

Jan Baumbach  
Associate Professor  
Department of Mathematics and Computer Science (IMADA)  
Computer Science  
SDU eScience Centre  
Campusvej 55  
5230 Odense M  
Denmark  
E-mail: jbaumbac@imada.sdu.dk  
Phone: +45-6550-2309  
Web address: <http://www.baumbachlab.net>

## Publications

### **Estimating motion artifacts of HR-pQCT scans using automatically derived standard parameters of bone structure- and density-quantification**

Albrecht, E., Bartosik, M., Simon, A., Baumbach, J., Barvencik, F., Amling, M., Oheim, R., Tsoy, O. & von Brackel, F. N., Jul 2026, In: *Bone*. 208, 9 p., 117878.

### **Astrocyte-specific FoxF2 modulates immune and myelin repair: Evidence from multiple sclerosis lesions and an animal model**

Damsbo, K., Reyahi, A., Nik, A. M., Oubounyt, M., Weber, A., Hyrlov, K. H., Kingo, C., Foged, M. L., Waede, M., Baumbach, J., Reynolds, R., Carlsson, P., Illes, Z. & Elkjaer, M. L., Jun 2026, In: *Journal of Neuroimmunology*. 415, 578896.

### **Older adults with osteoarthritis show lower functional performance compared to those with diabetes or hypertension: Evidence from the SHARE dataset**

Rafiei, M., Probul, N., Baumbach, J. & Baumbach, L., Jun 2026, In: *Osteoarthritis and Cartilage Open*. 8, 2, 8 p., 100781.

### **DysRegNet: Patient-specific and confounder-aware dysregulated network inference towards precision therapeutics**

Kersting, J., Lazareva, O., Louadi, Z., Baumbach, J., Blumenthal, D. B. & List, M., Apr 2026, In: *British Journal of Pharmacology*. 183, 8, p. 1709-1724

### **On the power and limits of foundation model image embeddings for privacy-preserving federated learning**

Lohmann, J. J. G., Witte, A., Maier, A., Saak, C. C., Sauter, G., Zimmermann, M., Bonn, S. & Baumbach, J., Mar 2026, In: *Array*. 29, 10 p., 100725.

### **Privacy-preserving federated prediction of health outcomes using multi-center survey data**

Das, S., Rafiei, M., Kammer, P. T., Skou, S. T., Grønne, D. T., Roos, E. M., Hajek, A., König, H.-H., Ullah, M. S., Probul, N., Baumbach, J. & Baumbach, L., 4. Feb 2026, In: *BMC Medical Research Methodology*. 26, 46.

### **Farthest better or nearest worse optimizer: a novel metaheuristic algorithm**

Taheri, A., RahimiZadeh, K., Baumbach, J., Beheshti, A., Zolotareva, O., Al-Betar, M. A., Mirjalili, S. & Gandomi, A. H., Feb 2026, In: *Artificial Intelligence Review*. 59, 2, 41 p., 79.

### **Detection of alternative splicing: deep sequencing or deep learning?**

Hackl, L. M., Neuhaus, F., Ameling, S., Völker, U., Baumbach, J. & Tsoy, O., 1. Jan 2026, In: *Briefings in Bioinformatics*. 27, 1, 12 p., bbaf705.

### **Long-term outcome and predictors for recurrence after medical and interventional treatment of arrhythmias at the UniverSity Heart CenTer Hamburg (TRUST): design and patient profile snapshot of a prospective clinical cohort study**

Obergassel, J., Rieß, J. L., Jaeckle, S., van Elferen, S., Nies, M., Schenker, N., Lemoine, M. D., Welcker, A., Kany, S., Rottner, L., Ismaili, D., Sommerfeld, L. C., Petersen, J., Govorov, K., Schoof, L., Tsoy, O., Baumbach, J., Pecha, S., Zeller, T. & Blankenberg, S. & 6 others, Fabritz, L., Reißmann, B., Ouyang, F., Rillig, A., Metzner, A. & Kirchhof, P., 1. Jan 2026, In: *European Heart Journal Open*. 6, 1, 21 p., oeg002.

### **ViMOP: a user-friendly and field-applicable pipeline for untargeted viral genome nanopore sequencing**

Petersen, N. P., Le, M., Renevey, A., Emua, E., Ryter, S., Annibaldi, G., Camara, J., Boumbaly, S., Erameh, C., Laske, T., Baumbach, J., Lemey, P., Günther, S., Duraffour, S. & Kafetzopoulou, L. E., 1. Jan 2026, In: *Bioinformatics*. 42, 1, 5 p., btaf687.

### **High-Resolution Spatial Map of the Human Facial Sebaceous Gland Reveals Marker Genes and Decodes Sebocyte Differentiation**

Düz, T., Torocsik, D., Simmering, A., Wolf, P., Gallinat, S., Baumbach, J. & Holzscheck, N., Jan 2026, In: *Journal of Investigative Dermatology*. 146, 1, p. 40-54 e14.

### **Privacy-by-Design with Federated Learning will drive future Rare Disease Research**

Süwer, S., Ullah, M. S., Probul, N., Maier, A. & Baumbach, J., Jan 2026, In: *Journal of Neuromuscular Diseases*. 13, 1, p. 6-19

### **A microenvironment-determined risk continuum refines subtyping in meningioma and reveals determinants of machine learning-based tumor classification**

The German "Aggressive Meningiomas" Consortium (KAM), 2026, In: *Nature Genetics*. 58, 2, p. 341–354 58.

### **Drugst.One DREAM—Drug repurposing through expert annotation and modification**

Spindler, L. M., Kersting, J., Manz, Q., Hartung, M., Maier, A., Mamdouh, Z. M., Casas, A. I., Baumbach, J. & List, M., Jul 2026, In: *British Journal of Pharmacology*. 183, 13, p. 3503-3516

### **The power and limits of predicting inter-protein exon-exon interactions using protein 3D structures**

Liebold, J., Del Moral-Morales, A., Manalastas-Cantos, K., Tsoy, O., Kurtz, S., Baumbach, J. & Newaz, K., 2026, In: *Bioinformatics Advances*. 6, 1, 13 p., vbag032.

### **FedscGen: privacy-preserving federated batch effect correction of single-cell RNA sequencing data**

Bakhtiari, M., Bonn, S., Theis, F., Zolotareva, O. & Baumbach, J., Dec 2025, In: *Genome Biology*. 26, 1, 29 p., 216.

### **Phenotypic Changes in a Monocyte Cluster with High Interleukin-1 Beta Expression during Long-Term Anti-CD20 Therapy**

Waede, M., Kingo, C., Damsbo, K., Joergensen, M. U., Oubounyt, M., Gjerstorff, M., Thomassen, M., Baumbach, J., Moeller, J. B., Elkjaer, M. L. & Illes, Z., Dec 2025, In: *Annals of Neurology*. 98, 6, p. 1283-1298

### **Systematic Comparison of Bone Proteome Extraction Methods to Allow for Integrated Proteomics–Metabolomics Correlation**

Wiltzsch, V., Schmidt, J. R., Adamowicz, K., Lauterbach, T., Lehmann, J., Baumbach, J., Laske, T. & Kalkhof, S., 5. Sept 2025, In: *Journal of Proteome Research*. 24, 9, p. 4362-4376

### **Comprehensive benchmark of differential transcript usage analysis for bulk and single-cell RNA sequencing**

Lio, C. T., Düz, T., Hoffmann, M., Willruth, L. L., Baumbach, J., List, M. & Tsoy, O., Sept 2025, In: *NAR Genomics and Bioinformatics*. 7, 3, 13 p., lqaf117.

### **Drug Repurposing for Kala-Azar**

Arsić, B., Ilić, B. S., Maier, A., Hartung, M., Janjić, J., Milićević, J. & Baumbach, J., Aug 2025, In: *Pharmaceutics*. 17, 8, 23 p., 1021.

### **Pathology-oriented multiplexing enables integrative disease mapping**

Kuehl, M., Okabayashi, Y., Wong, M. N., Gernhold, L., Gut, G., Kaiser, N., Schwerk, M., Gräfe, S. K., Ma, F. Y., Tanevski, J., Schäfer, P. S. L., Mezher, S., Sarabia del Castillo, J., Goldbeck-Strieder, T., Zolotareva, O., Hartung, M., Delgado Chaves, F. M., Klinkert, L., Gnirck, A. C. & Spehr, M. & 55 others, Fleck, D., Joodaki, M., Parra, V., Shaigan, M., Diebold, M., Prinz, M., Kranz, J., Kux, J. M., Braun, F., Kretz, O., Wu, H., Grahhammer, F., Heins, S., Zimmermann, M., Haas, F., Kyliès, D., Wanner, N., Czogalla, J., Dumoulin, B., Zolotarev, N., Lindenmeyer, M., Karlson, P., Nyengaard, J. R., Sebode, M., Weidemann, S., Wiech, T., Groene, H. J., Tomas, N. M., Meyer-Schwesinger, C., Kuppe, C., Kramann, R., Karras, A., Bruneval, P., Tharoux, P. L., Pastene, D., Yard, B., Schaub, J. A., McCown, P. J., Pyle, L., Choi, Y. J., Yokoo, T., Baumbach, J., Sáez, P. J., Costa, I., Turner, J. E., Hodgkin, J. B., Saez-Rodríguez, J., Huber, T. B., Bjornstad, P., Kretzler, M., Lenoir, O., Nikolic-Paterson, D. J., Pelkmans, L., Bonn, S. & Puelles, V. G., Aug 2025, In: *Nature*. 644, 8076, p. 516-526

**Privacy-preserving multicenter differential protein abundance analysis with FedProt**

Burankova, Y., Abele, M., Bakhtiari, M., von Toerne, C., Barth, T. K., Schweizer, L., Giesbertz, P., Schmidt, J. R., Kalkhof, S., Müller-Deile, J., van Veelen, P. A., Mohammed, Y., Hammer, E., Arend, L., Adamowicz, K., Laske, T., Hartebrodt, A., Frisch, T., Meng, C. & Matschinske, J. & 11 others, Späth, J., Röttger, R., Schwämmle, V., Hauck, S. M., Lichtenthaler, S. F., Imhof, A., Mann, M., Ludwig, C., Kuster, B., Baumbach, J. & Zolotareva, O., Aug 2025, In: Nature Computational Science. 5, 8, p. 675-688

**DIGGER 2.0: Digging into the functional impact of differential splicing on human and mouse disorders**

Albrecht, E., Pelz, K., Gress, A., Trung, H. N., Kalinina, O. V., Kacprowski, T., Baumbach, J., List, M. & Tsoy, O., 7. Jul 2025, In: Nucleic Acids Research. 53, W1, p. 245-252

**Endogenous dysregulated energy and amino acid metabolism delay scaffold-guided large volume bone regeneration in a diabetic rat model with Leptin receptor deficiency**

Dias, D. B., Chan, W. L., Ellinghaus, A., Fritsche-Guenther, R., Wiebach, J., Bembennek, A., Laske, T., Baumbach, J., Duda, G. N., Kirwan, J. A. & Poh, P. S. P., 1. Jun 2025, In: Acta Biomaterialia. 199, p. 108-119

**Meta-analysis of genomic characteristics for antiviral influenza defective interfering particle prioritization**

Lohmann, J. J. G., Le, M., Alnaji, F. G., Zolotareva, O., Baumbach, J. & Laske, T., 1. Jun 2025, In: NAR Genomics and Bioinformatics. 7, 2, 18 p., lqaf031.

**Synergistic Network Pharmacology: Preclinical Validation and Clinical Safety in Acute Ischemic Stroke**

Casas, A. I., Nogales, C., Szepanowski, R. D., Elbatreek, M. H., Anastasi, E., Sadegh, S., Skelton, J., Frank, B., Wipat, A., Baumbach, J., Kleinschnitz, C. & Schmidt, H. H. H. W., 20. May 2025, In: Journal of the American Heart Association. 14, 10, 16 p., e039098.

**Are Changes in Physical Activity, Pain, and Quality of Life in Patients with Knee Osteoarthritis After Exercise Therapy and Education Beyond Normal Fluctuations? A Comparative Study**

Rafiei, M., Das, S., Roos, E. M., Skou, S. T., Baumbach, J. & Baumbach, L., 13. May 2025, In: Journal of Clinical Medicine. 14, 10, 19 p., 3406.

**Systematic evaluation of normalization approaches in tandem mass tag and label-free protein quantification data using PRONE**

Arend, L., Adamowicz, K., Schmidt, J. R., Burankova, Y., Zolotareva, O., Tsoy, O., Pauling, J. K., Kalkhof, S., Baumbach, J., List, M. & Laske, T., 1. May 2025, In: Briefings in Bioinformatics. 26, 3, 16 p., bba201.

**Personalized Predictions for Changes in Knee Pain Among Patients With Osteoarthritis Participating in Supervised Exercise and Education: Prognostic Model Study**

Rafiei, M., Das, S., Bakhtiari, M., Roos, E. M., Skou, S. T., Grønne, D. T., Baumbach, J. & Baumbach, L., 21. Mar 2025, In: JMIR Rehabilitation and Assistive Technologies. 12, 18 p., e60162.

