

# Galaxy: a comprehensive approach for supporting accessible and transparent computational research in the life sciences

Genome Biology

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Using Galaxy to Perform Large-Scale Interactive Data Analyses. <i>Current Protocols in Bioinformatics</i> , 2007, 19, Unit 10.5.	25.8	100
2	Bacterial population genomics and infectious disease diagnostics. <i>Trends in Biotechnology</i> , 2010, 28, 611-618.	4.9	44
3	BiologicalNetworks 2.0 - an integrative view of genome biology data. <i>BMC Bioinformatics</i> , 2010, 11, 610.	1.2	21
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6	Putting epigenome comparison into practice. <i>Nature Biotechnology</i> , 2010, 28, 1053-1056.	9.4	7
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8	Taming complex bioinformatics workflows with weaver, makeflow, and starch. , 2010, , .		12
9	Relational database index choices for genome annotation data. , 2010, , .		3
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1859	A Workflow Management System for Scalable Data Mining on Clouds. <i>IEEE Transactions on Services Computing</i> , 2018, 11, 480-492.	3.2	78
1860	A resource provisioning framework for bioinformatics applications in multi-cloud environments. <i>Future Generation Computer Systems</i> , 2018, 78, 379-391.	4.9	23
1861	The future of scientific workflows. <i>International Journal of High Performance Computing Applications</i> , 2018, 32, 159-175.	2.4	104
1862	Phloem fibres as motors of gravitropic behaviour of flax plants: level of transcriptome. <i>Functional Plant Biology</i> , 2018, 45, 203.	1.1	18
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1864	A Combination of Stable Isotope Probing, Illumina Sequencing, and Co-occurrence Network to Investigate Thermophilic Acetate- and Lactate-Utilizing Bacteria. <i>Microbial Ecology</i> , 2018, 75, 113-122.	1.4	32
1865	Functional interrelationship between TFIIA and E2F transcription factors at specific cell cycle gene loci. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 712-722.	1.2	8
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1873	The Recent Trends, Techniques and Methods of Cloud Security. <i>Smart Innovation, Systems and Technologies</i> , 2018, , 594-601.	0.5	0
1874	Cloud Computing in Bioinformatics and Big Data Analytics: Current Status and Future Research. <i>Advances in Intelligent Systems and Computing</i> , 2018, , 629-640.	0.5	6
1875	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. <i>Analytical Chemistry</i> , 2018, 90, 649-656.	3.2	50
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1877	Rapid startup of thermophilic anaerobic digester to remove tetracycline and sulfonamides resistance genes from sewage sludge. <i>Science of the Total Environment</i> , 2018, 612, 788-798.	3.9	90
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1879	A multidisciplinary study of a Late Pleistocene arctic ground squirrel ( <i>Urocyon parryi</i> ) midden from Yukon, Canada. <i>Quaternary Research</i> , 2018, 89, 333-351.	1.0	3
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1882	The effects of pastoral intensification on the feeding interactions of generalist predators in streams. <i>Molecular Ecology</i> , 2018, 27, 590-602.	2.0	9
1883	Iron Age Italic population genetics: the Piceni from Novilara (8th-7th century BC). <i>Annals of Human Biology</i> , 2018, 45, 34-43.	0.4	13
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1885	Diversity and dynamics of lactic acid bacteria in Atole agrio, a traditional maize-based fermented beverage from South-Eastern Mexico, analysed by high throughput sequencing and culturing. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 385-399.	0.7	28
1886	Rhizobia inhabiting nodules and rhizosphere soils of alfalfa: A strong selection of facultative microsymbionts. <i>Soil Biology and Biochemistry</i> , 2018, 116, 340-350.	4.2	23
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1896	DagOn*: Executing Direct Acyclic Graphs as Parallel Jobs on Anything. , 2018, , .		19
1897	Fine-Grained Attribute Level Locking Scheme for Collaborative Scientific Workflow Development. , 2018, , .		1
1898	DataPackageR: Reproducible data preprocessing, standardization and sharing using R/Bioconductor for collaborative data analysis. <i>Gates Open Research</i> , 2018, 2, 31.	2.0	6
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1900	Quantitative Approach in Clinical Microbiology: A Paradigm Shift Toward Culture-Free Methods. , 2018, , 599-615.		1
1901	SyNDI: synchronous network data integration framework. <i>BMC Bioinformatics</i> , 2018, 19, 403.	1.2	1
1902	A Putative Zn2Cys6 Transcription Factor Is Associated With Isoprothiolane Resistance in <i>Magnaporthe oryzae</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2608.	1.5	24
1903	Haploinsufficiency of the intellectual disability gene SETD5 disturbs developmental gene expression and cognition. <i>Nature Neuroscience</i> , 2018, 21, 1717-1727.	7.1	65
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1905	Maser: one-stop platform for NGS big data from analysis to visualization. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	42
1906	Intestinal Microbiome in Irritable Bowel Syndrome before and after Gut-Directed Hypnotherapy. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3619.	1.8	29
