016**, 25, 767-74 | 4 | 29 |

| | | | |
|---|---|---|---|
| 273 | Software tools for single-cell tracking and quantification of cellular and molecular properties. *Nature Biotechnology*, **2016**, 34, 703-6 | 44.5 | 108 |
| 272 | Separation of Uncorrelated Stationary time series using Autocovariance Matrices. *Journal of Time Series Analysis*, **2016**, 37, 337-354 | 0.8 | 25 |
| 271 | Quantitative comparison of competing PDE models for Pomlp dynamics in fission yeast * *The authors acknowledge financial support from the Postdoctoral Fellowship Program (PFP) of the Helmholtz Zentrum Munchen.. *IFAC-PapersOnLine*, **2016**, 49, 264-269 | 0.7 | 2 |
| 270 | Metabolomics reveals effects of maternal smoking on endogenous metabolites from lipid metabolism in cord blood of newborns. *Metabolomics*, **2016**, 12, 76 | 4.7 | 13 |
| 269 | Computational approaches for systems metabolomics. *Current Opinion in Biotechnology*, **2016**, 39, 198-206 | 11.4 | 42 |
| 268 | Metabolomics screening identifies reduced L-carnitine to be associated with progressive emphysema. *Clinical Science*, **2016**, 130, 273-87 | 6.5 | 28 |
| 267 | Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. *Nature Biotechnology*, **2015**, 33, 155-60 | 44.5 | 778 |
| 266 | Fast clonal expansion and limited neural stem cell self-renewal in the adult subependymal zone. *Nature Neuroscience*, **2015**, 18, 490-2 | 25.5 | 138 |
| 265 | Identifying latent dynamic components in biological systems. *IET Systems Biology*, **2015**, 9, 193-203 | 1.4 | 4 |
| 264 | Transcriptional Mechanisms of Proneural Factors and REST in Regulating Neuronal Reprogramming of Astrocytes. *Cell Stem Cell*, **2015**, 17, 74-88 | 18 | 118 |
| 263 | Multi-omic signature of body weight change: results from a population-based cohort study. *BMC Medicine*, **2015**, 13, 48 | 11.4 | 51 |
| 262 | Metabolism gene signatures and surgical site infections in abdominal surgery. *International Journal of Surgery*, **2015**, 14, 67-74 | 7.5 | 2 |
| 261 | Neurodevelopment. Live imaging of adult neural stem cell behavior in the intact and injured zebrafish brain. *Science*, **2015**, 348, 789-93 | 33.3 | 125 |
| 260 | Next-generation sequencing reveals novel differentially regulated mRNAs, lncRNAs, miRNAs, sdRNAs and a piRNA in pancreatic cancer. *Molecular Cancer*, **2015**, 14, 94 | 42.1 | 171 |
| 259 | Network plasticity of pluripotency transcription factors in embryonic stem cells. *Nature Cell Biology* , **2015**, 17, 1235-46 | 23.4 | 98 |
| 258 | Stem-cell-like properties and epithelial plasticity arise as stable traits after transient Twist1 activation. *Cell Reports*, **2015**, 10, 131-9 | 10.6 | 118 |
| 257 | SimiRa: A tool to identify coregulation between microRNAs and RNA-binding proteins. *RNA Biology*, **2015**, 12, 998-1009 | 4.8 | 12 |
| 256 | Reconstructing gene regulatory dynamics from high-dimensional single-cell snapshot data. *Bioinformatics*, **2015**, 31, i89-96 | 7.2 | 106 |

| | | | |
|---|---|---|---|
| 255 | RAMONA: a Web application for gene set analysis on multilevel omics data. *Bioinformatics*, **2015**, 31, 128-30 | 7.2 | 6 |
| 254 | Network-based approach for analyzing intra- and interfluid metabolite associations in human blood, urine, and saliva. *Journal of Proteome Research*, **2015**, 14, 1183-94 | 5.6 | 33 |
| 253 | Atrx promotes heterochromatin formation at retrotransposons. *EMBO Reports*, **2015**, 16, 836-50 | 6.5 | 79 |
| 252 | Inference of spatiotemporal effects on cellular state transitions from time-lapse microscopy. *BMC Systems Biology*, **2015**, 9, 61 | 3.5 | 3 |
| 251 | MicroRNA-Target Network Inference and Local Network Enrichment Analysis Identify Two microRNA Clusters with Distinct Functions in Head and Neck Squamous Cell Carcinoma. *International Journal of Molecular Sciences*, **2015**, 16, 30204-22 | 6.3 | 10 |
| 250 | Integrative Analysis of MicroRNA and mRNA Data Reveals an Orchestrated Function of MicroRNAs in Skeletal Myocyte Differentiation in Response to TNF-α or IGF1. *PLoS ONE*, **2015**, 10, e0135284 | 3.7 | 17 |
| 249 | Diffusion maps for high-dimensional single-cell analysis of differentiation data. *Bioinformatics*, **2015** , 31, 2989-98 | 7.2 | 378 |
| 248 | Opposing effects of allogrooming on disease transmission in ant societies. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2015**, 370, | 5.8 | 33 |
| 247 | Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. *Cell Stem Cell*, **2015**, 16, 712-24 | 18 | 286 |
| 246 | Quantification of regenerative potential in primary human mammary epithelial cells. *Development (Cambridge)*, **2015**, 142, 3239-51 | 6.6 | 86 |
| 245 | Gender-specific pathway differences in the human serum metabolome. *Metabolomics*, **2015**, 11, 1815-1833 | 4.7 | 130 |
| 244 | Anatomic-landmark detection using graphical context modelling **2015**, | | 1 |
| 243 | Decoding the regulatory network of early blood development from single-cell gene expression measurements. *Nature Biotechnology*, **2015**, 33, 269-276 | 44.5 | 268 |
| 242 | Model selection using limiting distributions of second-order blind source separation algorithms. *Signal Processing*, **2015**, 113, 95-103 | 4.4 | 22 |
| 241 | Data-Driven Modelling of Biological Multi-Scale Processes. *Journal of Coupled Systems and Multiscale Dynamics*, **2015**, 3, 101-121 | | 25 |
| 240 | The Human Blood Metabolome-Transcriptome Interface. *PLoS Genetics*, **2015**, 11, e1005274 | 6 | 65 |
| 239 | A critical period for postnatal adaptive plasticity in a model of motor axon miswiring. *PLoS ONE*, **2015**, 10, e0123643 | 3.7 | 5 |
| 238 | An Affine Equivariant Robust Second-Order BSS Method. *Lecture Notes in Computer Science*, **2015**, 328-335 | 0.9 | 2 |