**A platform for the biomedical application of large language models**

Lobentanzer, S., Feng, S., Bruderer, N., Maier, A., BioChatter Consortium, Wang, C., Baumbach, J., Abreu-Vicente, J., Krehl, N., Ma, Q., Lemberger, T. & Saez-Rodriguez, J., Feb 2025, In: Nature Biotechnology. 43, 2, p. 166-169

**Exploring common mechanisms of adverse drug reactions and disease phenotypes through network-based analysis**

Firoozbakht, F., Elkjaer, M. L., Handy, D. E., Wang, R. S., Chervontseva, Z., Rarey, M., Loscalzo, J., Baumbach, J. & Tsoy, O., Feb 2025, In: Cell Reports Methods. 5, 2, 20 p., 100990.

**Unveiling the interplay between soluble guanylate cyclase activation and redox signalling in stroke pathophysiology and treatment**

Grønning, A. G., Vonhof, S. E., Elbatreek, M., Hamker, A., Szepanowski, R. D., Erkelenz, S. C., Langhauser, F., Egea, J., Lopez, M. G., Baumbach, J., Kleinschnitz, C. & Casas, A. I., Feb 2025, In: Biomedicine and Pharmacotherapy. 183, 11 p., 117829.

### **Transforming literature screening: The emerging role of large language models in systematic reviews**

Delgado-Chaves, F. M., Jennings, M. J., Atalaia, A., Wolff, J., Horvath, R., Mamdouh, Z. M., Baumbach, J. & Baumbach, L., 6. Jan 2025, In: Proceedings of the National Academy of Sciences of the United States of America. 122, 2, 10 p., e2411962122.

### **Transcription factor prediction using protein 3D secondary structures**

Liebold, J., Neuhaus, F., Geiser, J., Kurtz, S., Baumbach, J. & Newaz, K., 1. Jan 2025, In: Bioinformatics. 41, 1, 11 p., btac762.

### **From Literature to Knowledge Graphs to Drug Repurposing**

Delgado-Chaves, F. M., Süwer, S., Bagemihl, K., Dicunta, L., Liebold, J., Baier, S., Rodríguez-Eguren, A., Bueno-Fernandez, C., Cervelló, I., Maier, A., List, M., Baumbach, L. & Baumbach, J., 2025, *REXPO25 Conference*. REPO4EU, 2 p.

### **Comparative evaluation of feature reduction methods for drug response prediction**

Firoozbakht, F., Yousefi, B., Tsoy, O., Baumbach, J. & Schwikowski, B., Dec 2024, In: Scientific Reports. 14, 1, 11 p., 30885.

### **AI in microbiome-related healthcare**

Probul, N., Huang, Z., Saak, C. C., Baumbach, J. & List, M., Nov 2024, In: Microbial Biotechnology. 17, 11, 10 p., e70027.

### **Network medicine-based epistasis detection in complex diseases: Ready for quantum computing**

Hoffmann, M., Poschenrieder, J. M., Incudini, M., Baier, S., Fritz, A., Maier, A., Hartung, M., Hoffmann, C., Trummer, N., Adamowicz, K., Picciani, M., Scheibling, E., Harl, M. V., Lesch, I., Frey, H., Kayser, S., Wissenberg, P., Schwartz, L., Hafner, L. & Acharya, A. & 28 others, Hackl, L., Grabert, G., Lee, S. G., Cho, G., Cloward, M. E., Jankowski, J., Lee, H. K., Tsoy, O., Wenke, N., Pedersen, A. G., Bønnelykke, K., Mandarino, A., Melograna, F., Schulz, L., Climente-González, H., Wilhelm, M., Iapichino, L., Wienbrandt, L., Ellinghaus, D., Van Steen, K., Grossi, M., Furth, P. A., Hennighausen, L., Di Pierro, A., Baumbach, J., Kacprowski, T., List, M. & Blumenthal, D. B., 23. Sept 2024, In: Nucleic Acids Research. 52, 17, p. 10144-10160

### **Prognostic importance of splicing-triggered aberrations of protein complex interfaces in cancer**

Newaz, K., Schaefer, C., Weisel, K., Baumbach, J. & Frishman, D., Sept 2024, In: NAR Genomics and Bioinformatics. 6, 3, 13 p., lqae133.

### **Drugst.One - a plug-and-play solution for online systems medicine and network-based drug repurposing**

Maier, A., Hartung, M., Abovsky, M., Adamowicz, K., Bader, G. D., Baier, S., Blumenthal, D. B., Chen, J., Elkjaer, M. L., Garcia-Hernandez, C., Helmy, M., Hoffmann, M., Jurisica, I., Kotlyar, M., Lazareva, O., Levi, H., List, M., Lobentanzer, S., Loscalzo, J. & Malod-Dognin, N. & 20 others, Manz, Q., Matschinske, J., Mee, M., Oubounyt, M., Pastrello, C., Pico, A. R., Pillich, R. T., Poschenrieder, J. M., Pratt, D., Pržulj, N., Sadegh, S., Saez-Rodriguez, J., Sarkar, S., Shaked, G., Shamir, R., Trummer, N., Turhan, U., Wang, R. S., Zolotareva, O. & Baumbach, J., 5. Jul 2024, In: Nucleic Acids Research. 52, W1, p. W481-W488

### **Single-Cell Multi-Omics Map of Cell Type-Specific Mechanistic Drivers of Multiple Sclerosis Lesions**

Elkjaer, M. L., Hartebrodt, A., Oubounyt, M., Weber, A., Vitved, L., Reynolds, R., Thomassen, M., Rottger, R., Baumbach, J. & Illes, Z., 1. May 2024, In: Neurology(R) neuroimmunology & neuroinflammation. 11, 3, 15 p., e200213.

### **Partial reinforcement optimizer: An evolutionary optimization algorithm[Formula presented]**

Taheri, A., RahimiZadeh, K., Beheshti, A., Baumbach, J., Rao, R. V., Mirjalili, S. & Gandomi, A. H., 15. Mar 2024, In: Expert Systems with Applications. 238, Part F, 20 p., 122070.

### **On the limits of 16S rRNA gene-based metagenome prediction and functional profiling**

Matchado, M. S., Rühlemann, M., Reitmeier, S., Kacprowski, T., Frost, F., Haller, D., Baumbach, J. & List, M., 1. Feb 2024, In: Microbial Genomics. 10, 2, 14 p., 001203.

### **Blood transcriptomics analysis offers insights into variant-specific immune response to SARS-CoV-2**

Hoffmann, M., Willruth, L. L., Dietrich, A., Lee, H. K., Knabl, L., Trummer, N., Baumbach, J., Furth, P. A., Hennighausen, L. & List, M., Feb 2024, In: Scientific Reports. 14, 1, p. 2808 11 p.

### **Inference of differential gene regulatory networks using boosted differential trees**

Galindez, G., List, M., Baumbach, J., Völker, U., Mäder, U., Blumenthal, D. B. & Kacprowski, T., 2024, In: *Bioinformatics Advances*. 4, 1, 20 p., vbae034.

### **Key Proteins for Regeneration in *A. mexicanum*: Transcriptomic Insights From Aged and Juvenile Limbs**

Del Moral-Morales, A., Sámano, C., Ocampo-Cervantes, J. A., Topf, M., Baumbach, J., Hernández, J., Torres-Arciga, K., González-Barrios, R. & Soto-Reyes, E., 2024, In: *Scientifica*. 2024, 5460694.

### **Meta-analysis of proteomics data from osteoblasts, bone, and blood: Insights into druggable targets, active factors, and potential biomarkers for bone biomaterial design**

Schmidt, J. R., Adamowicz, K., Arend, L., Lehmann, J., List, M., Poh, P. S. P., Baumbach, J., Kalkhof, S. & Laske, T., 2024, In: *Journal of Tissue Engineering*. 15, p. 1-26

### **NeDRex-Web: An Interactive Web Tool for Drug Repurposing by Exploring Heterogeneous Molecular Networks**

Maier, A., Rafiei, M., Anastasi, E., Zolotareva, O., Skelton, J., Elkjaer, M. L., Casas, A. I., Nogales, C., Schmidt, H. H. H. W., Kacprowski, T., Blumenthal, D. B., Wipat, A., Sadegh, S. & Baumbach, J., 2024, *2024 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*. IEEE, p. 429-434

### **Proteomic meta-study harmonization, mechanotyping and drug repurposing candidate prediction with ProHarMeD**

Adamowicz, K., Arend, L., Maier, A., Schmidt, J. R., Kuster, B., Tsoy, O., Zolotareva, O., Baumbach, J. & Laske, T., Dec 2023, In: *npj Systems Biology and Applications*. 9, 1, 49.

### **New Enhancing MRI Lesions Associate with IL-17, Neutrophil Degranulation and Integrin Microparticles: Multi-Omics Combined with Frequent MRI in Multiple Sclerosis**

Illes, Z., Jørgensen, M. M., Bæk, R., Bente, L. M., Lauridsen, J. T., Hyrlov, K. H., Aboo, C., Baumbach, J., Kacprowski, T., Cotton, F., Guttman, C. R. G. & Stensballe, A., 28. Nov 2023, In: *Biomedicine*. 11, 12, 21 p., 3170.

### **Inference of differential key regulatory networks and mechanistic drug repurposing candidates from scRNA-seq data with SCANet**

Oubounyt, M., Adlung, L., Patroni, F., Wenke, N. K., Maier, A., Hartung, M., Baumbach, J. & Elkjaer, M. L., Nov 2023, In: *Bioinformatics*. 39, 11, 10 p., btad644.

### **Alternative splicing impacts microRNA regulation within coding regions**

Hackl, L. M., Fenn, A., Louadi, Z., Baumbach, J., Kacprowski, T., List, M. & Tsoy, O., 1. Sept 2023, In: *NAR Genomics and Bioinformatics*. 5, 3, 12 p., lqad081.

### **Multi-scale systems genomics analysis predicts pathways, cell types, and drug targets involved in normative variation in peri-adolescent human cognition**

Pai, S., Hui, S., Weber, P., Narayan, S., Whitley, O., Li, P., Labrie, V., Baumbach, J., Wheeler, A. L. & Bader, G. D., 1. Jul 2023, In: *Cerebral Cortex*. 33, 13, p. 8581-8593

### **A YAP/TAZ-ARHGAP29-RhoA Signaling Axis Regulates Podocyte Protrusions and Integrin Adhesions**

Rogg, M., Maier, J. I., Helmstädter, M., Sammarco, A., Kliewe, F., Kretz, O., Weißer, L., Van Wymersch, C., Findeisen, K., Koessinger, A. L., Tsoy, O., Baumbach, J., Grabbert, M., Werner, M., Huber, T. B., Endlich, N., Schilling, O. & Schell, C., Jul 2023, In: *Cells*. 12, 13, 21 p., 1795.

### **Alternative splicing analysis benchmark with DICAST**

Fenn, A., Tsoy, O., Faro, T., Rößler, F. L. M., Dietrich, A., Kersting, J., Louadi, Z., Lio, C. T., Völker, U., Baumbach, J., Kacprowski, T. & List, M., 1. Jun 2023, In: *NAR Genomics and Bioinformatics*. 5, 2, 10 p., lqad044.

### **Laminarin-triggered defence responses are geographically dependent in natural populations of *Solanum chilense***

Kahlon, P. S., Förner, A., Muser, M., Oubounyt, M., Gigl, M., Hammerl, R., Baumbach, J., Hüchelhoven, R., Dawid, C. & Stam, R., 19. May 2023, In: *Journal of Experimental Botany*. 74, 10, p. 3240-3254

### **TF-Prioritizer: a Java pipeline to prioritize condition-specific transcription factors**

Hoffmann, M., Trummer, N., Schwartz, L., Jankowski, J., Lee, H. K., Willruth, L.-L., Lazareva, O., Yuan, K., Baumgarten, N., Schmidt, F., Baumbach, J., Schulz, M. H., Blumenthal, D. B., Hennighausen, L. & List, M., 3. May 2023, In: *GigaScience*. 12, 15 p., giad026.

### **Hierarchical association of COPD to principal genetic components of biological systems**

Carlin, D. E., Larsen, S. J., Sirupurapu, V., Cho, M. H., Silverman, E. K., Baumbach, J. & Ideker, T., May 2023, In: *PLOS ONE*. 18, 5, 19 p., e0286064.

### **spongEffects: ceRNA modules offer patient-specific insights into the miRNA regulatory landscape**

Boniolo, F., Hoffmann, M., Roggendorf, N., Tercan, B., Baumbach, J., Castro, M. A. A., Robertson, A. G., Saur, D. & List, M., May 2023, In: *Bioinformatics*. 39, 5, 10 p., btad276.

### **Lacking mechanistic disease definitions and corresponding association data hamper progress in network medicine and beyond**

Sadegh, S., Skelton, J., Anastasi, E., Maier, A., Adamowicz, K., Möller, A., Kriege, N. M., Kronberg, J., Haller, T., Kacprowski, T., Wipat, A., Baumbach, J. & Blumenthal, D. B., 25. Mar 2023, In: *Nature Communications*. 14, 1, 15 p., 1662.