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1910	Comparative transcriptomic analysis of bovine papillomatosis. <i>BMC Genomics</i> , 2018, 19, 949.	1.2	5
1911	RGAAT: A Reference-based Genome Assembly and Annotation Tool for New Genomes and Upgrade of Known Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 373-381.	3.0	15
1912	Developing reproducible bioinformatics analysis workflows for heterogeneous computing environments to support African genomics. <i>BMC Bioinformatics</i> , 2018, 19, 457.	1.2	33
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1916	Targeting the BRD4-HOXB13 Coregulated Transcriptional Networks with Bromodomain-Kinase Inhibitors to Suppress Metastatic Castration-Resistant Prostate Cancer. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 2796-2810.	1.9	26
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1919	Single Nucleotide Polymorphism Analysis Indicates Genetic Distinction and Reduced Diversity of Swine-Associated Methicillin Resistant <i>Staphylococcus aureus</i> (MRSA) ST5 Isolates Compared to Clinical MRSA ST5 Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 2078.	1.5	28
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1922	Immune-suppression by OsHV-1 viral infection causes fatal bacteraemia in Pacific oysters. <i>Nature Communications</i> , 2018, 9, 4215.	5.8	217
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1929	Computational tools to unmask transposable elements. <i>Nature Reviews Genetics</i> , 2018, 19, 688-704.	7.7	173
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1931	EasyQC: Tool with Interactive User Interface for Efficient Next-Generation Sequencing Data Quality Control. <i>Journal of Computational Biology</i> , 2018, 25, 1301-1311.	0.8	8
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1933	Analytical Approaches for Exome Sequence Data. <i>Translational Bioinformatics</i> , 2018, , 121-136.	0.0	0
1934	Neutral variation does not predict immunogenetic variation in the European grayling ( <i>Thymallus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	8
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1936	A Microbial Signature of Psychological Distress in Irritable Bowel Syndrome. <i>Psychosomatic Medicine</i> , 2018, 80, 698-709.	1.3	75
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1939	High level of genetic connectivity in a deep-water reef fish, <i>Caulolatilus microps</i> . <i>Journal of Fish Biology</i> , 2018, 93, 766-777.	0.7	3
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1941	Copy number variants implicate cardiac function and development pathways in earthquake-induced stress cardiomyopathy. <i>Scientific Reports</i> , 2018, 8, 7548.	1.6	8
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1945	Nonsynonymous Polymorphism in Guanine Monophosphate Synthetase Is a Risk Factor for Unfavorable Thiopurine Metabolite Ratios in Patients With Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 2606-2612.	0.9	4
1946	Selective nanopore sequencing of human BRCA1 by Cas9-assisted targeting of chromosome segments (CATCH). <i>Nucleic Acids Research</i> , 2018, 46, e87-e87.	6.5	98
1947	ASaiM: a Galaxy-based framework to analyze microbiota data. <i>GigaScience</i> , 2018, 7, .	3.3	25
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1949	Selecting Fully Modified XNA Aptamers Using Synthetic Genetics. <i>Current Protocols in Chemical Biology</i> , 2018, 10, e44.	1.7	16
1950	Managing Complex Workflows in Bioinformatics: An Interactive Toolkit With GPU Acceleration. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 199-208.	2.2	17
1951	Tellurium notebooks – An environment for reproducible dynamical modeling in systems biology. <i>PLoS Computational Biology</i> , 2018, 14, e1006220.	1.5	41
1952	The helicase Ded1p controls use of near-cognate translation initiation codons in 5' UTRs. <i>Nature</i> , 2018, 559, 130-134.	13.7	143
1953	Computational Techniques in Data Integration and Big Data Handling in Omics. , 2018, , 209-222.		0
1954	Histone methylation changes are required for life cycle progression in the human parasite <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2018, 14, e1007066.	2.1	57
1955	Analysis of the resistance mechanisms in sugarcane during <i>Sporisorium scitamineum</i> infection using RNA-seq and microscopy. <i>PLoS ONE</i> , 2018, 13, e0197840.	1.1	37
1956	A lightweight rapid application development framework for biomedical image analysis. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 164, 193-205.	2.6	12
1957	Cross-domain similarity assessment for workflow improvement to handle Big Data challenge in workflow management. <i>Journal of Big Data</i> , 2018, 5, .	6.9	0
1958	Genomic functions of developmental pluripotency associated factor 4 (Dppa4) in pluripotent stem cells and cancer. <i>Stem Cell Research</i> , 2018, 31, 83-94.	0.3	14
1959	Ethylene-Related Gene Expression Networks in Wood Formation. <i>Frontiers in Plant Science</i> , 2018, 9, 272.	1.7	48
1960	The Agave Platform. , 2018, , .		22
1961	Understanding Forest Health with Remote Sensing, Part III: Requirements for a Scalable Multi-Source Forest Health Monitoring Network Based on Data Science Approaches. <i>Remote Sensing</i> , 2018, 10, 1120.	1.8	63