| | | | |
|---|---|---|---|
| 237 | Approximate Bayesian Computation for Stochastic Single-Cell Time-Lapse Data Using Multivariate Test Statistics. *Lecture Notes in Computer Science*, **2015**, 52-63 | 0.9 | 3 |
| 236 | Method of conditional moments (MCM) for the Chemical Master Equation: a unified framework for the method of moments and hybrid stochastic-deterministic models. *Journal of Mathematical Biology*, **2014**, 69, 687-735 | 2 | 72 |
| 235 | Probabilistic PCA of censored data: accounting for uncertainties in the visualization of high-throughput single-cell qPCR data. *Bioinformatics*, **2014**, 30, 1867-75 | 7.2 | 16 |
| 234 | An atlas of genetic influences on human blood metabolites. *Nature Genetics*, **2014**, 46, 543-550 | 36.3 | 695 |
| 233 | Hypothalamic miR-103 protects from hyperphagic obesity in mice. *Journal of Neuroscience*, **2014**, 34, 10659-74 | 6.6 | 50 |
| 232 | Bayesian blind source separation for data with network structure. *Journal of Computational Biology*, **2014**, 21, 855-65 | 1.7 | 3 |
| 231 | Cytokine-regulated GADD45G induces differentiation and lineage selection in hematopoietic stem cells. *Stem Cell Reports*, **2014**, 3, 34-43 | 8 | 34 |
| 230 | Parameterizing cell-to-cell regulatory heterogeneities via stochastic transcriptional profiles. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E626-35 | 11.5 | 29 |
| 229 | miR-335 promotes mesendodermal lineage segregation and shapes a transcription factor gradient in the endoderm. *Development (Cambridge)*, **2014**, 141, 514-25 | 6.6 | 16 |
| 228 | Mouse IDGenes: a reference database for genetic interactions in the developing mouse brain. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014, | 5 | 2 |
| 227 | Allergic contact dermatitis in psoriasis patients: typical, delayed, and non-interacting. *PLoS ONE*, **2014**, 9, e101814 | 3.7 | 24 |
| 226 | Proteome-wide analysis reveals an age-associated cellular phenotype of in situ aged human fibroblasts. *Aging*, **2014**, 6, 856-78 | 5.6 | 46 |
| 225 | ODE constrained mixture modelling: a method for unraveling subpopulation structures and dynamics. *PLoS Computational Biology*, **2014**, 10, e1003686 | 5 | 31 |
| 224 | Feature ranking of type 1 diabetes susceptibility genes improves prediction of type 1 diabetes. *Diabetologia*, **2014**, 57, 2521-9 | 10.3 | 85 |
| 223 | Uncertainty Analysis for Non-identifiable Dynamical Systems: Profile Likelihoods, Bootstrapping and More. *Lecture Notes in Computer Science*, **2014**, 61-72 | 0.9 | 19 |
| 222 | MCA: Multiresolution Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data. *BMC Bioinformatics*, **2014**, 15, 240 | 3.6 | 9 |
| 221 | Intraindividual genome expression analysis reveals a specific molecular signature of psoriasis and eczema. *Science Translational Medicine*, **2014**, 6, 244ra90 | 17.5 | 128 |
| 220 | Novel genetic associations with serum level metabolites identified by phenotype set enrichment analyses. *Human Molecular Genetics*, **2014**, 23, 5847-57 | 5.6 | 23 |