### **De-novo reconstruction and identification of transcriptional gene regulatory network modules differentiating single-cell clusters**

Oubounyt, M., Elkjaer, M. L., Laske, T., Grønning, A. G. B., Moeller, M. J. & Baumbach, J., Mar 2023, In: *NAR Genomics and Bioinformatics*. 5, 1, 17 p., lqad018.

### **Systematic analysis of alternative splicing in time course data using Spycone**

Lio, C. T., Grabert, G., Louadi, Z., Fenn, A., Baumbach, J., Kacprowski, T., List, M. & Tsoy, O., Jan 2023, In: *Bioinformatics*. 39, 1, 9 p., btac846.

### **CircRNA-sponging: A pipeline for extensive analysis of circRNA expression and their role in miRNA sponging**

Hoffmann, M., Schwartz, L., Ciora, O. A., Trummer, N., Willruth, L. L., Jankowski, J., Lee, H. K., Baumbach, J., Furth, P. A., Hennighausen, L. & List, M., 2023, In: *Bioinformatics Advances*. 3, 1, 9 p., vbad093.

### **CTCF and Its Multi-Partner Network for Chromatin Regulation**

Del Moral-Morales, A., Salgado-Albarrán, M., Sánchez-Pérez, Y., Wenke, N. K., Baumbach, J. & Soto-Reyes, E., 2023, In: *Cells*. 12, 10, p. 1357-1369.

### **Federated Machine Learning, Privacy-Enhancing Technologies, and Data Protection Laws in Medical Research: Scoping Review**

Brauneck, A., Schmalhorst, L., Majdabadi, M. M. K., Bakhtiari, M., Völker, U., Baumbach, J., Baumbach, L. & Buchholtz, G., 2023, In: *Journal of Medical Internet Research*. 25, 18 p., e41588.

### **Human-in-the-Loop Integration with Domain-Knowledge Graphs for Explainable Federated Deep Learning**

Holzinger, A., Saranti, A., Hauschild, A. C., Beinecke, J., Heider, D., Roettger, R., Mueller, H., Baumbach, J. & Pfeifer, B., 2023, *Machine Learning and Knowledge Extraction - 7th IFIP TC 5, TC 12, WG 8.4, WG 8.9, WG 12.9 International Cross-Domain Conference, CD-MAKE 2023, Proceedings*. Holzinger, A., Holzinger, A., Holzinger, A., Kieseberg, P., Cabitza, F., Campagner, A., Tjoa, A. M., Weippl, E. & Weippl, E. (eds.). Springer Science+Business Media, p. 45-64 (Lecture Notes in Computer Science, Vol. 14065 LNCS).

### **Network-based approaches for modeling disease regulation and progression**

Galindez, G., Sadegh, S., Baumbach, J., Kacprowski, T. & List, M., 2023, In: *Computational and Structural Biotechnology Journal*. 21, p. 780-795

### **The FeatureCloud Platform for Federated Learning in Biomedicine: Unified Approach**

Matschinske, J., Späth, J., Bakhtiari, M., Probul, N., Majdabadi, M. M. K., Nasirigerdeh, R., Torkzadehmahani, R., Hartebrodt, A., Orban, B. A., Fejér, S. J., Zolotareva, O., Das, S., Baumbach, L., Pauling, J. K., Tomašević, O., Bihari, B., Bloice, M., Donner, N. C., Fdhila, W. & Frisch, T. & 19 others, Hauschild, A. C., Heider, D., Holzinger, A., Hötzeneder,

W., Hospes, J., Kacprowski, T., Kastelitz, M., List, M., Mayer, R., Moga, M., Müller, H., Pustozerova, A., Röttger, R., Saak, C. C., Saranti, A., Schmidt, H. H. W., Tschohl, C., Wenke, N. K. & Baumbach, J., 2023, In: Journal of Medical Internet Research. 25, 16 p., e42621.

#### **Hypothesis of a potential BrainBiota and its relation to CNS autoimmune inflammation**

Elkjaer, M. L., Simon, L., Frisch, T., Bente, L. M., Kacprowski, T., Thomassen, M., Reynolds, R., Baumbach, J., Röttger, R. & Illes, Z., 2. Dec 2022, In: Frontiers in Immunology. 13, 1043579.

#### **CTCF regulates the PI3K-Akt pathway and it is a target for personalized ovarian cancer therapy**

Salgado-Albarrán, M., Späth, J., González-Barrios, R., Baumbach, J. & Soto-Reyes, E., Dec 2022, In: npj Systems Biology and Applications. 8, 1, 10 p., 5.

#### **Federated machine learning for a facilitated implementation of Artificial Intelligence in healthcare - a proof of concept study for the prediction of coronary artery calcification scores**

Wolff, J., Matschinske, J., Baumgart, D., Pytlík, A., Keck, A., Natarajan, A., von Schacky, C. E., Pauling, J. K. & Baumbach, J., Dec 2022, In: Journal of Integrative Bioinformatics. 19, 4, 14 p., 20220032.

#### **The limits of molecular signatures for pancreatic ductal adenocarcinoma subtyping**

Lautizi, M., Baumbach, J., Weichert, W., Steiger, K., List, M., Pfarr, N. & Kacprowski, T., Dec 2022, In: NAR Cancer. 4, 4, zcac030.

#### **Un-biased housekeeping gene panel selection for high-validity gene expression analysis**

Casas, A. I., Hassan, A. A., Manz, Q., Wiwie, C., Kleikers, P., Egea, J., López, M. G., List, M., Baumbach, J. & Schmidt, H. H. W., Dec 2022, In: Scientific Reports. 12, 1, 12324.

#### **Not quite the same: How alternative splicing affects protein interactions**

Louadi, Z., Tsoy, O., Baumbach, J., Kacprowski, T. & List, M., 19. Nov 2022, *Protein Interactions: The Molecular Basis of Interactomics*. Wiley, p. 359-379

#### **dsMTL: a computational framework for privacy-preserving, distributed multi-task machine learning**

Cao, H., Zhang, Y., Baumbach, J., Burton, P. R., Dwyer, D., Koutsouleris, N., Matschinske, J., Marcon, Y., Rajan, S., Rieg, T., Ryser-Welch, P., Späth, J., Herrmann, C. & Schwarz, E., 1. Nov 2022, In: Bioinformatics. 38, 21, p. 4919-4926

#### **Cancer driver drug interaction explorer**

Hartung, M., Anastasi, E., Mamdouh, Z. M., Nogales, C., Schmidt, H. H. W., Baumbach, J., Zolotareva, O. & List, M., 5. Jul 2022, In: Nucleic Acids Research. 50, W1, p. W138-W144

#### **Online in silico validation of disease and gene sets, clusterings or subnetworks with DIGEST**

Adamowicz, K., Maier, A., Baumbach, J. & Blumenthal, D. B., Jul 2022, In: Briefings in Bioinformatics. 23, 4, bbac247.

#### **Privacy-Preserving Artificial Intelligence Techniques in Biomedicine**

Torkzadehmahani, R., Nasirigerdeh, R., Blumenthal, D. B., Kacprowski, T., List, M., Matschinske, J., Spaeth, J., Wenke, N. K. & Baumbach, J., Jun 2022, In: Methods of Information in Medicine. 61, S01, p. e12-e27

#### **MoSBI: Automated signature mining for molecular stratification and subtyping**

Rose, T. D., Bechtler, T., Ciora, O. A., Anh Lilian Le, K., Molnar, F., Köhler, N., Baumbach, J., Röttger, R. & Pauling, J. K., 19. Apr 2022, In: PNAS. 119, 16, p. e2118210119 10 p., e2118210119.

#### **Federated Random Forests can improve local performance of predictive models for various healthcare applications**

Hauschild, A. C., Lemanczyk, M., Matschinske, J., Frisch, T., Zolotareva, O., Holzinger, A., Baumbach, J. & Heider, D., 15. Apr 2022, In: Bioinformatics. 38, 8, p. 2278-2286

#### **Robust disease module mining via enumeration of diverse prize-collecting Steiner trees**

Bernett, J., Krupke, D., Sadegh, S., Baumbach, J., Fekete, S. P., Kacprowski, T., List, M. & Blumenthal, D. B., 15. Mar 2022, In: Bioinformatics. 38, 6, p. 1600-1606 7 p.

**A systematic review of tissue and single cell transcriptome/proteome studies of the brain in multiple sclerosis**

Elkjaer, M. L., Röttger, R., Baumbach, J. & Illes, Z., 2. Mar 2022, In: *Frontiers in Immunology*. 13, 761225.

**sPLINK: a hybrid federated tool as a robust alternative to meta-analysis in genome-wide association studies**

Nasirigerdeh, R., Torkzadehmahani, R., Matschinske, J., Frisch, T., List, M., Späth, J., Weiss, S., Völker, U., Pitkänen, E., Heider, D., Wenke, N. K., Kaissis, G., Rueckert, D., Kacprowski, T. & Baumbach, J., 24. Jan 2022, In: *Genome Biology*. 23, 32.

**A systematic comparison of novel and existing differential analysis methods for CyTOF data**

Arend, L., Bennett, J., Manz, Q., Klug, M., Lazareva, O., Baumbach, J., Bongiovanni, D. & List, M., Jan 2022, In: *Briefings in Bioinformatics*. 23, 1, bbab471.

**KeyPathwayMiner: De Novo Pathway Enrichment in the R Ecosystem**

Mechteridis, K., Lauber, M., Baumbach, J. & List, M., Jan 2022, In: *Frontiers in Genetics*. 12, 14 p., 812853.

**Mucosal microbiota adapts to ATF6-induced alterations in host lipid metabolism with prognostic value in colorectal cancer**

Bierwirth, S., Sorbie, A., Coleman, O., Reuß, E., Weber, P., Köhler, N., Kacprowski, T., Dunkel, A., Pauling, J., Ecker, J., Baumbach, J., Rosenstiel, P., Steiger, K., Wirbel, J., Zeller, G., Janssen, K. P. & Haller, D., 2022, In: *Journal of Crohn's and Colitis*. 16, Supplement\_1, p. i167 1 p., P057 .

**Namco: a microbiome explorer**

Dietrich, A., Machado, M. S., Zwiebel, M., Ölke, B., Lauber, M., Lagkouvardos, I., Baumbach, J., Haller, D., Brandl, B., Skurk, T., Hauner, H., Reitmeier, S. & List, M., 2022, In: *Microbial Genomics*. 8, 8, 000852.

**Functional enrichment of alternative splicing events with NEASE reveals insights into tissue identity and diseases**

Louadi, Z., Elkjaer, M. L., Klug, M., Lio, C. T., Fenn, A., Illes, Z., Bongiovanni, D., Baumbach, J., Kacprowski, T., List, M. & Tsoy, O., 2. Dec 2021, In: *Genome Biology*. 22, 22 p., 327.

**Flimma: a federated and privacy-aware tool for differential gene expression analysis**

Zolotareva, O., Nasirigerdeh, R., Matschinske, J., Torkzadehmahani, R., Bakhtiari, M., Frisch, T., Späth, J., Blumenthal, D. B., Abbasinejad, A., Tieri, P., Kaissis, G., Rückert, D., Wenke, N. K., List, M. & Baumbach, J., Dec 2021, In: *Genome Biology*. 22, 1, 26 p., 338.

**Network medicine for disease module identification and drug repurposing with the NeDRex platform**

Sadegh, S., Skelton, J., Anastasi, E., Bennett, J., Blumenthal, D. B., Galindez, G., Salgado-Albarrán, M., Lazareva, O., Flanagan, K., Cockell, S., Nogales, C., Casas, A. I., Schmidt, H. H. W., Baumbach, J., Wipat, A. & Kacprowski, T., Dec 2021, In: *Nature Communications*. 12, 1, 12 p., 6848.

**The AIME registry for artificial intelligence in biomedical research**

Matschinske, J., Alcaraz, N., Benis, A., Golebiewski, M., Grimm, D. G., Heumos, L., Kacprowski, T., Lazareva, O., List, M., Louadi, Z., Pauling, J. K., Pfeifer, N., Röttger, R., Schwämmle, V., Sturm, G., Traverso, A., Van Steen, K., de Freitas, M. V., Villalba Silva, G. C. & Wee, L. & 5 others, Wenke, N. K., Zanin, M., Zolotareva, O., Baumbach, J. & Blumenthal, D. B., Oct 2021, In: *Nature Methods*. 18, 10, p. 1128–1131

**Unbiased examination of genome-wide human endogenous retrovirus transcripts in MS brain lesions**

Elkjaer, M. L., Frisch, T., Tonazzolli, A., Röttger, R., Reynolds, R., Baumbach, J. & Illes, Z., Oct 2021, In: *Multiple Sclerosis Journal*. 27, 12, p. 1829-1837

**ASimulator: splice-aware RNA-Seq data simulation**

Manz, Q., Tsoy, O., Fenn, A., Baumbach, J., Völker, U., List, M. & Kacprowski, T., 15. Sept 2021, In: *Bioinformatics*. 37, 18, p. 3008–3010

**On the limits of active module identification**

Lazareva, O., Baumbach, J., List, M. & Blumenthal, D. B., Sept 2021, In: *Briefings in Bioinformatics*. 22, 5, 11 p., bbab066.

