

# Yufeng Wu

## List of Publications by Year in descending order

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36  
papers

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citations

623734

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h-index

580821

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g-index

39  
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39  
docs citations

39  
times ranked

884  
citing authors

#	ARTICLE	IF	CITATIONS
1	Alterations of host-gut microbiome interactions in multiple sclerosis. <i>EBioMedicine</i> , 2022, 76, 103798.	6.1	59
2	Accurate and efficient cell lineage tree inference from noisy single cell data: the maximum likelihood perfect phylogeny approach. <i>Bioinformatics</i> , 2020, 36, 742-750.	4.1	21
3	Inference of population admixture network from local gene genealogies: a coalescent-based maximum likelihood approach. <i>Bioinformatics</i> , 2020, 36, i326-i334.	4.1	6
4	HPV-EM: an accurate HPV detection and genotyping EM algorithm. <i>Scientific Reports</i> , 2020, 10, 14340.	3.3	3
5	Inferring the ancestry of parents and grandparents from genetic data. <i>PLoS Computational Biology</i> , 2020, 16, e1008065.	3.2	9
6	InvBFM: finding genomic inversions from high-throughput sequence data based on feature mining. <i>BMC Genomics</i> , 2020, 21, 173.	2.8	4
7	Detecting circular RNA from high-throughput sequence data with de Bruijn graph. <i>BMC Genomics</i> , 2020, 21, 749.	2.8	11
8	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
9	GAPPadder: a sensitive approach for closing gaps on draft genomes with short sequence reads. <i>BMC Genomics</i> , 2019, 20, 426.	2.8	15
10	DeepSV: accurate calling of genomic deletions from high-throughput sequencing data using deep convolutional neural network. <i>BMC Bioinformatics</i> , 2019, 20, 665.	2.6	27
11	CLADES: A classification-based machine learning method for species delimitation from population genetic data. <i>Molecular Ecology Resources</i> , 2018, 18, 1144-1156.	4.8	13
12	CircMarker: a fast and accurate algorithm for circular RNA detection. <i>BMC Genomics</i> , 2018, 19, 572.	2.8	25
13	An improved approach for reconstructing consensus repeats from short sequence reads. <i>BMC Genomics</i> , 2018, 19, 566.	2.8	1
14	STELLS2: fast and accurate coalescent-based maximum likelihood inference of species trees from gene tree topologies. <i>Bioinformatics</i> , 2017, 33, 1789-1797.	4.1	14
15	RENT+: an improved method for inferring local genealogical trees from haplotypes with recombination. <i>Bioinformatics</i> , 2017, 33, 1021-1030.	4.1	22
16	GAPPadder: A sensitive approach for closing gaps on draft genomes with short sequence reads. , 2017, , .		1
17	REPdenovo: Inferring De Novo Repeat Motifs from Short Sequence Reads. <i>PLoS ONE</i> , 2016, 11, e0150719.	2.5	45
18	Concod: Accurate consensus-based approach of calling deletions from high-throughput sequencing data. , 2016, , .		2

#	ARTICLE	IF	CITATIONS
19	An algorithm for computing the gene tree probability under the multispecies coalescent and its application in the inference of population tree. <i>Bioinformatics</i> , 2016, 32, i225-i233.	4.1	12
20	Fast Construction of Near Parsimonious Hybridization Networks for Multiple Phylogenetic Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 565-570.	3.0	5
21	A coalescent-based method for population tree inference with haplotypes. <i>Bioinformatics</i> , 2015, 31, 691-698.	4.1	9
22	Genomic takeover by transposable elements in the Strawberry poison frog. <i>Molecular Biology and Evolution</i> , 2014, 35, 2913-2927.	8.9	45
23	An SVM-based approach for discovering splicing junctions with RNA-Seq. , 2014, , .		0
24	GINDEL: Accurate Genotype Calling of Insertions and Deletions from Low Coverage Population Sequence Reads. <i>PLoS ONE</i> , 2014, 9, e113324.	2.5	22
25	An Algorithm for Constructing Parsimonious Hybridization Networks with Multiple Phylogenetic Trees. <i>Journal of Computational Biology</i> , 2013, 20, 792-804.	1.6	19
26	Workshop: Calling Structural Variation with low-coverage sequencing data by mapping to focal region. , 2012, , .		0
27	COALESCENT-BASED SPECIES TREE INFERENCE FROM GENE TREE TOPOLOGIES UNDER INCOMPLETE LINEAGE SORTING BY MAXIMUM LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 763-775.	2.3	128
28	Identifying interacting SNPs with parallel fish-agent based logic regression. , 2011, , .		2
29	New Methods for Inference of Local Tree Topologies with Recombinant SNP Sequences in Populations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 182-193.	3.0	14
30	Linkage disequilibrium based genotype calling from low-coverage shotgun sequencing reads. <i>BMC Bioinformatics</i> , 2011, 12, S53.	2.6	9
31	Close lower and upper bounds for the minimum reticulate network of multiple phylogenetic trees. <i>Bioinformatics</i> , 2010, 26, i140-i148.	4.1	40
32	Exact Computation of Coalescent Likelihood for Panmictic and Subdivided Populations under the Infinite Sites Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 611-618.	3.0	11
33	A practical method for exact computation of subtree prune and regraft distance. <i>Bioinformatics</i> , 2009, 25, 190-196.	4.1	68
34	A new recombination lower bound and the minimum perfect phylogenetic forest problem. <i>Journal of Combinatorial Optimization</i> , 2008, 16, 229-247.	1.3	3
35	Association Mapping of Complex Diseases with Ancestral Recombination Graphs: Models and Efficient Algorithms. <i>Journal of Computational Biology</i> , 2008, 15, 667-684.	1.6	9
36	Efficient computation of close lower and upper bounds on the minimum number of recombinations in biological sequence evolution. <i>Bioinformatics</i> , 2005, 21, i413-i422.	4.1	45