| | | | |
|---|---|---|---|
| 219 | Radial Basis Function Approximations of Bayesian Parameter Posterior Densities for Uncertainty Analysis. *Lecture Notes in Computer Science*, **2014**, 73-85 | 0.9 | 3 |
| 218 | Metabolite profiling reveals new insights into the regulation of serum urate in humans. *Metabolomics*, **2014**, 10, 141-151 | 4.7 | 36 |
| 217 | A strategy to find gene combinations that identify children who progress rapidly to type 1 diabetes after islet autoantibody seroconversion. *Acta Diabetologica*, **2014**, 51, 403-11 | 3.9 | 18 |
| 216 | Posttranscriptional regulatory networks: from expression profiling to integrative analysis of mRNA and microRNA data. *Methods in Molecular Biology*, **2014**, 1160, 165-88 | 1.4 | 8 |
| 215 | Centroid Clustering of Cellular Lineage Trees. *Lecture Notes in Computer Science*, **2014**, 15-29 | 0.9 | 3 |
| 214 | Effects of smoking and smoking cessation on human serum metabolite profile: results from the KORA cohort study. *BMC Medicine*, **2013**, 11, 60 | 11.4 | 77 |
| 213 | Sharpening of expression domains induced by transcription and microRNA regulation within a spatio-temporal model of mid-hindbrain boundary formation. *BMC Systems Biology*, **2013**, 7, 48 | 3.5 | 12 |
| 212 | Metabolomic profiles in individuals with negative affectivity and social inhibition: a population-based study of Type D personality. *Psychoneuroendocrinology*, **2013**, 38, 1299-309 | 5 | 23 |
| 211 | An automatic method for robust and fast cell detection in bright field images from high-throughput microscopy. *BMC Bioinformatics*, **2013**, 14, 297 | 3.6 | 71 |
| 210 | Modeling of 2D diffusion processes based on microscopy data: parameter estimation and practical identifiability analysis. *BMC Bioinformatics*, **2013**, 14 Suppl 10, S7 | 3.6 | 13 |
| 209 | Dependent component analysis. *Eurasip Journal on Advances in Signal Processing*, **2013**, 2013, | 1.9 | 2 |
| 208 | Visualizing edge-edge relations in graphs **2013**, | | 4 |
| 207 | Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54 | 36.3 | 505 |
| 206 | Wound-healing growth factor, basic FGF, induces Erk1/2-dependent mechanical hyperalgesia. *Pain*, **2013**, 154, 2216-2226 | 8 | 27 |
| 205 | High-dimensional Bayesian parameter estimation: case study for a model of JAK2/STAT5 signaling. *Mathematical Biosciences*, **2013**, 246, 293-304 | 3.9 | 43 |
| 204 | Integrative genetic and metabolite profiling analysis suggests altered phosphatidylcholine metabolism in asthma. *Allergy: European Journal of Allergy and Clinical Immunology*, **2013**, 68, 629-36 | 9.3 | 57 |
| 203 | Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. *Nature Cell Biology*, **2013**, 15, 363-72 | 23.4 | 221 |
| 202 | Live imaging of astrocyte responses to acute injury reveals selective juxtavascular proliferation. *Nature Neuroscience*, **2013**, 16, 580-6 | 25.5 | 271 |

| | | | |
|---|---|---|---|
| 201 | Statistical methods for the analysis of high-throughput metabolomics data. *Computational and Structural Biotechnology Journal*, **2013**, 4, e201301009 | 6.8 | 176 |
| 200 | iVUN: interactive Visualization of Uncertain biochemical reaction Networks. *BMC Bioinformatics*, **2013**, 14 Suppl 19, S2 | 3.6 | 5 |
| 199 | A modular framework for gene set analysis integrating multilevel omics data. *Nucleic Acids Research* , **2013**, 41, 9622-33 | 20.1 | 27 |
| 198 | Truth-Content and Phase Transitions of Random Boolean Networks with Generic Logics. *SIAM Journal on Applied Dynamical Systems*, **2013**, 12, 315-351 | 2.8 | 1 |
| 197 | The human transcriptome is enriched for miRNA-binding sites located in cooperativity-permitting distance. *RNA Biology*, **2013**, 10, 1125-35 | 4.8 | 30 |
| 196 | A Vine-copula Based Adaptive MCMC Sampler for Efficient Inference of Dynamical Systems. *Bayesian Analysis*, **2013**, 8, | 2.3 | 15 |
| 195 | Joining forces of Bayesian and frequentist methodology: a study for inference in the presence of non-identifiability. *Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences*, **2013**, 371, 20110544 | 3 | 62 |
| 194 | Lessons learned from quantitative dynamical modeling in systems biology. *PLoS ONE*, **2013**, 8, e74335 | 3.7 | 174 |
| 193 | Multi-scale modeling of GMP differentiation based on single-cell genealogies. *FEBS Journal*, **2012**, 279, 3488-500 | 5.7 | 15 |
| 192 | ICA over finite fields□Separability and algorithms. *Signal Processing*, **2012**, 92, 1796-1808 | 4.4 | 24 |
| 191 | The signal separation evaluation campaign (2007□010): Achievements and remaining challenges. *Signal Processing*, **2012**, 92, 1928-1936 | 4.4 | 95 |
| 190 | Systematic Complexity Reduction of Signaling Models and Application to a CD95 Signaling Model for Apoptosis **2012**, 57-84 | | |
| 189 | The dynamic range of the human metabolome revealed by challenges. *FASEB Journal*, **2012**, 26, 2607-19 | 0.9 | 226 |
| 188 | Bayesian independent component analysis recovers pathway signatures from blood metabolomics data. *Journal of Proteome Research*, **2012**, 11, 4120-31 | 5.6 | 18 |
| 187 | Identification and quantification of 1-hydroxybutene-2-yl mercapturic acid in human urine by UPLC-HILIC-MS/MS as a novel biomarker for 1,3-butadiene exposure. *Chemical Research in Toxicology*, **2012**, 25, 1565-7 | 4 | 12 |
| 186 | A strategy for combining minor genetic susceptibility genes to improve prediction of disease in type 1 diabetes. *Genes and Immunity*, **2012**, 13, 549-55 | 4.4 | 54 |
| 185 | On the hypothesis-free testing of metabolite ratios in genome-wide and metabolome-wide association studies. *BMC Bioinformatics*, **2012**, 13, 120 | 3.6 | 70 |
| 184 | Bayesian model selection validates a biokinetic model for zirconium processing in humans. *BMC Systems Biology*, **2012**, 6, 95 | 3.5 | 17 |