**Differential lncRNA expression profiling of cognitive function in middle and old aged monozygotic twins using generalized association analysis**

Mohammadnejad, A., Baumbach, J., Li, W., Lund, J., Larsen, M. J., Li, S., Mengel-From, J., Sheldrick-Michel, T. M., Christiansen, L., Christensen, K., Hjelmberg, J. & Tan, Q., Aug 2021, In: *Journal of Psychiatric Research*. 140, p. 197-204

**EWASex: An efficient R-package to predict sex in epigenome-wide association studies**

Lund, J., Li, W., Mohammadnejad, A., Li, S., Baumbach, J. & Tan, Q., 15. Jul 2021, In: *Bioinformatics*. 37, 14, p. 2075-2076

**On the Privacy of Federated Pipelines**

Nasirigerdeh, R., Torkzadehmahani, R., Baumbach, J. & Blumenthal, D. B., 11. Jul 2021, *SIGIR 2021 - Proceedings of the 44th International ACM SIGIR Conference on Research and Development in Information Retrieval*. Association for Computing Machinery, p. 1975-1979 3462996

**Global Gene Expression Profiling and Transcription Factor Network Analysis of Cognitive Aging in Monozygotic Twins**

Mohammadnejad, A., Li, W., Lund, J. B., Li, S., Larsen, M. J., Mengel-From, J., Sheldrick-Michel, T. M., Christiansen, L., Christensen, K., Hjelmberg, J. V. B., Baumbach, J. & Tan, Q., 14. Jun 2021, In: *Frontiers in Genetics*. 12, 9 p., 675587.

**An Integrated Database of Small RNAs and Their Interplay With Transcriptional Gene Regulatory Networks in *Corynebacteria***

Parise, M. T. D., Parise, D., Aburjaile, F. F., Pinto Gomide, A. C., Kato, R. B., Raden, M., Backofen, R., Azevedo, V. A. D. C. & Baumbach, J., Jun 2021, In: *Frontiers in Microbiology*. 12, 14 p., 656435.

**Clinical epigenetics settings for cancer and cardiovascular diseases: real-life applications of network medicine at the bedside**

Sarno, F., Benincasa, G., List, M., Barabasi, A. L., Baumbach, J., Ciardiello, F., Filetti, S., Glass, K., Loscalzo, J., Marchese, C., Maron, B. A., Paci, P., Parini, P., Petrillo, E., Silverman, E. K., Verrienti, A., Altucci, L., Napoli, C. & The International Network Medicine Consortium, Mar 2021, In: *Clinical Epigenetics*. 13, 1, 38 p., 66.

**Primer, Pipelines, Parameters: Issues in 16S rRNA Gene Sequencing**

Abellan-Schneyder, I., Machado, M. S., Reitmeier, S., Sommer, A., Sewald, Z., Baumbach, J., List, M. & Neuhaus, K., 24. Feb 2021, In: *mSphere*. 6, 1, 22 p., e01202-20.

**CSF proteome in multiple sclerosis subtypes related to brain lesion transcriptomes**

Elkjaer, M. L., Nawrocki, A., Kacprowski, T., Lassen, P., Simonsen, A. H., Marignier, R., Sejbaek, T., Nielsen, H. H., Wermuth, L., Rashid, A. Y., Høgh, P., Sellebjerg, F., Reynolds, R., Baumbach, J., Larsen, M. R. & Illes, Z., 18. Feb 2021, In: *Scientific Reports*. 11, 13 p., 4132.

**Novel DNA methylation marker discovery by assumption-free genome-wide association analysis of cognitive function in twins**

Mohammadnejad, A., Sørensen, M., Baumbach, J., Mengel-From, J., Li, W., Lund, J., Li, S., Christiansen, L., Christensen, K., Hjelmberg, J. V. B. & Tan, Q., Feb 2021, In: *Aging Cell*. 20, 2, 12 p., e13293.

**The transcriptional regulatory network of *Corynebacterium pseudotuberculosis***

Parise, D., Parise, M. T. D., Gomide, A. C. P., Aburjaile, F. F., Kato, R. B., Salgado-Albarrán, M., Tauch, A., Azevedo, V. A. D. C. & Baumbach, J., Feb 2021, In: *Microorganisms*. 9, 2, 16 p., 415.

**DIGGER: exploring the functional role of alternative splicing in protein interactions**

Louadi, Z., Yuan, K., Gress, A., Tsoy, O., Kalinina, O. V., Baumbach, J., Kacprowski, T. & List, M., 8. Jan 2021, In: *Nucleic Acids Research*. 49, D1, p. D309-D318

**Comparative transcriptome analysis reveals key epigenetic targets in SARS-CoV-2 infection**

Salgado-Albarrán, M., Navarro-Delgado, E. I., Del Moral-Morales, A., Alcaraz, N., Baumbach, J., González-Barrios, R. & Soto-Reyes, E., 2021, In: *npj Systems Biology and Applications*. 7, 1, 14 p., 21.

### **Enabling single-cell trajectory network enrichment**

Grønning, A. G. B., Oubounyt, M., Kanev, K., Lund, J., Kacprowski, T., Zehn, D., Röttger, R. & Baumbach, J., 2021, In: *Nature Computational Science*. 1, 2, p. 153-163

### **Lessons from the COVID-19 pandemic for advancing computational drug repurposing strategies**

Galindez, G., Matschinske, J., Rose, T. D., Sadegh, S., Salgado-Albarrán, M., Späth, J., Baumbach, J. & Pauling, J. K., 2021, In: *Nature Computational Science*. 1, 1, p. 33-41

### **Machine learning for deciphering cell heterogeneity and gene regulation**

Scherer, M., Schmidt, F., Lazareva, O., Walter, J., Baumbach, J., Schulz, M. H. & List, M., 2021, In: *Nature Computational Science*. 1, 3, p. 183-191

### **netDx: Software for building interpretable patient classifiers by multi-omic data integration using patient similarity networks**

Pai, S., Weber, P., Isserlin, R., Kaka, H., Hui, S., Shah, M. A., Giudice, L., Giugno, R., Nøhr, A. K., Baumbach, J. & Bader, G. D., 2021, In: *F1000Research*. 9, 42 p., 1239.

### **Network analysis methods for studying microbial communities: A mini review**

Matchado, M. S., Lauber, M., Reitmeier, S., Kacprowski, T., Baumbach, J., Haller, D. & List, M., 2021, In: *Computational and Structural Biotechnology Journal*. 19, p. 2687-2698

### **Network Medicine-Based Unbiased Disease Modules for Drug and Diagnostic Target Identification in ROSopathies**

Nogales, C., Grønning, A. G. B., Sadegh, S., Baumbach, J. & Schmidt, H. H. H. W., 2021, *Reactive Oxygen Species: Network Pharmacology and Therapeutic Applications*. Schmidt, H. H. H. W., Ghezzi, P. & Cuadrado, A. (eds.). Springer, p. 49-68 (Handbook of Experimental Pharmacology, Vol. 264).

### **Global Gene Expression Profiling of Body-Mass Index in Middle-Aged Danish Twins**

Li, W., Baumbach, J., Mohammadnejad, A., Lund, J., Larsen, M. J., Hjelmberg, J. V. B., Mengel-From, J., Christensen, K., Christiansen, L. & Tan, Q., 4. Dec 2020, In: *Genetics and Genomics*. p. 1-8 8 p.

### **Exploring the SARS-CoV-2 virus-host-drug interactome for drug repurposing**

Sadegh, S., Matschinske, J., Blumenthal, D. B., Galindez, G., Kacprowski, T., List, M., Nasirigerdeh, R., Oubounyt, M., Pichlmair, A., Rose, T. D., Salgado-Albarrán, M., Späth, J., Stukalov, A., Wenke, N. K., Yuan, K., Pauling, J. K. & Baumbach, J., 1. Dec 2020, In: *Nature Communications*. 11, 3518.

### **Methylation profile of locally advanced rectal carcinomas and neoadjuvant chemoradiotherapy response**

Matos do Canto, L., Barros-Filho, M. C., Marinho, D., Kupper, B. E. C., Begnami, M. F. S., Scapulatempo-Neto, C., Havelund, B. M., Lindebjerg, J., Marchi, F. A., Baumbach, J., Aguiar, Jr., S. & Rogatto, S. R., 1. Dec 2020, In: *European Journal of Human Genetics*. 28, Suppl. 1, p. 756 1 p., P20.65.B.

### **Generalized correlation coefficient for genome-wide association analysis of cognitive ability in twins**

Mohammadnejad, A., Nygaard, M., Li, S., Zhang, D., Xu, C., Li, W., Lund, J., Christiansen, L., Baumbach, J., Christensen, K., Hjelmberg, J. V. B. & Tan, Q., 24. Nov 2020, In: *Aging*. 12, 22, p. 22457-22494

### **Weighted Gene Coregulation Network Analysis of Promoter DNA Methylation on All-Cause Mortality in Old-Aged Birth Cohorts Finds Modules of High-Risk Associated Biomarkers**

Lund, J., Li, S., Baumbach, J., Christensen, K., Li, W., Mohammadnejad, A., Pattie, A., Marioni, R. E., Deary, I. J. & Tan, Q., 13. Nov 2020, In: *The Journals of Gerontology Series A*. 75, 12, p. 2249-2257

### **NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype**

Elbatreek, M. H., Sadegh, S., Anastasi, E., Guney, E., Nogales, C., Kacprowski, T., Hassan, A. A., Teubner, A., Huang, P. H., Hsu, C. Y., Schiffers, P. M. H., Janssen, G. M., Kleikers, P. W. M., Wipat, A., Baumbach, J., De Mey, J. G. R. & Schmidt, H. H. H. W., 10. Nov 2020, In: *PLOS Biology*. 18, 11, 25 p., e3000885.

### **Molecular networks in Network Medicine: Development and applications**

Silverman, E. K., Schmidt, H. H. H. W., Anastasiadou, E., Altucci, L., Angelini, M., Badimon, L., Balligand, J. L., Benincasa, G., Capasso, G., Conte, F., Di Costanzo, A., Farina, L., Fiscon, G., Gatto, L., Gentili, M., Loscalzo, J., Marchese, C., Napoli, C., Paci, P. & Petti, M. & 6 others, Quackenbush, J., Tieri, P., Viggiano, D., Vilahur, G., Glass, K. & Baumbach, J., Nov 2020, In: *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*. 12, 6, 38 p., e1489.

### **Comprehensive analysis of DNA methylation and prediction of response to neoadjuvant therapy in locally advanced rectal cancer**

Canto, L. M. D., Barros-Filho, M. C., Rainho, C. A., Marinho, D., Kupper, B. E. C., Begnami, M. D. F. D. S., Scapulatempo-Neto, C., Havelund, B. M., Lindebjerg, J., Marchi, F. A., Baumbach, J., Aguiar, S. & Rogatto, S. R., 22. Oct 2020, In: *Cancers*. 12, 11, 19 p., 3079.

### **Balsam—an interactive online platform for breath analysis, visualization and classification**

Weber, P., Pauling, J. K., List, M. & Baumbach, J., Oct 2020, In: *Metabolites*. 10, 10, 16 p., 393.

### **Inflammatory breast cancer: Clinical implications of genomic alterations and mutational profiling**

Faldoni, F. L. C., Villacis, R. A. R., Canto, L. M., Fonseca-Alves, C. E., Cury, S. S., Larsen, S. J., Aagaard, M. M., Souza, C. P., Scapulatempo-Neto, C., Osório, C. A. B. T., Baumbach, J., Marchi, F. A. & Rogatto, S. R., Oct 2020, In: *Cancers*. 12, 10, 21 p., 2816.

### **Differential long noncoding RNA profiling of BMI in twins**

Li, W., Baumbach, J., Larsen, M. J., Mohammadnejad, A., Lund, J., Christensen, K., Christiansen, L. & Tan, Q., Sept 2020, In: *Epigenomics*. 12, 17, p. 1531-1541

### **DeepCLIP: predicting the effect of mutations on protein-RNA binding with deep learning**

Grønning, A. G. B., Doktor, T. K., Larsen, S. J., Petersen, U. S. S., Holm, L. L., Bruun, G. H., Hansen, M. B., Hartung, A.-M., Baumbach, J. & Andresen, B. S., 27. Jul 2020, In: *Nucleic Acids Research*. 48, 13, p. 7099-7118

### **Methylation profile of locally advanced rectal carcinomas and neoadjuvant chemoradiotherapy response**

Canto, L. M. D., Barros-Filho, M. C., Almeida, D. M., Kupper, B. E. C., Begnami, M. D. F. D. S., Scapulatempo-Neto, C., Havelund, B. M., Lindebjerg, J., Marchi, F. A., Baumbach, J., Aguiar, S. & Rogatto, S. R., Jun 2020.

