

Leonid Chindelevitch

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

1,852
citations

758635

12
h-index

476904

29
g-index

57
all docs

57
docs citations

57
times ranked

3085
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273. | 3.4 | 114 |
| 2 | Inferring the effectiveness of government interventions against COVID-19. <i>Science</i> , 2021, 371, . | 6.0 | 730 |
| 3 | Fast median computation for symmetric, orthogonal matrices under the rank distance. <i>Linear Algebra and Its Applications</i> , 2021, 614, 394-414. | 0.4 | 1 |
| 4 | SplitStrains, a tool to identify and separate mixed Mycobacterium tuberculosis infections from WGS data. <i>Microbial Genomics</i> , 2021, 7, . | 1.0 | 7 |
| 5 | Predicting drug resistance in <i>M. tuberculosis</i> using a long-term recurrent convolutional network. , 2021, , . | | 1 |
| 6 | INGOT-DR: an interpretable classifier for predicting drug resistance in <i>M. tuberculosis</i> . <i>Algorithms for Molecular Biology</i> , 2021, 16, 17. | 0.3 | 9 |
| 7 | Understanding the effectiveness of government interventions against the resurgence of COVID-19 in Europe. <i>Nature Communications</i> , 2021, 12, 5820. | 5.8 | 135 |
| 8 | Network science inspires novel tree shape statistics. <i>PLoS ONE</i> , 2021, 16, e0259877. | 1.1 | 7 |
| 9 | Computing the distribution of the Robinson-Foulds distance. <i>Computational Biology and Chemistry</i> , 2020, 87, 107284. | 1.1 | 1 |
| 10 | PathOGIST: A Novel Method for Clustering Pathogen Isolates by Combining Multiple Genotyping Signals. <i>Lecture Notes in Computer Science</i> , 2020, , 108-124. | 1.0 | 0 |
| 11 | Towards better prediction of Mycobacterium tuberculosis lineages from MIRU-VNTR data. <i>Infection, Genetics and Evolution</i> , 2019, 72, 59-66. | 1.0 | 9 |
| 12 | MCS2: minimal coordinated supports for fast enumeration of minimal cut sets in metabolic networks. <i>Bioinformatics</i> , 2019, 35, i615-i623. | 1.8 | 4 |
| 13 | A cubic algorithm for the generalized rank median of three genomes. <i>Algorithms for Molecular Biology</i> , 2019, 14, 16. | 0.3 | 0 |
| 14 | Generalizations of the Genomic Rank Distance to Indels. <i>Lecture Notes in Computer Science</i> , 2019, , 152-164. | 1.0 | 0 |
| 15 | Counting Sorting Scenarios and Intermediate Genomes for the Rank Distance. <i>Lecture Notes in Computer Science</i> , 2019, , 137-151. | 1.0 | 1 |
| 16 | Deconvoluting the diversity of within-host pathogen strains in a multi-locus sequence typing framework. <i>BMC Bioinformatics</i> , 2019, 20, 637. | 1.2 | 3 |
| 17 | A new resolution function to evaluate tree shape statistics. <i>PLoS ONE</i> , 2019, 14, e0224197. | 1.1 | 4 |
| 18 | A new resolution function to evaluate tree shape statistics. , 2019, 14, e0224197. | | 0 |

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|----|---|-----|-----------|
| 19 | A new resolution function to evaluate tree shape statistics. , 2019, 14, e0224197. | | 0 |
| 20 | A new resolution function to evaluate tree shape statistics. , 2019, 14, e0224197. | | 0 |
| 21 | Relatedness of the incidence decay with exponential adjustment (IDEA) model, "Farr's law" and SIR compartmental difference equation models. Infectious Disease Modelling, 2018, 3, 1-12. | 1.2 | 14 |
| 22 | The MONGOOSE Rational Arithmetic Toolbox. Methods in Molecular Biology, 2018, 1716, 77-99. | 0.4 | 0 |
| 23 | A Cubic Algorithm for the Generalized Rank Median of Three Genomes. Lecture Notes in Computer Science, 2018, , 3-27. | 1.0 | 0 |
| 24 | Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. Scientific Reports, 2018, 8, 15382. | 1.6 | 75 |
| 25 | On the rank-distance median of 3 permutations. BMC Bioinformatics, 2018, 19, 142. | 1.2 | 3 |
| 26 | MentalIST " A fast MLST caller for large MLST schemes. Microbial Genomics, 2018, 4, . | 1.0 | 55 |
| 27 | A standardised method for interpreting the association between mutations and phenotypic drug resistance in Mycobacterium tuberculosis. European Respiratory Journal, 2017, 50, 1701354. | 3.1 | 273 |
| 28 | Polyclonal Pulmonary Tuberculosis Infections and Risk for Multidrug Resistance, Lima, Peru. Emerging Infectious Diseases, 2017, 23, 1887-1890. | 2.0 | 11 |
| 29 | On the Rank-Distance Median of 3 Permutations. Lecture Notes in Computer Science, 2017, , 256-276. | 1.0 | 1 |
| 30 | Vision Screening Results in a Cohort of Bhopal Gas Disaster Survivors. Current Science, 2017, 112, 2085. | 0.4 | 0 |
| 31 | ClassTR: Classifying Within-Host Heterogeneity Based on Tandem Repeats with Application to Mycobacterium tuberculosis Infections. PLoS Computational Biology, 2016, 12, e1004475. | 1.5 | 14 |
| 32 | Reply to Chen et al. Journal of Infectious Diseases, 2016, 214, 1287-1288. | 1.9 | 0 |
| 33 | Within-Host Heterogeneity of Mycobacterium tuberculosis Infection Is Associated With Poor Early Treatment Response: A Prospective Cohort Study. Journal of Infectious Diseases, 2016, 213, 1796-1799. | 1.9 | 45 |
| 34 | Reply to "Do genome-scale models need exact solvers or clearer standards?". Molecular Systems Biology, 2015, 11, 830. | 3.2 | 7 |
| 35 | Evaluating the potential impact of enhancing HIV treatment and tuberculosis control programmes on the burden of tuberculosis. Journal of the Royal Society Interface, 2015, 12, 20150146. | 1.5 | 9 |
| 36 | An exact arithmetic toolbox for a consistent and reproducible structural analysis of metabolic network models. Nature Communications, 2014, 5, 4893. | 5.8 | 37 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Optimizing a global alignment of protein interaction networks. <i>Bioinformatics</i> , 2013, 29, 2765-2773. | 1.8 | 53 |
| 38 | MetaMerge: scaling up genome-scale metabolic reconstructions, with application to <i>Mycobacterium tuberculosis</i> . <i>Genome Biology</i> , 2012, 13, R6. | 13.9 | 31 |
| 39 | Metabolic Network Analysis Demystified. <i>Lecture Notes in Computer Science</i> , 2011, , 31-33. | 1.0 | 0 |
| 40 | LOCAL OPTIMIZATION FOR GLOBAL ALIGNMENT OF PROTEIN INTERACTION NETWORKS. , 2009, , 123-132. | | 25 |
| 41 | Inverting the Viterbi algorithm. , 2008, , . | | 14 |
| 42 | Error analysis and preconditioning for an enhanced DtN-FE algorithm for exterior scattering problems. <i>Journal of Computational and Applied Mathematics</i> , 2007, 204, 493-504. | 1.1 | 5 |
| 43 | ON THE INFERENCE OF PARSIMONIOUS INDEL EVOLUTIONARY SCENARIOS. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 721-744. | 0.3 | 24 |