| | | | |
|---|---|---|---|
| 183 | Stability and multiattractor dynamics of a toggle switch based on a two-stage model of stochastic gene expression. *Biophysical Journal*, **2012**, 102, 19-29 | 2.9 | 61 |
| 182 | Uniqueness of linear factorizations into independent subspaces. *Journal of Multivariate Analysis*, **2012**, 112, 48-62 | 1.4 | 4 |
| 181 | Body fat free mass is associated with the serum metabolite profile in a population-based study. *PLoS ONE*, **2012**, 7, e40009 | 3.7 | 77 |
| 180 | The Sox17-mCherry fusion mouse line allows visualization of endoderm and vascular endothelial development. *Genesis*, **2012**, 50, 496-505 | 1.9 | 25 |
| 179 | Social transfer of pathogenic fungus promotes active immunisation in ant colonies. *PLoS Biology*, **2012**, 10, e1001300 | 9.7 | 126 |
| 178 | A novel approach for resolving differences in single-cell gene expression patterns from zygote to blastocyst. *Bioinformatics*, **2012**, 28, i626-i632 | 7.2 | 44 |
| 177 | Specific temperature-induced perturbations of secondary mRNA structures are associated with the cold-adapted temperature-sensitive phenotype of influenza A virus. *RNA Biology*, **2012**, 9, 1266-74 | 4.8 | 14 |
| 176 | A unilateral negative feedback loop between miR-200 microRNAs and Sox2/E2F3 controls neural progenitor cell-cycle exit and differentiation. *Journal of Neuroscience*, **2012**, 32, 13292-308 | 6.6 | 83 |
| 175 | Mining the unknown: a systems approach to metabolite identification combining genetic and metabolic information. *PLoS Genetics*, **2012**, 8, e1003005 | 6 | 126 |
| 174 | PhenomiR: microRNAs in human diseases and biological processes. *Methods in Molecular Biology*, **2012**, 822, 249-60 | 1.4 | 51 |
| 173 | Joint Diagonalization of Several Scatter Matrices for ICA. *Lecture Notes in Computer Science*, **2012**, 172-179 | 0.9 | 2 |
| 172 | Bayesian Fuzzy Clustering of Colored Graphs. *Lecture Notes in Computer Science*, **2012**, 528-535 | 0.9 | 2 |
| 171 | Bayesian Inference of Latent Causes in Gene Regulatory Dynamics. *Lecture Notes in Computer Science*, **2012**, 520-527 | 0.9 | |
| 170 | To Infinity and Beyond: On ICA over Hilbert Spaces. *Lecture Notes in Computer Science*, **2012**, 180-187 | 0.9 | |
| 169 | An ensemble approach for inferring semi-quantitative regulatory dynamics for the differentiation of mouse embryonic stem cells using prior knowledge. *Advances in Experimental Medicine and Biology*, **2012**, 736, 247-60 | 3.6 | 4 |
| 168 | Systems Biology Meets Metabolism **2012**, 281-313 | | 1 |
| 167 | Uniqueness of Non-Gaussianity-Based Dimension Reduction. *IEEE Transactions on Signal Processing*, **2011**, 59, 4478-4482 | 4.8 | 7 |
| 166 | The nature and perception of fluctuations in human musical rhythms. *PLoS ONE*, **2011**, 6, e26457 | 3.7 | 55 |

| | | | |
|---|---|---|---|
| 165 | Gaussian graphical modeling reveals specific lipid correlations in glioblastoma cells **2011**, | | 1 |
| 164 | The Heckscher–Ohlin model and the network structure of international trade. *International Review of Economics and Finance*, **2011**, 20, 135-145 | 2.8 | 32 |
| 163 | Theoretical analysis of time-to-peak responses in biological reaction networks. *Bulletin of Mathematical Biology*, **2011**, 73, 978-1003 | 2.1 | 4 |
| 162 | Effective parameters determining the information flow in hierarchical biological systems. *Bulletin of Mathematical Biology*, **2011**, 73, 706-25 | 2.1 | 4 |
| 161 | MicroRNAs coordinately regulate protein complexes. *BMC Systems Biology*, **2011**, 5, 136 | 3.5 | 48 |
| 160 | Gaussian graphical modeling reconstructs pathway reactions from high-throughput metabolomics data. *BMC Systems Biology*, **2011**, 5, 21 | 3.5 | 207 |
| 159 | Steady-state robustness of qualitative gene regulation networks. *International Journal of Robust and Nonlinear Control*, **2011**, 21, 1742-1758 | 3.6 | 3 |
| 158 | Dynamic mathematical modeling of IL13-induced signaling in Hodgkin and primary mediastinal B-cell lymphoma allows prediction of therapeutic targets. *Cancer Research*, **2011**, 71, 693-704 | 10.1 | 61 |
| 157 | Dynamic regimes of random fuzzy logic networks. *New Journal of Physics*, **2011**, 13, 013041 | 2.9 | 1 |
| 156 | Vertex centralities in input-output networks reveal the structure of modern economies. *Physical Review E*, **2011**, 83, 046127 | 2.4 | 82 |
| 155 | Huge splicing frequency in human Y chromosomal UTY gene. *OMICS A Journal of Integrative Biology*, **2011**, 15, 141-54 | 3.8 | 10 |
| 154 | MIPS: curated databases and comprehensive secondary data resources in 2010. *Nucleic Acids Research*, **2011**, 39, D220-4 | 20.1 | 65 |
| 153 | Complex principal component and correlation structure of 16 yeast genomic variables. *Molecular Biology and Evolution*, **2011**, 28, 2501-12 | 8.3 | 9 |
| 152 | miTALOS: analyzing the tissue-specific regulation of signaling pathways by human and mouse microRNAs. *Rna*, **2011**, 17, 809-19 | 5.8 | 44 |
| 151 | Discovery of sexual dimorphisms in metabolic and genetic biomarkers. *PLoS Genetics*, **2011**, 7, e10022156 | | 256 |
| 150 | Hierarchical differentiation of myeloid progenitors is encoded in the transcription factor network. *PLoS ONE*, **2011**, 6, e22649 | 3.7 | 103 |
| 149 | Tissue-specific target analysis of disease-associated microRNAs in human signaling pathways. *PLoS ONE*, **2010**, 5, e11154 | 3.7 | 14 |
| 148 | The structure of borders in a small world. *PLoS ONE*, **2010**, 5, e15422 | 3.7 | 107 |