### **Exploratory analysis of age and sex dependent DNA methylation patterns on the X-chromosome in whole blood samples**

Li, S., Lund, J., Christensen, K., Baumbach, J., Mengel-From, J., Kruse, T. A., Li, W., Mohammadnejad, A., Pattie, A., Marioni, R. E., Deary, I. J. & Tan, Q., 28. Apr 2020, In: *Genome Medicine*. 12, 39, 13 p., 39.

### **Age-dependent DNA methylation patterns on the Y chromosome in elderly males**

Lund, J. B., Li, S., Christensen, K., Mengel-From, J., Thinggaard, M. S., Marioni, R. E., Starr, J., Pattie, A., Deary, I. J., Baumbach, J. & Tan, Q., Feb 2020, In: *Aging Cell*. 19, 2, 8 p., e12907.

### **De Novo and Supervised Endophenotyping Using Network-Guided Ensemble Learning**

Larsen, S. J., Schmidt, H. H. H. W. & Baumbach, J., Feb 2020, In: *Network and Systems Medicine*. 3, 1, p. 8-21

### **Multiple Sclerosis Atlas: A Molecular Map of Brain Lesion Stages in Progressive Multiple Sclerosis**

Frisch, T., Elkjaer, M. L., Reynolds, R., Michel, T. M., Kacprowski, T., Burton, M., Kruse, T. A., Thomassen, M., Baumbach, J. & Illes, Z., 2020, In: *Network and Systems Medicine*. 3, 1, p. 122-129 8 p.

### **Molecular signature of different lesion types in the brain white matter of patients with progressive multiple sclerosis**

Elkjaer, M. L., Frisch, T., Reynolds, R., Kacprowski, T., Burton, M., Kruse, T. A., Thomassen, M., Baumbach, J. & Illes, Z., 11. Dec 2019, In: *Acta Neuropathologica Communications*. 7, 17 p., 205.

### **DNA methylome profiling in identical twin pairs discordant for body mass index**

Li, W., Zhang, D., Wang, W., Wu, Y., Mohammadnejad, A., Lund, J., Baumbach, J., Christiansen, L. & Tan, Q., Dec 2019, In: *International Journal of Obesity*. 43, 12, p. 2491-2499

BioAtlas verbindet Mikrobiomsequenzdaten und GEO-Informationen  
Lund, J., List, M., Wenke, N. K., Tan, Q. & Baumbach, J., 1. Nov 2019, In: BioSpektrum. 25, 7, 1 p., 795.

#### **Molecular signatures of different lesions types in the white matter of SPMS**

Elkjaer, M. L., Frisch, T., Reynolds, R., Kacprowski, T., Burton, M., Kruse, T., Thomassen, M., Baumbach, J. & Illes, Z., 1. Sept 2019, In: Multiple Sclerosis Journal. 25, 2 Suppl. 1, p. 76 1 p., 211.

#### **The MS Atlas - A molecular map of brain lesion stages in secondary progressive MS**

Frisch, T., Elkjaer, M. L., Reynolds, R., Michel, T. M., Kacprowski, T., Burton, M., Kruse, T. A., Thomassen, M., Baumbach, J. & Illes, Z., 1. Sept 2019, In: Multiple Sclerosis Journal. 25, 2 Suppl. 1, p. 379-380 P749.

#### **Development of a cGMP phospho-protein biomarker panel for patient stratification**

Nogales, C., Anastasi, E., Gronning, A. G. B., Petraino, A., Flannagan, K., Stevanoska, M., Chenine, S., Casas, A. I., Baumbach, J., Wipat, A. & Schmidt, H. H. H. W., 15. Aug 2019, In: Journal of Translational Medicine. 17, Suppl 2, p. P28

#### **Unraveling of the mechanism behind PKG dependent regulation of NOX4/5 gene expression for improved ischemic stroke therapy**

Casas, A. I., Gronning, A. G., Langhauser, F., Kleinschnitz, C., Baumbach, J. & Schmidt, H. H., 15. Aug 2019, In: Journal of Translational Medicine. 17, Suppl 2, P7.

#### **Community effort endorsing multiscale modelling, multiscale data science and multiscale computing for systems medicine**

Zanin, M., Chorbev, I., Stres, B., Stalidzans, E., Vera, J., Tieri, P., Castiglione, F., Groen, D., Zheng, H., Baumbach, J., Schmid, J. A., Basilio, J., Klimek, P., Debeljak, N., Rozman, D. & Schmidt, H. H. H. W., 21. May 2019, In: Briefings in Bioinformatics. 20, 3, p. 1057-1062

#### **Increased levels of genomic instability and mutations in homologous recombination genes in locally advanced rectal carcinomas**

Do Canto, L. M., Larsen, S. J., Kupper, B. E. C., De Souza Begnami, M. D. F., Scapulatempo-Neto, C., Petersen, A. H., Aagaard, M. M., Baumbach, J., Aguiar, S. & Rogatto, S. R., 14. May 2019, In: Frontiers in Oncology. 9, 9 p., 00395.

#### **Genomic profiling in ovarian cancer retreated with platinum based chemotherapy presented homologous recombination deficiency and copy number imbalances of CCNE1 and RB1 genes**

da Costa, A. A. B. A., do Canto, L. M., Larsen, S. J., Ribeiro, A. R. G., Stecca, C. E., Petersen, A. H., Aagaard, M. M., de Brot, L., Baumbach, J., Baiocchi, G., Achatz, M. I. & Rogatto, S. R., 6. May 2019, In: BMC Cancer. 19, 1, 10 p., 422.

#### **TiCoNE 2: A Composite Clustering Model for Robust Cluster Analyses on Noisy Data**

Wiwie, C., Röttger, R. & Baumbach, J., 28. Apr 2019, In: arxiv.org.

#### **From single drug targets to synergistic network pharmacology in ischemic stroke**

Casas, A. I., Hassan, A. A., Larsen, S. J., Gomez-Rangel, V., Elbatreek, M., Kleikers, P. W. M., Guney, E., Egea, J., López, M. G., Baumbach, J. & Schmidt, H. H. H. W., 2. Apr 2019, In: PNAS. 116, 14, p. 7129-7136

#### **Author Correction: Osteogenesis depends on commissioning of a network of stem cell transcription factors that act as repressors of adipogenesis (Nature Genetics, (2019), 51, 4, (716-727), 10.1038/s41588-019-0359-1)**

Rauch, A., Haakonsson, A. K., Madsen, J. G. S., Larsen, M., Forss, I., Madsen, M. R., Van Hauwaert, E. L., Wiwie, C., Jespersen, N. Z., Tencerova, M., Nielsen, R., Larsen, B. D., Röttger, R., Baumbach, J., Scheele, C., Kassem, M. & Mandrup, S., 1. Apr 2019, In: Nature Genetics. 51, 4, p. 766

#### **Enriched power of disease-concordant twin-case-only design in detecting interactions in genome-wide association studies**

Li, W., Baumbach, J., Mohammadnejad, A., Brasch-Andersen, C., Vandin, F., Korbel, J. O. & Tan, Q., 1. Apr 2019, In: European Journal of Human Genetics. 27, 4, p. 631-636

#### **Osteogenesis depends on commissioning of a network of stem cell transcription factors that act as repressors of adipogenesis**

Rauch, A., Haakonsson, A. K., Madsen, J. G. S., Larsen, M., Forss, I., Madsen, M. R., Van Hauwaert, E. L., Wiwie, C., Jespersen, N. Z., Tencerova, M., Nielsen, R., Larsen, B. D., Röttger, R., Baumbach, J., Scheele, C., Kassem, M. & Mandrup, S., Apr 2019, In: *Nature Genetics*. 51, 4, p. 716-727

**Methylation-based classifier of response to neoadjuvant chemoradiotherapy in locally advanced rectal carcinomas (oral presentation)**

Canto, L. M. D., Barros-Filho, M. C., Almeida, D. M., Kupper, B. E. C., Begnami, M. D. F. D. S., Scapulatempo-Neto, C., Marchi, F. A., Baumbach, J., Aguiar, S. & Rogatto, S. R., Mar 2019.

**The Selection of a Hepatocyte Cell Line Susceptible to Plasmodium falciparum Sporozoite Invasion That Is Associated With Expression of Glypican-3**

Tweedell, R. E., Tao, D., Hamerly, T., Robinson, T. M., Larsen, S., Grønning, A. G. B., Norris, A. M., King, J. G., Law, H. C. H., Baumbach, J., Bergmann-Leitner, E. S. & Dinglasan, R. R., 28. Feb 2019, In: *Frontiers in Microbiology*. 10, FEB, 16 p., 127.

**DNA methylome profiling of all-cause mortality in comparison with age-associated methylation patterns**

Lund, J., Li, S., Baumbach, J., Svane, A. M., Hjelmberg, J. V. B., Christiansen, L., Christensen, K., Redmond, P., Marioni, R. E., Deary, I. J. & Tan, Q., 8. Feb 2019, In: *Clinical Epigenetics*. 11, 8 p., 23.

**E. coli gene regulatory networks are inconsistent with gene expression data**

Larsen, S. J., Röttger, R., Schmidt, H. H. H. W. & Baumbach, J., 10. Jan 2019, In: *Nucleic Acids Research*. 47, 1, p. 85-92

**Time-Resolved Systems Medicine Reveals Viral Infection-Modulating Host Targets**

Wiwie, C., Kuznetsova, I., Mostafa, A., Rauch, A., Haakonsson, A., Barrio-Hernandez, I., Blagoev, B., Mandrup, S., Schmidt, H. H. H. W., Pleschka, S., Röttger, R. & Baumbach, J., 2019, In: *Systems medicine (New Rochelle, N.Y.)*. 2, 1, 9 p.

**On the power of epigenome-wide association studies using a disease-discordant twin design**

Li, W., Christiansen, L., Hjelmberg, J. V. B., Baumbach, J. & Tan, Q., 1. Dec 2018, In: *Bioinformatics*. 34, 23, p. 4073-4078

**Weighted gene co-expression network analysis of microarray mRNA expression profiling in response to electroacupuncture**

Mohammadnejad, A., Li, S., Duan, H., Lund, J., Li, W., Baumbach, J. & Tan, Q., Dec 2018, *Proceedings of the 2018 IEEE International Conference on Bioinformatics and Biomedicine*. Schmidt, H., Griol, D., Wang, H., Baumbach, J., Zheng, H., Callejas, Z., Hu, X., Dickerson, J. & Zhang, L. (eds.). IEEE, p. 1876-1883 8621258

**Gene methylation co-regulation network analysis of all-cause mortality in ageing individuals**

Lund, J., Baumbach, J. & Tan, Q., 16. Oct 2018.

**Molecular signature of brain lesion evolution and fate in progressive MS**

Elkjaer, M. L., Frisch, T., Burton, M., Reynolds, R., Kruse, T., Thomassen, M., Baumbach, J. & Illes, Z., 1. Oct 2018, In: *Multiple Sclerosis Journal*. 24, Suppl. 2, p. 182-183 2 p.

**Temporal changes of inflammation and endothelial dysfunction in multiple sclerosis related to the evolution of enhancing lesions on frequent MRI**

Stensballe, A., Kastaniegaard, K., Jorgensen, M., Baek, R., Sejbaek, T., Bennike, T., Wiwie, C., Baumbach, J., Cotton, F., Guttmann, C. & Illes, Z., 1. Oct 2018, In: *Multiple Sclerosis Journal*. 24, Suppl. 2, p. 457-458 2 p.

**A simulation study on power of epigenome-wide association analysis using disease-discordant twin design**

Li, W., Baumbach, J., Christiansen, L. & Tan, Q., Oct 2018, In: *European Journal of Human Genetics*. 26, Suppl 1, p. 767-768 2 p., P18.18B.

**Association study between gene expression and body mass index for middle aged Danish twins using weighted correlation network analysis**

Li, W., Baumbach, J., Christiansen, L. & Tan, Q., Oct 2018.

**Polygenic analysis of genome-wide SNP data identifies common variants on allergic rhinitis**

Mohammadnejad, A., Brasch-Andersen, C., Haagerup, A., Vestbo, J., Baumbach, J. & Tan, Q., Oct 2018, In: *European Journal of Human Genetics*. 26, S, p. 781 1 p., P18.49A.

**Using neural networks to predict effects of mutations on protein binding**

Gronning, A. G. B., Doktor, T. K., Larsen, S. J., Bruun, G. H., Baumbach, J. & Andresen, B. S., Oct 2018, In: *European Journal of Human Genetics*. 26, p. 719 1 p.

**Network analysis of DNA methylation of visceral adipose tissue comparing obese individuals with and without type 2 diabetes**

Mohammadnejad, A., Li, W., Lund, J., Baumbach, J. & Tan, Q., 25. Sept 2018.

