

Ionas Erb

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,088
citations

394421

19
h-index

361022

35
g-index

45
all docs

45
docs citations

45
times ranked

4151
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | The Information-Geometric Perspective of Compositional Data Analysis. , 2021, , 21-43. | | 5 |
| 2 | Examining microbeâ€“metabolite correlations by linear methods. Nature Methods, 2021, 18, 37-39. | 19.0 | 15 |
| 3 | Multiple Sequence Alignment Computation Using the T-Coffee Regressive Algorithm Implementation. Methods in Molecular Biology, 2021, 2231, 89-97. | 0.9 | 6 |
| 4 | Amalgams: data-driven amalgamation for the dimensionality reduction of compositional data. NAR Genomics and Bioinformatics, 2020, 2, lqaa076. | 3.2 | 19 |
| 5 | Interpretable Log Contrasts for the Classification of Health Biomarkers: a New Approach to Balance Selection. MSystems, 2020, 5, . | 3.8 | 16 |
| 6 | Partial correlations in compositional data analysis. Applied Computing and Geosciences, 2020, 6, 100026. | 2.2 | 15 |
| 7 | Editorial:Â“Compositional data analysis and related methods applied to genomicsâ€”a first special issue from<i>NAR Genomics and Bioinformatics</i>. NAR Genomics and Bioinformatics, 2020, 2, lqaa103. | 3.2 | 10 |
| 8 | A field guide for the compositional analysis of any-omics data. GigaScience, 2019, 8, . | 6.4 | 187 |
| 9 | Pergola-web: a web server for the visualization and analysis of longitudinal behavioral data using repurposed genomics tools and standards. Nucleic Acids Research, 2019, 47, W600-W604. | 14.5 | 2 |
| 10 | Impaired development of neocortical circuits contributes to the neurological alterations in DYRK1A haploinsufficiency syndrome. Neurobiology of Disease, 2019, 127, 210-222. | 4.4 | 35 |
| 11 | Large multiple sequence alignments with a root-to-leaf regressive method. Nature Biotechnology, 2019, 37, 1466-1470. | 17.5 | 25 |
| 12 | Protocol for Measuring Compulsive-like Feeding Behavior in Mice. Bio-protocol, 2019, 9, e3308. | 0.4 | 1 |
| 13 | Extinction and reinstatement of an operant responding maintained by food in different models of obesity. Addiction Biology, 2018, 23, 544-555. | 2.6 | 11 |
| 14 | Timeâ€“course and dynamics of obesityâ€“related behavioral changes induced by energyâ€“dense foods in mice. Addiction Biology, 2018, 23, 531-543. | 2.6 | 13 |
| 15 | Understanding sequencing data as compositions: an outlook and review. Bioinformatics, 2018, 34, 2870-2878. | 4.1 | 224 |
| 16 | Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. IScience, 2018, 9, 244-257. | 4.1 | 5 |
| 17 | Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251. | 8.8 | 131 |
| 18 | Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. Genome Biology, 2016, 17, 32. | 8.8 | 166 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | How should we measure proportionality on relative gene expression data?. Theory in Biosciences, 2016, 135, 21-36. | 1.4 | 77 |
| 20 | Multiple sequence alignment modeling: methods and applications. Briefings in Bioinformatics, 2016, 17, 1009-1023. | 6.5 | 153 |
| 21 | Combined Treatment With Environmental Enrichment and (-)-Epigallocatechin-3-Gallate Ameliorates Learning Deficits and Hippocampal Alterations in a Mouse Model of Down Syndrome. ENeuro, 2016, 3, ENEURO.0103-16.2016. | 1.9 | 42 |
| 22 | Principal Component Analysis of the Effects of Environmental Enrichment and (-)-epigallocatechin-3-gallate on Age-Associated Learning Deficits in a Mouse Model of Down Syndrome. Frontiers in Behavioral Neuroscience, 2015, 9, 330. | 2.0 | 44 |
| 23 | Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179. | 1.1 | 97 |
| 24 | Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089. | 5.5 | 102 |
| 25 | T-Coffee: Tree-Based Consistency Objective Function for Alignment Evaluation. Methods in Molecular Biology, 2014, 1079, 117-129. | 0.9 | 56 |
| 26 | Efficient and Interpretable Prediction of Protein Functional Classes by Correspondence Analysis and Compact Set Relations. PLoS ONE, 2013, 8, e75542. | 2.5 | 7 |
| 27 | Use of ChIP-Seq data for the design of a multiple promoter-alignment method. Nucleic Acids Research, 2012, 40, e52-e52. | 14.5 | 23 |
| 28 | MotEvo: integrated Bayesian probabilistic methods for inferring regulatory sites and motifs on multiple alignments of DNA sequences. Bioinformatics, 2012, 28, 487-494. | 4.1 | 114 |
| 29 | Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. Nature Protocols, 2011, 6, 1669-1682. | 12.0 | 87 |
| 30 | BlastRâ€”fast and accurate database searches for non-coding RNAs. Nucleic Acids Research, 2011, 39, 6886-6895. | 14.5 | 28 |
| 31 | Transcription Factor Binding Site Positioning in Yeast: Proximal Promoter Motifs Characterize TATA-Less Promoters. PLoS ONE, 2011, 6, e24279. | 2.5 | 30 |
| 32 | The functional importance of telomere clustering: Global changes in gene expression result from SIR factor dispersion. Genome Research, 2009, 19, 611-625. | 5.5 | 110 |
| 33 | Genome-wide Expression Profiling, In Vivo DNA Binding Analysis, and Probabilistic Motif Prediction Reveal Novel Abf1 Target Genes during Fermentation, Respiration, and Sporulation in Yeast. Molecular Biology of the Cell, 2008, 19, 2193-2207. | 2.1 | 29 |
| 34 | SwissRegulon: a database of genome-wide annotations of regulatory sites. Nucleic Acids Research, 2007, 35, D127-D131. | 14.5 | 123 |
| 35 | On a Notion of Linear Replicator Equations. Journal of Dynamics and Differential Equations, 2005, 17, 427-451. | 1.9 | 12 |
| 36 | Multi-Information in the Thermodynamic Limit. Journal of Statistical Physics, 2004, 115, 949-976. | 1.2 | 13 |