| | | | |
|---|---|---|---|
| 147 | From Binary to Multivalued to Continuous Models: The lac Operon as a Case Study. *Journal of Integrative Bioinformatics*, **2010**, 7, | 3.8 | 8 |
| 146 | MicroRNA loss enhances learning and memory in mice. *Journal of Neuroscience*, **2010**, 30, 14835-42 | 6.6 | 244 |
| 145 | Patterns of subnet usage reveal distinct scales of regulation in the transcriptional regulatory network of Escherichia coli. *PLoS Computational Biology*, **2010**, 6, e1000836 | 5 | 14 |
| 144 | . *IEEE Transactions on Circuits and Systems I: Regular Papers*, **2010**, 57, 1463-1474 | 3.9 | 6 |
| 143 | PhenomiR: a knowledgebase for microRNA expression in diseases and biological processes. *Genome Biology*, **2010**, 11, R6 | 18.3 | 207 |
| 142 | The a(d) coefficient as a descriptive measure of the within-group agreement of ratings. *British Journal of Mathematical and Statistical Psychology*, **2010**, 63, 341-60 | 2.8 | 4 |
| 141 | Information-Theoretic Model Selection for Independent Components. *Lecture Notes in Computer Science*, **2010**, 254-262 | 0.9 | |
| 140 | Odefy--from discrete to continuous models. *BMC Bioinformatics*, **2010**, 11, 233 | 3.6 | 84 |
| 139 | Structuring heterogeneous biological information using fuzzy clustering of k-partite graphs. *BMC Bioinformatics*, **2010**, 11, 522 | 3.6 | 16 |
| 138 | Knowledge-based matrix factorization temporally resolves the cellular responses to IL-6 stimulation. *BMC Bioinformatics*, **2010**, 11, 585 | 3.6 | 10 |
| 137 | Intronic microRNAs support their host genes by mediating synergistic and antagonistic regulatory effects. *BMC Genomics*, **2010**, 11, 224 | 4.5 | 106 |
| 136 | Biologically meaningful update rules increase the critical connectivity of generalized Kauffman networks. *Journal of Theoretical Biology*, **2010**, 266, 436-48 | 2.3 | 5 |
| 135 | From binary to multivalued to continuous models: the lac operon as a case study. *Journal of Integrative Bioinformatics*, **2010**, 7, | 3.8 | 7 |
| 134 | The 2010 Signal Separation Evaluation Campaign (SiSEC2010): Audio Source Separation. *Lecture Notes in Computer Science*, **2010**, 114-122 | 0.9 | 17 |
| 133 | Second Order Subspace Analysis and Simple Decompositions. *Lecture Notes in Computer Science*, **2010**, 370-377 | 0.9 | 4 |
| 132 | Robust Second-Order Source Separation Identifies Experimental Responses in Biomedical Imaging. *Lecture Notes in Computer Science*, **2010**, 466-473 | 0.9 | 4 |
| 131 | ICA over Finite Fields. *Lecture Notes in Computer Science*, **2010**, 645-652 | 0.9 | 6 |
| 130 | The 2010 Signal Separation Evaluation Campaign (SiSEC2010): Biomedical Source Separation. *Lecture Notes in Computer Science*, **2010**, 123-130 | 0.9 | 2 |