**A Case-only Genome-Wide Association Study on Gene-Sex Interaction in Allergic Rhinitis**

Mohammadnejad, A., Brasch-Andersen, C., Li, W., Haagerup, A., Baumbach, J. & Tan, Q., Sept 2018, In: *Annals of Allergy, Asthma & Immunology*. 121, 3, p. 366-367.e2

**Mutational profile and genomic instability according to response to therapy in rectal carcinomas**

Do Canto, L. M., Larsen, S. J., Catin Kupper, B. E., Ferreira de Souza Begnami, M. D., Scapulatempo Neto, C., Baumbach, J., Petersen, A. H., Jorgensen, M. M. A., Aguiar, S. & Rogatto, S. R., Jul 2018, In: *Cancer Research*. 78, Suppl. 13, 5360.

**Guiding biomedical clustering with ClustEval**

Wiwie, C., Baumbach, J. & Röttger, R., 1. Jun 2018, In: *Nature Protocols*. 13, 6, p. 1429-1444

**CoNVaQ: a web tool for copy number variation-based association studies**

Larsen, S. J., do Canto, L. M., Rogatto, S. R. & Baumbach, J., 18. May 2018, In: *BMC Genomics*. 19, 9 p., 369.

**DNA methylation linked to all-cause mortality in older people: An epigenome-wide association study.**

Lund, J., Baumbach, J. & Tan, Q., Mar 2018.

**Detecting the Association Between DNA Methylation and Body Mass Index Using Co-Twin Design and Reduced Representation Bisulfite Sequencing Technology**

Li, W., Baumbach, J., Christiansen, L. & Tan, Q., 2018.

**DIMmer: Discovery of Differentially Methylated Regions in Epigenome-Wide Association Study (EWAS) Data**

Frisch, T., Møller Gøttcke, J., Röttger, R., Tan, Q. & Baumbach, J., 2018, *Data Mining for Systems Biology: Methods and Protocols*. Mamitsuka, H. (ed.). Humana Press, p. 51-62 (Methods in Molecular Biology, Vol. 1807).

**Elucidation of time-dependent systems biology cell response patterns with time course network enrichment**

Wiwie, C., Rauch, A., Haakonsson, A., Barrio-Hernandez, I., Blagoev, B., Mandrup, S., Röttger, R. & Baumbach, J., 2018, In: *arxiv.org*.

**Online interactive microbial classification and geospatial distributional analysis using BioAtlas**

Lund, J., Tan, Q. & Baumbach, J., 2018, *Data Mining for Systems Biology: Methods and Protocols*. Mamitsuka, H. (ed.). New York: Humana Press, Vol. 1807. p. 21-35 (Methods in Molecular Biology, Vol. 1807).

**Orthologous proteins of experimental de- and remyelination are differentially regulated in the CSF proteome of multiple sclerosis subtypes**

Martin, N. A., Nawrocki, A., Molnar, V., Elkjaer, M. L., Thygesen, E. K., Palkovits, M., Acs, P., Sejbaek, T., Nielsen, H. H., Hegedus, Z., Sellebjerg, F., Molnar, T., Barbosa, E. G. V., Alcaraz, N., Gallyas, F., Svenningsen, A. F., Baumbach, J., Lassmann, H., Larsen, M. R. & Illes, Z., 2018, In: *PLOS ONE*. 13, 8, p. 1-26 e0202530.

**The druggable pocketome of *Corynebacterium diphtheriae*: A new approach for in silico putative druggable targets**  
Hassan, S. S., Jamal, S. B., Radusky, L. G., Tiwari, S., Ullah, A., Ali, J., Behramand, de Carvalho, P. V. S. D., Shams, R., Khan, S., Figueiredo, H. C. P., Barh, D., Ghosh, P., Silva, A., Baumbach, J., Röttger, R., Turjanski, A. G. & Azevedo, V. A. C., 2018, In: *Frontiers in Genetics*. 9, 9 p., 44.

**The End of Medicine as We Know It: Introduction to the New Journal, *Systems Medicine***  
Baumbach, J. & Schmidt, H. H. H. W., 2018, In: *Network and Systems Medicine*. 1, 1, p. 1-2

**A case-only genome-wide association study for assessing gene-sex interaction in Allergic rhinitis**  
Mohammadnejad, A., Brasch-Andersen, C., Haagerup, A., Vestbo, J., Baumbach, J. & Tan, Q., Aug 2017.

**Elucidation of altered pathways in tumor-initiating cells of triple-negative breast cancer: A useful cell model system for drug screening**  
Christensen, A. G., Ehmsen, S., Terp, M. G., Batra, R., Alcaraz, N., Baumbach, J., Noer, J. B., Moreira, J. M. A., Leth-Larsen, R., Larsen, M. R. & Ditzel, H. J., Aug 2017, In: *Stem Cells*. 35, 8, p. 1898–1912

**BioAtlas: Interactive web service for microbial distribution analysis**  
Lund, J., List, M. & Baumbach, J., 21. Jul 2017.

**CytoMCS: A Multiple Maximum Common Subgraph Detection Tool for Cytoscape**  
Larsen, S. & Baumbach, J., 21. Jul 2017, In: *Journal of Integrative Bioinformatics*. 14, 2, 8 p., 20170014.

**Interactive microbial distribution analysis using BioAtlas**  
Lund, J., List, M. & Baumbach, J., 3. Jul 2017, In: *Nucleic Acids Research*. 45, W1, p. W509–W513

**Enriched power of case-only design in detecting gene-gene interaction using disease concordant twins**  
Li, W., Vandin, F., Baumbach, J. & Tan, Q., 22. Jun 2017.

**Association of X chromosome-linked DNA-methylation with mortality in the elderly.**  
Lund, J., Baumbach, J. & Tan, Q., Jun 2017.

**A simulation study on power of epigenome-wide association analysis using disease-discordant twin design**  
Li, W., Baumbach, J., Christiansen, L. & Tan, Q., 28. May 2017.

**Polygenic analysis of genome-wide SNP data identifies common variants on allergic rhinitis**  
Mohammadnejad, A., Brasch-Andersen, C., Haagerup, A., Vestbo, J., Baumbach, J. & Tan, Q., May 2017. 1 p.

**Efficient detection of differentially methylated regions using DIMmeR**  
Almeida, D. M., Uhrenfeldt Skov, I., Silva, A., Vandin, F., Tan, Q., Röttger, R. & Baumbach, J., 15. Feb 2017, In: *Bioinformatics*. 33, 4, p. 549-551

**An integrative in-silico approach for therapeutic target identification in the human pathogen *Corynebacterium diphtheriae***  
Jamal, S. B., Hassan, S. S., Tiwari, S., Viana, M. V., De Jesus Benevides, L., Ullah, A., Turjanski, A. G., Barh, D., Ghosh, P., Costa, D. A., Silva, A., Röttger, R., Baumbach, J. & Azevedo, V. A. C., 2017, In: *PLOS ONE*. 12, 10, 25 p., e0186401.

**De novo pathway-based biomarker identification**  
Alcaraz, N., List, M., Batra, R., Vandin, F., Ditzel, H. J. & Baumbach, J., 2017, In: *Nucleic Acids Research*. 45, 16, 11 p., e151.

**Drug repurposing by integrated literature mining and drug-gene-disease triangulation**  
Sun, P., Guo, J., Winnenburg, R. & Baumbach, J., 2017, In: *Drug Discovery Today*. 22, 4, p. 615-619

### **Efficient Management of High-Throughput Screening Libraries with SAVANAH**

List, M., Elnegaard, M. P., Schmidt, S., Christiansen, H., Tan, Q., Mollenhauer, J. & Baumbach, J., 2017, In: Journal of Biomolecular Screening. 22, 2, p. 196-202

### **LifeStyle-Specific-Islands (LISSI): Integrated Bioinformatics Platform for Genomic Island Analysis**

Barbosa, E., Röttger, R., Hauschild, A.-C., Soares, S. D. C., Boecker, S., Azevedo, V. & Baumbach, J., 2017, In: Journal of Integrative Bioinformatics. 14, 2, 7 p.

### **On the performance of de novo pathway enrichment**

Batra, R., Alcaraz, N., Gitzhofer, K., Pauling, J., Ditzel, H. J., Hellmuth, M., Baumbach, J. & List, M., 2017, In: n p j Systems Biology and Applications. 3, 6.

### **On the performance of pre-microRNA detection algorithms**

Saçar Demirci, M. D., Baumbach, J. & Allmer, J., 2017, In: Nature Communications. 8, 9 p., 330.

### **A systematic review of breath analysis and detection of volatile organic compounds in COPD**

Christiansen, A., Davidsen, J. R., Titlestad, I., Vestbo, J. & Baumbach, J., 31. Aug 2016, In: Journal of Breath Research. 10, 3, 034002.

### **PetriScope: A plugin for discrete Petri net simulations in Cytoscape**

Almeida, D., Azevedo, V., Silva, A. & Baumbach, J., 4. Jun 2016, In: Journal of Integrative Bioinformatics. 13, 1, 6 p., 284.

### **A Simulated Annealing Algorithm for Maximum Common Edge Subgraph Detection in Biological Networks**

Larsen, S., Alkær sig, F. G., Ditzel, H., Jurisica, I., Alcaraz, N. & Baumbach, J., 2016, *GECCO 2016 - Proceedings of the 2016 Genetic and Evolutionary Computation Conference*. Friedrich, T. (ed.). Association for Computing Machinery, p. 341-348

### **Comprehensive analysis of high-throughput screens with HiTSeekR**

List, M., Schmidt, S., Christiansen, H., Rehmsmeier, M., Tan, Q., Mollenhauer, J. & Baumbach, J., 2016, In: Nucleic Acids Research. 44, 14, p. 6639-6648

### **CytoGEDEVO: Global alignment of biological networks with Cytoscape**

Malek, M., Ibragimov, R., Albrecht, M. & Baumbach, J., 2016, In: Bioinformatics. 32, 8, p. 1259-1261

### **Differentially Methylated Genomic Regions in Birth-Weight Discordant Twin Pairs**

Chen, M., Baumbach, J., Vandin, F., Röttger, R., Vieira Barbosa, E. G., Dong, M., Nielsen, M. F. M., Christiansen, L. & Tan, Q., 2016, In: Annals of Human Genetics. 80, 2, p. 81-87

### **DiMmeR: Discovery of Multiple Differentially Methylated Regions**

Almeida, D. M., Skov, I., Silva, A., Vandin, F., Tan, Q., Röttger, R. & Baumbach, J., 2016.

### **GIPSy: Genomic island prediction software**

Soares, S. C., Geyik, H., Ramos, R. T. J., de Sá, P. H. C. G., Barbosa, E. G. V., Baumbach, J., Figueiredo, H. C. P., Miyoshi, A., Tauch, A., Silva, A. & Azevedo, V., 2016, In: Journal of Biotechnology. 232, p. 2-11

### **Jllumina: A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and MethylationEPIC data processing**

Almeida, D. M., Uhrenfeldt Skov, I., Lund, J., Mohammadnejad, A., Silva, A., Vandin, F., Tan, Q., Baumbach, J. & Röttger, R., 2016, In: Journal of Integrative Bioinformatics. 13, 4, p. 294 9 p., 294.

### **KeyPathwayMinerWeb: online multi-omics network enrichment**

List, M., Alcaraz, N., Dissing-Hansen, M., Ditzel, H. J., Mollenhauer, J. & Baumbach, J., 2016, In: Nucleic Acids Research. 44, W1, p. W98-W104

**Metagenomic evidence for the presence of phototrophic Gemmatimonadetes bacteria in diverse environments**

Zeng, Y., Baumbach, J., Barbosa, E. G. V., Azevedo, V., Zhang, C. & Koblížek, M., 2016, In: Environmental Microbiology Reports. 8, 1, p. 139-149

**Robust and on-line multi-omics de novo pathway enrichment with KeyPathwayMiner**

Alcaraz, N., List, M., Dissing-Hansen, M., Rehmsmeier, M., Tan, Q., Mollenhauer, J., Ditzel, H. & Baumbach, J., 2016.

**Robust de novo pathway enrichment with KeyPathwayMiner 5: [version 1; peer review: 2 approved]**

Alcaraz, N., List, M., Dissing-Hansen, M., Rehmsmeier, M., Tan, Q., Mollenhauer, J., Ditzel, H. & Baumbach, J., 2016, In: F1000Research. 5, 9 p., 1531.

**Comparing the performance of biomedical clustering methods**

Wiwie, C., Baumbach, J. & Röttger, R., Nov 2015, In: Nature Methods. 12, 11, p. 1033-1038

**KeyPathwayMiner - De-novo network enrichment by combining multiple OMICS data and biological networks**

Baumbach, J., Alcaraz, N., Pauling, J. K., Batra, R., Vieira Barbosa, E. G., Christensen, A. G. L. & Ditzel, H., 10. Jul 2015.

**Carotta: Revealing Hidden Confounder Markers in Metabolic Breath Profiles**

Hauschild, A.-C., Frisch, T., Baumbach, J. I. & Baumbach, J., 2015, In: Metabolites. 5, 2, p. 344-363

**CMRegNet-An interspecies reference database for corynebacterial and mycobacterial regulatory networks**

Abreu, V. A. C., Almeida, S., Tiwari, S., Hassan, S. S., Mariano, D., Silva, A., Baumbach, J., Azevedo, V. & Röttger, R., 2015, In: BMC Genomics. 16, 452.