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1964	Identification of Bisphenol A-Assimilating Microorganisms in Mixed Microbial Communities Using $^{13}\text{C}$ -DNA Stable Isotope Probing. <i>Environmental Science &amp; Technology</i> , 2018, 52, 9128-9135.	4.6	17
1965	An FRMD4B variant suppresses dysplastic photoreceptor lesions in models of enhanced S-cone syndrome and of Nrl deficiency. <i>Human Molecular Genetics</i> , 2018, 27, 3340-3352.	1.4	6
1966	27nt-RNAs guide histone variant deposition via $\alpha$ -RNA-induced DNA replication interference <sup>TM</sup> and thus transmit parental genome partitioning in <i>Stylonychia</i> . <i>Epigenetics and Chromatin</i> , 2018, 11, 31.	1.8	6
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1968	Western Indian Rural Gut Microbial Diversity in Extreme Prakriti Endo-Phenotypes Reveals Signature Microbes. <i>Frontiers in Microbiology</i> , 2018, 9, 118.	1.5	68
1969	A Guide to the Chloroplast Transcriptome Analysis Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2018, 1829, 295-313.	0.4	12
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1974	De novo transcriptome assembly of <i>Pueraria montana</i> var. <i>lobata</i> and <i>Neustanthus phaseoloides</i> for the development of eSSR and SNP markers: narrowing the US origin(s) of the invasive kudzu. <i>BMC Genomics</i> , 2018, 19, 439.	1.2	11
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1976	Bystro: rapid online variant annotation and natural-language filtering at whole-genome scale. <i>Genome Biology</i> , 2018, 19, 14.	3.8	29
1977	IRProfiler $\hat{=}$ a software toolbox for high throughput immune receptor profiling. <i>BMC Bioinformatics</i> , 2018, 19, 144.	1.2	7
1978	Effect of Bmi1 over-expression on gene expression in adult and embryonic murine neural stem cells. <i>Scientific Reports</i> , 2018, 8, 7464.	1.6	19
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1982	KREAP: an automated Galaxy platform to quantify in vitro re-epithelialization kinetics. <i>GigaScience</i> , 2018, 7, .	3.3	3
1983	Riluzole reduces amyloid beta pathology, improves memory, and restores gene expression changes in a transgenic mouse model of early-onset Alzheimer's disease. <i>Translational Psychiatry</i> , 2018, 8, 153.	2.4	64
1984	Adaptations to marine versus terrestrial low temperature environments as revealed by comparative genomic analyses of the genus <i>Psychrobacter</i> . <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	17
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1986	pyPaSWAS: Python-based multi-core CPU and GPU sequence alignment. <i>PLoS ONE</i> , 2018, 13, e0190279.	1.1	13
1987	Higher sequence diversity in the vaginal tract than in blood at early HIV-1 infection. <i>PLoS Pathogens</i> , 2018, 14, e1006754.	2.1	16
1988	Expression Analysis of Genes Regulated by Thyroid Hormone in Neural Cells. <i>Methods in Molecular Biology</i> , 2018, 1801, 17-28.	0.4	2
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1995	Computational Systems Biology Applications. , 2019, , 66-73.		0
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2005	The Science Gateways Community Institute: Collaborations and efforts on international scale. <i>Future Generation Computer Systems</i> , 2019, 101, 951-958.	4.9	2
2006	TASKA: A modular task management system to support health research studies. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 121.	1.5	7
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2014	Dosage Compensation throughout the <i>Schistosoma mansoni</i> Lifecycle: Specific Chromatin Landscape of the Z Chromosome. <i>Genome Biology and Evolution</i> , 2019, 11, 1909-1922.	1.1	15
2015	Corvus: a framework for interfacing scientific software for spectroscopic and materials science applications. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 1694-1704.	1.0	5

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2054	The role of machine learning in scientific workflows. <i>International Journal of High Performance Computing Applications</i> , 2019, 33, 1128-1139.	2.4	21
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2058	Surface sterilization methods impact measures of internal microbial diversity in ticks. <i>Parasites and Vectors</i> , 2019, 12, 268.	1.0	81
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