| | | | |
|---|---|---|---|
| 129 | Second-Order Source Separation Based on Prior Knowledge Realized in a Graph Model. *Lecture Notes in Computer Science*, **2010**, 434-441 | 0.9 | 6 |
| 128 | Robust stability analysis and design under consideration of multiple feedback loops of the tryptophan regulatory network of Escherichia coli. *Advances in Experimental Medicine and Biology*, **2010**, 680, 189-97 | 3.6 | |
| 127 | Hypergraphs and cellular networks. *PLoS Computational Biology*, **2009**, 5, e1000385 | 5 | 209 |
| 126 | Spatial analysis of expression patterns predicts genetic interactions at the mid-hindbrain boundary. *PLoS Computational Biology*, **2009**, 5, e1000569 | 5 | 33 |
| 125 | Transforming Boolean models to continuous models: methodology and application to T-cell receptor signaling. *BMC Systems Biology*, **2009**, 3, 98 | 3.5 | 158 |
| 124 | Reconstruction of graphs based on random walks. *Theoretical Computer Science*, **2009**, 410, 3826-3838 | 1.1 | 3 |
| 123 | ICA, kernel methods and nonnegativity: New paradigms for dynamical component analysis of fMRI data. *Engineering Applications of Artificial Intelligence*, **2009**, 22, 497-504 | 7.2 | 7 |
| 122 | Blind source separation techniques for the decomposition of multiply labeled fluorescence images. *Biophysical Journal*, **2009**, 96, 3791-800 | 2.9 | 88 |
| 121 | Blind Source Separation Techniques For The Decomposition Of Multiply Labeled Fluorescence Images. *Biophysical Journal*, **2009**, 96, 32a | 2.9 | 3 |
| 120 | Zebrafish reward mutants reveal novel transcripts mediating the behavioral effects of amphetamine. *Genome Biology*, **2009**, 10, R81 | 18.3 | 62 |
| 119 | Soft Dimension Reduction for ICA by Joint Diagonalization on the Stiefel Manifold. *Lecture Notes in Computer Science*, **2009**, 354-361 | 0.9 | 18 |
| 118 | Estimating Hidden Influences in Metabolic and Gene Regulatory Networks. *Lecture Notes in Computer Science*, **2009**, 387-394 | 0.9 | 2 |
| 117 | Blind Decomposition of Spectral Imaging Microscopy: A Study on Artificial and Real Test Data. *Lecture Notes in Computer Science*, **2009**, 548-556 | 0.9 | 3 |
| 116 | Hierarchical Extraction of Independent Subspaces of Unknown Dimensions. *Lecture Notes in Computer Science*, **2009**, 259-266 | 0.9 | 5 |
| 115 | Analyzing M-CSF dependent monocyte/macrophage differentiation: expression modes and meta-modes derived from an independent component analysis. *BMC Bioinformatics*, **2008**, 9, 100 | 3.6 | 19 |
| 114 | An evolutionary and structural characterization of mammalian protein complex organization. *BMC Genomics*, **2008**, 9, 629 | 4.5 | 18 |
| 113 | A robust model for spatiotemporal dependencies. *Neurocomputing*, **2008**, 71, 2209-2216 | 5.4 | 9 |
| 112 | Hybridizing sparse component analysis with genetic algorithms for microarray analysis. *Neurocomputing*, **2008**, 71, 2356-2376 | 5.4 | 11 |

| | | | |
|---|---|---|---|
| 111 | Erythropoietin enhances hippocampal long-term potentiation and memory. *BMC Biology*, **2008**, 6, 37 | 7.3 | 102 |
| 110 | Money Circulation, Trackable Items, and the Emergence of Universal Human Mobility Patterns. *IEEE Pervasive Computing*, **2008**, 7, 28-35 | 1.3 | 45 |
| 109 | Knowledge-based gene expression classification via matrix factorization. *Bioinformatics*, **2008**, 24, 1688-97 | 7.2 | 30 |
| 108 | Gene regulatory networks simplified by nonlinear balanced truncation **2008**, | | 4 |
| 107 | Episode-specific differential gene expression of peripheral blood mononuclear cells in rapid cycling supports novel treatment approaches. *Molecular Medicine*, **2008**, 14, 546-52 | 6.2 | 24 |
| 106 | Effective Emission Tomography Image Reconstruction Algorithms for SPECT Data. *Lecture Notes in Computer Science*, **2008**, 741-748 | 0.9 | 25 |
| 105 | Sparse Nonnegative Matrix Factorization with Genetic Algorithms for Microarray Analysis. *Neural Networks (IJCNN), International Joint Conference on*, **2007**, | | 11 |
| 104 | Joint low-rank approximation for extracting non-Gaussian subspaces. *Signal Processing*, **2007**, 87, 1890-1903 | 4.4 | 9 |
| 103 | A bilinear algorithm for sparse representations. *Computational Optimization and Applications*, **2007**, 38, 249-259 | 1.4 | 6 |
| 102 | Sparse Component Analysis: a New Tool for Data Mining. *Springer Optimization and Its Applications*, **2007**, 91-116 | 0.4 | 14 |
| 101 | How to extract marker genes from microarray data sets. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, **2007**, 2007, 4215-8 | | 4 |
| 100 | Colored Subspace Analysis **2007**, 121-128 | | 1 |
| 99 | Independent Subspace Analysis Is Unique, Given Irreducibility **2007**, 49-56 | | 5 |
| 98 | Statistical Analysis of Sample-Size Effects in ICA **2007**, 416-425 | | |
| 97 | Exploiting Blind Matrix Decomposition Techniques to Identify Diagnostic Marker Genes. *Lecture Notes in Computer Science*, **2007**, 80-89 | 0.9 | |
| 96 | Blind Matrix Decomposition Via Genetic Optimization of Sparseness and Nonnegativity Constraints. *Lecture Notes in Computer Science*, **2007**, 799-808 | 0.9 | |
| 95 | Pivot Selection Strategies in Jacobi Joint Block-Diagonalization. *Lecture Notes in Computer Science*, **2007**, 177-184 | 0.9 | 5 |
| 94 | A Toolbox for Model-Free Analysis of fMRI Data. *Lecture Notes in Computer Science*, **2007**, 209-217 | 0.9 | 1 |