**Covering tree with stars**

Baumbach, J., Guo, J. & Ibragimov, R., 2015, In: Journal of Combinatorial Optimization. 29, 1, p. 141-152

**Modeling and analysis of innate immune responses induced by the host cells against hepatitis C virus infection**

Obaid, A., Ahmad, J., Naz, A., Awan, F. M., Paracha, R. Z., Tareen, S. H. K., Anjum, S., Raza, A., Baumbach, J. & Ali, A., 2015, In: Integrative Biology. 7, 5, p. 544-559

**OpenLabNotes: An Electronic Laboratory Notebook Extension for OpenLabFramework**

List, M., Franz, M., Tan, Q., Mollenhauer, J. & Baumbach, J., 2015, In: Journal of Integrative Bioinformatics. 12, 3, 10 p., 274.

**Computational Integrative Biology--on the joint analysis of diverse biological data sets**

Baumbach, J. & Röttger, R., 1. Nov 2014, In: Integrative Biology. 6, 11, p. 1008-1009

**Large scale sample management and data analysis via MIRACLE**

Block, I., List, M., Pedersen, M. L., Christiansen, H., Schmidt, S., Thomassen, M., Tan, Q., Baumbach, J. & Mollenhauer, J., 24. Oct 2014.

**Microarray R-based analysis of complex lysate experiments with MIRACLE**

List, M., Block, I., Pedersen, M. L., Christiansen, H., Schmidt, S., Thomassen, M., Tan, Q., Baumbach, J. & Mollenhauer, J., Sept 2014, In: Bioinformatics. 30, 17, p. i631-i638

**Elucidation of epithelial-mesenchymal transition-related pathways in a triple-negative breast cancer cell line model by multi-omics interactome analysis**

Pauling, J. K., Christensen, A. G., Batra, R., Alcaraz, N., Barbosa, E., Larsen, M. R., Beck, H. C., Leth-Larsen, R., Azevedo, V., Ditzel, H. J. & Baumbach, J., 15. Aug 2014, In: Integrative Biology. 6, 11, p. 1058-1068

### **Classification of Breast Cancer Subtypes by combining Gene Expression and DNA Methylation Data**

List, M., Hauschild, A.-C., Tan, Q., Kruse, T. A., Mollenhauer, J., Baumbach, J. & Batra, R., Jun 2014, In: Journal of Integrative Bioinformatics. 11, 2, p. 236

### **On the limits of computational functional genomics for bacterial lifestyle prediction**

Barbosa, E., Röttger, R., Hauschild, A.-C., Azevedo, V. & Baumbach, J., 22. May 2014, In: Briefings in Functional Genomics. 13, 5, p. 398-408

### **Efficient Sample Tracking With OpenLabFramework**

List, M., Schmidt, S., Trojnar, J., Thomas, J., Thomassen, M., Kruse, T. A., Tan, Q., Baumbach, J. & Mollenhauer, J., 4. Mar 2014, In: Scientific Reports. 4, 4278.

### **On the importance of statistics in breath analysis—hope or curse?**

Eckel, S. P., Baumbach, J. & Hauschild, A.-C., Mar 2014, In: Journal of Breath Research. 8, 1, p. 012001

### **BacillusRegNet: a transcriptional regulation database and analysis platform for Bacillus species**

Misirli, G., Hallinan, J., Röttger, R., Baumbach, J. & Wipat, A., 2014, In: Journal of Integrative Bioinformatics. 11, 2, p. 244

### **Bi-Force: large-scale bicluster editing and its application to gene expression data biclustering**

Sun, P., Speicher, N. K., Röttger, R., Guo, J. & Baumbach, J., 2014, In: Nucleic Acids Research. 42, 9, p. e78

### **Compactness-Preserving Mapping on Trees**

Baumbach, J., Guo, J. & Ibragimov, R., 2014, *Combinatorial Pattern Matching - 25th Annual Symposium, CPM 2014, Proceedings*. Kulikov, A. S., Kuznetsov, S. O. & Pevzner, P. (eds.). Springer, p. 162-171 10 p. (Lecture Notes in Computer Science, Vol. 8486).

### **Complexity of Dense Bicluster Editing Problems**

Sun, P., Guo, J. & Baumbach, J., 2014, *Computing and Combinatorics - 20th International Conference, COCOON 2014, Proceedings: 20th International Conference, COCOON 2014, Atlanta, GA, USA, August 4-6, 2014. Proceedings*. Cai, Z., Zelikovskiy, A. & Bourgeois, A. (eds.). Springer, p. 154-165 12 p. (Lecture Notes in Computer Science, Vol. 8591).

### **Current breathomics—a review on data pre-processing techniques and machine learning in metabolomics breath analysis**

Smolinska, A., Hauschild, A. C., Fijten, R. R. R., Dallinga, J. W., Baumbach, J. & van Schooten, F. J., 2014, In: Journal of Breath Research. 8, 2, p. 20

### **Efficient large-scale bicluster editing**

Sun, P., Baumbach, J. & Guo, J., 2014, *Proceedings of the German Conference on Bioinformatics 2014*. Hofstadt, R., Nattkemper, T. W. & Giegerich, R. (eds.). Gesellschaft für Informatik (GI) e.V., Vol. P-235. p. 54-60 (Lecture Notes in Informatics - Proceedings, Vol. P-235).

### **KeyPathwayMiner 4.0: condition-specific pathway analysis by combining multiple omics studies and networks with Cytoscape**

Alcaraz, N., Pauling, J., Batra, R., Barbosa, E., Junge, A., Christensen, A. G., Azevedo, V., Ditzel, H. J. & Baumbach, J., 2014, In: BMC Systems Biology. 8, 1, 6 p.

### **Massive fungal biodiversity data re-annotation with multi-level clustering**

Vu, D., Szoke, S., Wiwie, C., Baumbach, J., Cardinali, G., Röttger, R. & Robert, V., 2014, In: Scientific Reports. 4, 9 p., 6837.

### **MIMA—a software for analyte identification in MCC/IMS chromatograms by mapping accompanying GC/MS measurements**

Maurer, F., Hauschild, A. C., Eisinger, K., Baumbach, J., Mayor, A. & Baumbach, J. I., 2014, In: International Journal for Ion Mobility Spectrometry. 17, 2, p. 95-101 7 p.

### **Multiple Graph Edit Distance: Simultaneous Topological Alignment of Multiple Protein-protein Interaction Networks with an Evolutionary Algorithm**

Ibragimov, R., Malek, M., Baumbach, J. & Guo, J., 2014, *Proceedings of the 2014 Conference on Genetic and Evolutionary Computation*. Association for Computing Machinery, p. 277-284 8 p.

#### **On the limits of computational functional genomics for bacterial lifestyle prediction**

Barbosa, E., Röttger, R., Hauschild, A.-C., Azevedo, V. & Baumbach, J., 2014, *German Conference on Bioinformatics 2014*. Giegerich, R., Hofestädt, R. & Nattkemper, T. W. (eds.). Gesellschaft für Informatik (GI) e.V, p. 79-84 (Lecture Notes in Informatics - Proceedings, Vol. P-235).

#### **Value of a newly sequenced bacterial genome**

Barbosa, E., Aburjaile, F. F., Ramos, R. T., Carneiro, A. R., Le Loir, Y., Baumbach, J., Miyoshi, A., Silva, A. & Azevedo, V., 2014, In: *World Journal of Biological Chemistry*. 5, 2, p. 161-8 8 p.

#### **BiCluE - Exact and heuristic algorithms for weighted bi-cluster editing of biomedical data**

Sun, P., Guo, J. & Baumbach, J., 20. Dec 2013, In: *BMC Proceedings*. 7, Suppl 7, S9.

#### **Conserved host-pathogen PPIs. Globally conserved inter-species bacterial PPIs based conserved host-pathogen interactome derived novel target in *C. pseudotuberculosis*, *C. diphtheriae*, *M. tuberculosis*, *C. ulcerans*, *Y. pestis*, and *E. coli* targeted by Piper betel compounds**

Barh, D., Gupta, K., Jain, N., Khatri, G., León-Sicairos, N., Canizalez-Roman, A., Tiwari, S., Verma, A., Rahangdale, S., Shah Hassan, S., dos Santos, A. R., Ali, A., Guimarães, L. C., Thiago Jucá Ramos, R., Devarapalli, P., Barve, N., Bakhtiar, M., Kumavath, R., Ghosh, P. & Miyoshi, A. & 6 others, Silva, A., Kumar, A., Misra, A. N., Blum, K., Baumbach, J. & Azevedo, V., Mar 2013, In: *Integrative Biology*. 5, 3, p. 495-509 15 p.

#### **Density parameter estimation for finding clusters of homologous proteins-tracing actinobacterial pathogenicity lifestyles**

Röttger, R., Kalaghatgi, P., Sun, P., Soares, S. D. C., Azevedo, V., Wittkop, T. & Baumbach, J., 15. Jan 2013, In: *Bioinformatics*. 29, 2, p. 215-222

#### **Cluster editing**

Böcker, S. & Baumbach, J., 1. Jan 2013, *The Nature of Computation: Logic, Algorithms, Applications: 9th Conference on Computability in Europe, CIE 2013, Milan, Italy, July*. Bonizzoni, P., Brattka, V. & Löwe, B. (eds.). Springer, p. 33-44 12 p. (Lecture Notes in Computer Science, Vol. 7921).

#### **Neighborhood-preserving mapping between trees**

Baumbach, J., Ibragimov, R. & Guo, J.-Y., 1. Jan 2013, *Algorithms and Data Structures: 13th International Symposium, WADS 2013*. Dehne, F., Solis-Oba, R. & Sack, J.-R. (eds.). Springer, p. 427-438 12 p. (Lecture Notes in Computer Science, Vol. 8037).

#### **High-resolution detection of DNA binding sites of the global transcriptional regulator GlxR in *Corynebacterium glutamicum***

Jungwirth, B., Sala, C., Kohl, T. A., Uplekar, S., Baumbach, J., Cole, S. T., Pühler, A. & Tauch, A., Jan 2013, In: *Microbiology*. 159, Pt 1, p. 12-22 11 p.

#### **Analysis of the Airway Microbiota of Healthy Individuals and Patients with Chronic Obstructive Pulmonary Disease by T-RFLP and Clone Sequencing**

Zakharkina, T., Heinzl, E., Koczulla, R. A., Greulich, T., Rentz, K., Pauling, J. K., Baumbach, J., Herrmann, M., Grünewald, C., Dienemann, H., von Müller, L. & Bals, R., 2013, In: *PLOS ONE*. 8, 7, e68302.

#### **An integrative clinical database and diagnostics platform for biomarker identification and analysis in ion mobility spectra of human exhaled air**

Schneider, T., Hauschild, A.-C., Baumbach, J. I. & Baumbach, J., 2013, In: *Journal of Integrative Bioinformatics*. 10, 2, p. 218

#### **Covering tree with stars**

Baumbach, J., Guo, J.-Y. & Ibragimov, R., 2013, *Computing and Combinatorics: 19th International Conference, COCOON 2013, Hangzhou, China, June 21-23, 2013. Proceedings*. Du, D.-Z. & Zhang, G. (eds.). Springer, p. 373-384 12 p. (Lecture Notes in Computer Science, Vol. 7936).

### **GEDEVO: An Evolutionary Graph Edit Distance Algorithm for Biological Network Alignment**

Ibragimov, R., Malek, M., Guo, J. & Baumbach, J., 2013, *German Conference on Bioinformatics 2013*. Beißbarth, T., Kollmar, M., Leha, A., Morgenstern, B., Schultz, A.-K., Waack, S. & Wingender, E. (eds.). Schloss Dagstuhl-Leibniz-Zentrum fuer Informatik, Vol. 34. p. 68-79

### **Mature Epitope Density - A strategy for target selection based on immunoinformatics and exported prokaryotic proteins**

Santos, A. R., Pereira, V. B., Barbosa, E., Baumbach, J., Pauling, J., Röttger, R., Turk, M. Z., Silva, A., Miyoshi, A. & Azevedo, V., 2013, In: *BMC Genomics*. 14, Suppl. 6, p. 1-11 11 p., S4.

### **NABEECO: Biological network alignment with bee colony optimization algorithm**

Ibragimov, R., Martens, J., Guo, J.-Y. & Baumbach, J., 2013, *GECCO 2013 - Proceedings of the 2013 Genetic and Evolutionary Computation Conference Companion*. p. 43-44

### **Peak Detection Method Evaluation for Ion Mobility Spectrometry by Using Machine Learning Approaches**

Hauschild, A.-C., Kopczynski, D., D'Addario, M., Baumbach, J. I., Rahmann, S. & Baumbach, J., 2013, In: *Metabolites*. 3, 2, p. 277-293 17 p.

### **Efficient algorithms for extracting biological key pathways with global constraints**

Baumbach, J., Friedrich, T., Kötzing, T., Müller, J., Pauling, J. & Krohmer, A., 1. Jan 2012, *GECCO'12 - Proceedings of the 14th International Conference on Genetic and Evolutionary Computation*. p. 169-175 7 p.

### **Online transitivity clustering of biological data with missing values**

Röttger, R., Kreutzer, C., Vu, T. D., Wittkop, T. & Baumbach, J., 1. Jan 2012, *German Conference on Bioinformatics 2012, GCB 2012*. Böcker, S., Hufsky, F., Scheubert, K., Schleicher, J. & Schuster, S. (eds.). Schloss Dagstuhl-Leibniz-Zentrum fuer Informatik, p. 57-68 (OpenAccess Series in Informatics, Vol. 26).

### **Computational methods for metabolomic data analysis of ion mobility spectrometry data-reviewing the state of the art**

Hauschild, A.-C., Schneider, T., Pauling, J., Rupp, K., Jang, M., Baumbach, J. I. & Baumbach, J., 2012, In: *Metabolites*. 2, 4, p. 733-755 23 p.

### **CoryneRegNet 6.0: Updated database content, new analysis methods and novel features focusing on community demands**

Pauling, J., Röttger, R., Tauch, A., Azevedo, V. & Baumbach, J., 2012, In: *Nucleic Acids Research*. 40, Database Issue, p. D610-4

### **Efficient key pathway mining: combining networks and OMICS data**

Alcaraz, N., Friedrich, T., Kötzing, T., Krohmer, A., Müller, J., Pauling, J. & Baumbach, J., 2012, In: *Integrative Biology*. 4, 7, p. 756-64 9 p.

### **How Little Do We Actually Know? - On the Size of Gene Regulatory Networks**

Röttger, R., Ruckert, U., Taubert, J. & Baumbach, J., 2012, In: *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. 9, 5, p. 1293-1300

### **Integrated simultaneous analysis of different biomedical data types with exact weighted bi-cluster editing**

Sun, P., Guo, J. & Baumbach, J., 2012, In: *Journal of Integrative Bioinformatics*. 9, 2, p. 197

### **Integrated statistical learning of metabolic ion mobility spectrometry profiles for pulmonary disease identification**

Hauschild, A. C., Baumbach, J. & Baumbach, J., 2012, In: *Genetics and Molecular Research*. 11, 3, p. 2733-2744

### **Integrative computational biology**

Baumbach, J., 2012, In: *Integrative Biology*. 4, 7, p. 713-4 2 p.

Live sequence charts to model medical information

Aslakson, E., Szekely, S., Vernon, S. D., Bateman, L., Baumbach, J. & Setty, Y., 2012, In: *Theoretical Biology and Medical Modelling*. 9, 1, p. 22

On the trail of EHEC/EAEC--unraveling the gene regulatory networks of human pathogenic *Escherichia coli* bacteria  
Pauling, J., Röttger, R., Neuner, A., Salgado, H., Collado-Vides, J., Kalaghatgi, P., Azevedo, V., Tauch, A., Pühler, A. & Baumbach, J., 2012, In: *Integrative Biology*. 4, 7, p. 728-33

PIPS: pathogenicity island prediction software

Soares, S. C., Abreu, V. A. C., Ramos, R. T. J., Cerdeira, L., Silva, A., Baumbach, J., Trost, E., Tauch, A., Hirata, R., Mattos-Guaraldi, A. L., Miyoshi, A. & Azevedo, V., 2012, In: *PLOS ONE*. 7, 2, p. e30848

### **Stability and alignment of MCC/IMS devices**

Cumeras, R., Schneider, T., Favrod, P., Figueras, E., Gràcia, I., Maddula, S. & Baumbach, J., 2012, In: *International Journal for Ion Mobility Spectrometry*. 15, 1, p. 41-46

Analysis of quality raw data of second generation sequencers with Quality Assessment Software

Ramos, R. T., Carneiro, A. R., Baumbach, J., Azevedo, V., Schneider, M. P. & Silva, A., 2011, In: *BMC Research Notes*. 4, p. 130

A singular value decomposition approach for improved taxonomic classification of biological sequences

Santos, A. R., Santos, M. A., Baumbach, J., McCulloch, J. A., Oliveira, G. C., Silva, A., Miyoshi, A. & Azevedo, V., 2011, In: *BMC Genomics*. 12 Suppl 4, p. S11

clusterMaker: a multi-algorithm clustering plugin for Cytoscape

Morris, J. H., Apeltsin, L., Newman, A. M., Baumbach, J., Wittkop, T., Su, G., Bader, G. D. & Ferrin, T. E., 2011, In: *BMC Bioinformatics*. 12, p. 436

Comprehensive cluster analysis with Transitivity Clustering

Wittkop, T., Emig, D., Truss, A., Albrecht, M., Böcker, S. & Baumbach, J., 2011, In: *Nature Protocols*. 6, 3, p. 285-95 11 p.

Evidence for reductive genome evolution and lateral acquisition of virulence functions in two *Corynebacterium pseudotuberculosis* strains

Ruiz, J. C., D'Afonseca, V., Silva, A., Ali, A., Pinto, A. C., Santos, A. R., Rocha, A. A. M. C., Lopes, D. O., Dorella, F. A., Pacheco, L. G. C., Costa, M. P., Turk, M. Z., Seyffert, N., Moraes, P. M. R. O., Soares, S. C., Almeida, S. S., Castro, T. L. P., Abreu, V. A. C., Trost, E. & Baumbach, J. & 39 others, Tauch, A., Schneider, M. P. C., McCulloch, J., Cerdeira, L. T., Ramos, R. T. J., Zerlotini, A., Dominitini, A., Resende, D. M., Coser, E. M., Oliveira, L. M., Pedrosa, A. L., Vieira, C. U., Guimarães, C. T., Bartholomeu, D. C., Oliveira, D. M., Santos, F. R., Rabelo, É. M., Lobo, F. P., Franco, G. R., Costa, A. F., Castro, I. M., Dias, S. R. C., Ferro, J. A., Ortega, J. M., Paiva, L. V., Goulart, L. R., Almeida, J. F., Ferro, M. I. T., Carneiro, N. P., Falcão, P. R. K., Grynberg, P., Teixeira, S. M. R., Brommonschenkel, S., Oliveira, S. C., Meyer, R., Moore, R. J., Miyoshi, A., Oliveira, G. C. & Azevedo, V., 2011, In: *PLOS ONE*. 6, 4, p. e18551

Extension and Robustness of Transitivity Clustering for Protein-Protein Interaction Network Analysis

Wittkop, T., Rahmann, S., Röttger, R., Böcker, S. & Baumbach, J., 2011, In: *Internet Mathematics*. 7, 4, p. 255-273 19 p.

Rapid hybrid de novo assembly of a microbial genome using only short reads: *Corynebacterium pseudotuberculosis* I19 as a case study

Cerdeira, L. T., Carneiro, A. R., Ramos, R. T. J., de Almeida, S. S., D'Afonseca, V., Schneider, M. P. C., Baumbach, J., Tauch, A., McCulloch, J. A., Azevedo, V. A. C. & Silva, A., 2011, In: *Journal of Microbiological Methods*. 86, 2, p. 218-23 6 p.

RhizoRegNet--a database of rhizobial transcription factors and regulatory networks

Krol, E., Blom, J., Winnebold, J., Berhörster, A., Barnett, M. J., Goesmann, A., Baumbach, J. & Becker, A., 2011, In: *Arab Journal of Biotechnology*. 155, 1, p. 127-34 8 p.

AltAnalyze and DomainGraph: analyzing and visualizing exon expression data

Emig, D., Salomonis, N., Baumbach, J., Lengauer, T., Conklin, B. R. & Albrecht, M., 2010, In: Nucleic Acids Research. 38, Web Server issue, p. W755-62

Efficient online transcription factor binding site adjustment by integrating transitive graph projection with MoRAine 2.0

Wittkop, T., Rahmann, S. & Baumbach, J., 2010, In: Journal of Integrative Bioinformatics. 7, 3

On the power and limits of evolutionary conservation--unraveling bacterial gene regulatory networks

Baumbach, J., 2010, In: Nucleic Acids Research. 38, 22, p. 7877-84 8 p.

Partitioning biological data with transitivity clustering

Wittkop, T., Emig, D., Lange, S., Rahmann, S., Albrecht, M., Morris, J. H., Böcker, S., Stoye, J. & Baumbach, J., 2010, In: Nature Methods. 7, 6, p. 419-20 2 p.

From *Corynebacterium glutamicum* to *Mycobacterium tuberculosis*--towards transfers of gene regulatory networks and integrated data analyses with MycoRegNet

Krawczyk, J., Kohl, T. A., Goesmann, A., Kalinowski, J. & Baumbach, J., 2009, In: Nucleic Acids Research. 37, 14, p. e97

Integrated analysis and reconstruction of microbial transcriptional gene regulatory networks using CoryneRegNet

Baumbach, J., Wittkop, T., Kleindt, C. K. & Tauch, A., 2009, In: Nature Protocols. 4, 6, p. 992-1005 14 p.

MotifAdjuster: a tool for computational reassessment of transcription factor binding site annotations

Keilwagen, J., Baumbach, J., Kohl, T. A. & Grosse, I., 2009, In: Genome Biology. 10, 5, p. R46

Reliable transfer of transcriptional gene regulatory networks between taxonomically related organisms

Baumbach, J., Rahmann, S. & Tauch, A., 2009, In: BMC Systems Biology. 3, p. 8

Towards the integrated analysis, visualization and reconstruction of microbial gene regulatory networks

Baumbach, J., Tauch, A. & Rahmann, S., 2009, In: Briefings in Bioinformatics. 10, 1, p. 75-83 9 p.

Linking Cytoscape and the corynebacterial reference database CoryneRegNet

Baumbach, J. & Apeltsin, L., 2008, In: BMC Genomics. 9, p. 184

MoRAine--a web server for fast computational transcription factor binding motif re-annotation

Baumbach, J., Wittkop, T., Weile, J., Kohl, T. & Rahmann, S., 2008, In: Journal of Integrative Bioinformatics. 5, 2

The GlxR regulon of the amino acid producer *Corynebacterium glutamicum*: in silico and in vitro detection of DNA binding sites of a global transcription regulator

Kohl, T. A., Baumbach, J., Jungwirth, B., Pühler, A. & Tauch, A., 2008, In: Journal of Biotechnology. 135, 4, p. 340-50 11 p.

CoryneCenter - an online resource for the integrated analysis of corynebacterial genome and transcriptome data

Neuweger, H., Baumbach, J., Albaum, S., Bekel, T., Dondrup, M., Hüser, A. T., Kalinowski, J., Oehm, S., Pühler, A., Rahmann, S., Weile, J. & Goesmann, A., 2007, In: BMC Systems Biology. 1, p. 55

CoryneRegNet 3.0--an interactive systems biology platform for the analysis of gene regulatory networks in corynebacteria and *Escherichia coli*

Baumbach, J., Wittkop, T., Rademacher, K., Rahmann, S., Brinkrolf, K. & Tauch, A., 2007, In: Journal of Biotechnology. 129, 2, p. 279-89 11 p.

CoryneRegNet 4.0 - A reference database for corynebacterial gene regulatory networks

Baumbach, J., 2007, In: BMC Bioinformatics. 8, p. 429

Exact and heuristic algorithms for weighted cluster editing

Rahmann, S., Wittkop, T., Baumbach, J., Martin, M., Truss, A. & Böcker, S., 2007, *Computational Systems Bioinformatics: Proceedings of the CSB 2007 Conference, University of California, San Diego, USA, 13 – 17 August 2007*. Markstein, P. & Xu, Y. (eds.). Imperial College Press, Vol. 6. p. 391-401 11 p.

IMS2 -- An integrated medical software system for early lung cancer detection using ion mobility spectrometry data of human breath

Baumbach, J., Bunkowski, A., Lange, S., Oberwahrenbrock, T., Kleinbölting, N., Rahmann, S. & Baumbach, J. I., 2007, In: *Journal of Integrative Bioinformatics*. 4, 3, p. 75 1 p.

Large scale clustering of protein sequences with FORCE -A layout based heuristic for weighted cluster editing

Wittkop, T., Baumbach, J., Lobo, F. P. & Rahmann, S., 2007, In: *BMC Bioinformatics*. 8, p. 396

**CoryneRegNet 2: An integrative bioinformatics approach for reconstruction and comparison of transcriptional regulatory networks in prokaryotes**

Baumbach, J., Brinkrolf, K., Wittkop, T., Tauch, A. & Rahmann, S., 2006, In: *Journal of Integrative Bioinformatics*. 3, 2

CoryneRegNet - an ontology-based data warehouse of corynebacterial transcription factors and regulatory networks

Baumbach, J., Brinkrolf, K., Czaja, L. F., Rahmann, S. & Tauch, A., 2006, In: *BMC Genomics*. 7, p. 24

Graph-based analysis and visualization of experimental results with ONDEX

Köhler, J., Baumbach, J., Taubert, J., Specht, M., Skusa, A., Rüegg, A., Rawlings, C., Verrier, P. & Philippi, S., 2006, In: *Bioinformatics*. 22, 11, p. 1383-90 8 p.