| | | | |
|---|---|---|---|
| 93 | Identifiability Conditions and Subspace Clustering in Sparse BSS **2007**, 357-364 | | 2 |
| 92 | Blind Matrix Decomposition Techniques to Identify Marker Genes from Microarrays **2007**, 649-656 | | 3 |
| 91 | On the use of simulated annealing to automatically assign decorrelated components in second-order blind source separation. *IEEE Transactions on Biomedical Engineering*, **2006**, 53, 810-20 | 5 | 3 |
| 90 | Separation of water artifacts in 2D NOESY protein spectra using congruent matrix pencils. *Neurocomputing*, **2006**, 69, 497-522 | 5.4 | 7 |
| 89 | Denoising using local projective subspace methods. *Neurocomputing*, **2006**, 69, 1485-1501 | 5.4 | 29 |
| 88 | Median-based clustering for underdetermined blind signal processing. *IEEE Signal Processing Letters*, **2006**, 13, 96-99 | 3.2 | 17 |
| 87 | Robust Sparse Component Analysis Based on a Generalized Hough Transform. *Eurasip Journal on Advances in Signal Processing*, **2006**, 2007, 1 | 1.9 | 6 |
| 86 | Blind source separation based on self-organizing neural network. *Engineering Applications of Artificial Intelligence*, **2006**, 19, 305-311 | 7.2 | 2 |
| 85 | On the use of sparse signal decomposition in the analysis of multi-channel surface electromyograms. *Signal Processing*, **2006**, 86, 603-623 | 4.4 | 19 |
| 84 | Estimating Non-Gaussian Subspaces by Characteristic Functions. *Lecture Notes in Computer Science*, **2006**, 157-164 | 0.9 | 4 |
| 83 | Optimization Algorithms for Sparse Representations and Applications **2006**, 85-99 | | 1 |
| 82 | Uniqueness of Non-Gaussian Subspace Analysis. *Lecture Notes in Computer Science*, **2006**, 917-925 | 0.9 | 7 |
| 81 | Sparse Nonnegative Matrix Factorization Applied to Microarray Data Sets. *Lecture Notes in Computer Science*, **2006**, 254-261 | 0.9 | 4 |
| 80 | Region of Interest Based Independent Component Analysis. *Lecture Notes in Computer Science*, **2006**, 1048-1057 | 0.9 | 1 |
| 79 | Hybridizing Sparse Component Analysis with Genetic Algorithms for Blind Source Separation. *Lecture Notes in Computer Science*, **2005**, 137-148 | 0.9 | 3 |
| 78 | Sparse component analysis and blind source separation of underdetermined mixtures. *IEEE Transactions on Neural Networks*, **2005**, 16, 992-6 | | 211 |
| 77 | Extended Sparse Nonnegative Matrix Factorization. *Lecture Notes in Computer Science*, **2005**, 249-256 | 0.9 | 6 |
| 76 | On model identifiability in analytic postnonlinear ICA. *Neurocomputing*, **2005**, 64, 223-234 | 5.4 | 4 |

| | | | |
|---|---|---|---|
| 75 | A Hybridization of Simulated Annealing and Local PCA for Automatic Component Assignment Within ICA. *Lecture Notes in Computer Science*, **2005**, 1075-1082 | 0.9 | |
| 74 | A Fast and Efficient Method for Compressing fMRI Data Sets. *Lecture Notes in Computer Science*, **2005**, 769-777 | 0.9 | 1 |
| 73 | Functional MRI Analysis by a Novel Spatiotemporal ICA Algorithm. *Lecture Notes in Computer Science*, **2005**, 677-682 | 0.9 | 5 |
| 72 | 3D Spatial Analysis of fMRI Data on a Word Perception Task. *Lecture Notes in Computer Science*, **2004**, 977-984 | 0.9 | 4 |
| 71 | A new concept for separability problems in blind source separation. *Neural Computation*, **2004**, 16, 1827-50 | 2.9 | 27 |
| 70 | Spatial ICA of fMRI data in time windows. *AIP Conference Proceedings*, **2004**, | 0 | 4 |
| 69 | Denoising Using Local ICA and a Generalized Eigendecomposition with Time-Delayed Signals. *Lecture Notes in Computer Science*, **2004**, 993-1000 | 0.9 | 3 |
| 68 | A geometric algorithm for overcomplete linear ICA. *Neurocomputing*, **2004**, 56, 381-398 | 5.4 | 66 |
| 67 | Mobile decision support for transplantation patient data. *International Journal of Medical Informatics*, **2004**, 73, 461-4 | 5.3 | 14 |
| 66 | Uniqueness of complex and multidimensional independent component analysis. *Signal Processing*, **2004**, 84, 951-956 | 4.4 | 29 |
| 65 | Blind Source Separation of Linear Mixtures with Singular Matrices. *Lecture Notes in Computer Science*, **2004**, 121-128 | 0.9 | 4 |
| 64 | Postnonlinear Overcomplete Blind Source Separation Using Sparse Sources. *Lecture Notes in Computer Science*, **2004**, 718-725 | 0.9 | 4 |
| 63 | Second-Order Blind Source Separation Based on Multi-dimensional Autocovariances. *Lecture Notes in Computer Science*, **2004**, 726-733 | 0.9 | 7 |
| 62 | SOMICA and geometric ICA **2003**, | | 1 |
| 61 | A new ica method based on a lattice of the observation space **2003**, | | 1 |
| 60 | Removing water artefacts from 2D protein NMR spectra using GEVD with congruent matrix pencils **2003**, | | 1 |
| 59 | Mathematics in independent component analysis **2003**, | | 2 |
| 58 | Generalizing Geometric ICA to Nonlinear Settings. *Lecture Notes in Computer Science*, **2003**, 687-694 | 0.9 | 0 |

| | | | |
|---|---|---|---|
| 57 | Linear geometric ICA: fundamentals and algorithms. *Neural Computation*, **2003**, 15, 419-39 | 2.9 | 38 |
| 56 | An improved geometric overcomplete blind source separation algorithm. *Lecture Notes in Computer Science*, **2003**, 265-272 | 0.9 | |
| 55 | An Adaptive Approach to Blind Source Separation Using a Self-Organzing Map and a Neural Gas. *Lecture Notes in Computer Science*, **2003**, 695-702 | 0.9 | |
| 54 | Topological Constructions in the o-Graph Calculus. *Mathematische Nachrichten*, **2002**, 241, 170-186 | 0.8 | 1 |
| 53 | Comparison of maximum entropy and minimal mutual information in a nonlinear setting. *Signal Processing*, **2002**, 82, 971-980 | 4.4 | 2 |
| 52 | Overcomplete ICA with a Geometric Algorithm. *Lecture Notes in Computer Science*, **2002**, 1049-1054 | 0.9 | 3 |
| 51 | Pattern Repulsion Revisited. *Lecture Notes in Computer Science*, **2001**, 778-785 | 0.9 | 2 |
| 50 | Denoising using local ICA and kernel-PCA | | 2 |
| 49 | Kernel-PCA denoising of artifact-free protein NMR spectra | | 1 |
| 48 | Blind signal separation into groups of dependent signals using joint block diagonalization | | 19 |
| 47 | anndata: Annotated data | | 6 |
| 46 | CellRank for directed single-cell fate mapping | | 4 |
| 45 | Künstliche Intelligenz und maschinelles Lernen in der Diabetesforschung. *Diabetologe*,1 | 0.2 | |
| 44 | Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies | | 1 |
| 43 | Meeting the challenges of high-dimensional data analysis in immunology | | 1 |
| 42 | destiny – diffusion maps for large-scale single-cell data in R | | 5 |
| 41 | Diffusion pseudotime robustly reconstructs lineage branching | | 12 |
| 40 | Network-based metabolite ratios for an improved functional characterization of genome-wide association study results | | 2 |

| | | |
|---|---|---|
| 39 | Reconstructing cell cycle and disease progression using deep learning | 4 |
| 38 | Scalable parameter estimation for genome-scale biochemical reaction networks | 1 |
| 37 | Scanpy for analysis of large-scale single-cell gene expression data | 9 |
| 36 | Efficient parameterization of large-scale mechanistic models enables drug response prediction for cancer cell lines | 4 |
| 35 | Assessment of batch-correction methods for scRNA-seq data with a new test metric | 15 |
| 34 | Cell-type specific impact of glucocorticoid receptor activation on the developing brain | 2 |
| 33 | Integrated single cell analysis of human lung fibrosis resolves cellular origins of predictive protein signatures in body fluids | 4 |
| 32 | Design and power analysis for multi-sample single cell genomics experiments | 7 |
| 31 | Alterations of multiple alveolar macrophage states in chronic obstructive pulmonary disease | 7 |
| 30 | Swarm Learning as a privacy-preserving machine learning approach for disease classification | 3 |
| 29 | Query to reference single-cell integration with transfer learning | 26 |
| 28 | CellRank for directed single-cell fate mapping | 18 |
| 27 | Learning interpretable latent autoencoder representations with annotations of feature sets | 4 |
| 26 | Single-cell RNA sequencing reveals in vivo signatures of SARS-CoV-2-reactive T cells through reverse phenotyping | 2 |
| 25 | scCODA: A Bayesian model for compositional single-cell data analysis | 5 |
| 24 | Ultra-high sensitivity mass spectrometry quantifies single-cell proteome changes upon perturbation | 46 |
| 23 | Graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells | 23 |
| 22 | Beyond pseudotime: Following T-cell maturation in single-cell RNAseq time series | 2 |

| | | |
|---|---|---|
| 21 | MetaMap: An atlas of metatranscriptomic reads in human disease-related RNA-seq data | 1 |
| 20 | FASTGenomics: An analytical ecosystem for single-cell RNA sequencing data | 4 |
| 19 | Single cell RNA-seq denoising using a deep count autoencoder | 16 |
| 18 | Evaluation of Deep Learning Strategies for Nucleus Segmentation in Fluorescence Images | 17 |
| 17 | An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics | 5 |
| 16 | Generative modeling and latent space arithmetics predict single-cell perturbation response across cell types, studies and species | 10 |
| 15 | scSLAM-seq reveals core features of transcription dynamics in single cells | 2 |
| 14 | EpiScanpy: integrated single-cell epigenomic analysis | 12 |
| 13 | Deep learning does not outperform classical machine learning for cell-type annotation | 11 |
| 12 | Longitudinal single cell transcriptomics reveals Krt8+ alveolar epithelial progenitors in lung regeneration | 19 |
| 11 | Predicting antigen-specificity of single T-cells based on TCR CDR3 regions | 4 |
| 10 | Generalizing RNA velocity to transient cell states through dynamical modeling | 66 |
| 9 | A Sparse Deep Learning Approach for Automatic Segmentation of Human Vasculature in Multispectral Optoacoustic Tomography | 1 |
| 8 | scvi-tools: a library for deep probabilistic analysis of single-cell omics data | 18 |
| 7 | Compositional perturbation autoencoder for single-cell response modeling | 3 |
| 6 | Jointly learning T-cell receptor and transcriptomic information to decipher the immune response | 2 |
| 5 | Learning cell communication from spatial graphs of cells | 4 |
| 4 | Squidpy: a scalable framework for spatial single cell analysis | 26 |

# List of Publications

| | | |
|---|---|---|
| 3 | Over 1000 tools reveal trends in the single-cell RNA-seq analysis landscape | 1 |
| 2 | Multigrate: single-cell multi-omic data integration | 2 |
| 1 | Multi-omics and 3D-imaging reveal bone heterogeneity and unique calvaria cells in neuroinflammation | 1 |