# Yufeng Wu

## List of Publications by Year
## in descending order

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|---|---|---|---|
| 36 papers | 756 citations | 623734<br>14 h-index | 580821<br>25 g-index |
| 39 all docs | 39 docs citations | 39 times ranked | 884 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | COALESCENT-BASED SPECIES TREE INFERENCE FROM GENE TREE TOPOLOGIES UNDER INCOMPLETE LINEAGE SORTING BY MAXIMUM LIKELIHOOD. Evolution; International Journal of Organic Evolution, 2012, 66, 763-775. | 2.3 | 128 |
| 2 | A practical method for exact computation of subtree prune and regraft distance. Bioinformatics, 2009, 25, 190-196. | 4.1 | 68 |
| 3 | Alterations of host-gut microbiome interactions in multiple sclerosis. EBioMedicine, 2022, 76, 103798. | 6.1 | 59 |
| 4 | Efficient computation of close lower and upper bounds on the minimum number of recombinations in biological sequence evolution. Bioinformatics, 2005, 21, i413-i422. | 4.1 | 45 |
| 5 | Genomic takeover by transposable elements in the Strawberry poison frog. Molecular Biology and Evolution, 2014, 35, 2913-2927. | 8.9 | 45 |
| 6 | REPdenovo: Inferring De Novo Repeat Motifs from Short Sequence Reads. PLoS ONE, 2016, 11, e0150719. | 2.5 | 45 |
| 7 | Close lower and upper bounds for the minimum reticulate network of multiple phylogenetic trees. Bioinformatics, 2010, 26, i140-i148. | 4.1 | 40 |
| 8 | A draft genome sequence of the elusive giant squid, Architeuthis dux. GigaScience, 2020, 9, . | 6.4 | 37 |
| 9 | DeepSV: accurate calling of genomic deletions from high-throughput sequencing data using deep convolutional neural network. BMC Bioinformatics, 2019, 20, 665. | 2.6 | 27 |
| 10 | CircMarker: a fast and accurate algorithm for circular RNA detection. BMC Genomics, 2018, 19, 572. | 2.8 | 25 |
| 11 | RENT+: an improved method for inferring local genealogical trees from haplotypes with recombination. Bioinformatics, 2017, 33, 1021-1030. | 4.1 | 22 |
| 12 | GINDEL: Accurate Genotype Calling of Insertions and Deletions from Low Coverage Population Sequence Reads. PLoS ONE, 2014, 9, e113324. | 2.5 | 22 |
| 13 | Accurate and efficient cell lineage tree inference from noisy single cell data: the maximum likelihood perfect phylogeny approach. Bioinformatics, 2020, 36, 742-750. | 4.1 | 21 |
| 14 | An Algorithm for Constructing Parsimonious Hybridization Networks with Multiple Phylogenetic Trees. Journal of Computational Biology, 2013, 20, 792-804. | 1.6 | 19 |
| 15 | GAPPadder: a sensitive approach for closing gaps on draft genomes with short sequence reads. BMC Genomics, 2019, 20, 426. | 2.8 | 15 |
| 16 | New Methods for Inference of Local Tree Topologies with Recombinant SNP Sequences in Populations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 182-193. | 3.0 | 14 |
| 17 | STELLS2: fast and accurate coalescent-based maximum likelihood inference of species trees from gene tree topologies. Bioinformatics, 2017, 33, 1789-1797. | 4.1 | 14 |
| 18 | CLADES: A classification-based machine learning method for species delimitation from population genetic data. Molecular Ecology Resources, 2018, 18, 1144-1156. | 4.8 | 13 |

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|---|---------|-----|-----------|
| 19 | An algorithm for computing the gene tree probability under the multispecies coalescent and its application in the inference of population tree. Bioinformatics, 2016, 32, i225-i233. | 4.1 | 12 |
| 20 | Exact Computation of Coalescent Likelihood for Panmictic and Subdivided Populations under the Infinite Sites Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 611-618. | 3.0 | 11 |
| 21 | Detecting circular RNA from high-throughput sequence data with de Bruijn graph. BMC Genomics, 2020, 21, 749. | 2.8 | 11 |
| 22 | Association Mapping of Complex Diseases with Ancestral Recombination Graphs: Models and Efficient Algorithms. Journal of Computational Biology, 2008, 15, 667-684. | 1.6 | 9 |
| 23 | Linkage disequilibrium based genotype calling from low-coverage shotgun sequencing reads. BMC Bioinformatics, 2011, 12, S53. | 2.6 | 9 |
| 24 | A coalescent-based method for population tree inference with haplotypes. Bioinformatics, 2015, 31, 691-698. | 4.1 | 9 |
| 25 | Inferring the ancestry of parents and grandparents from genetic data. PLoS Computational Biology, 2020, 16, e1008065. | 3.2 | 9 |
| 26 | Inference of population admixture network from local gene genealogies: a coalescent-based maximum likelihood approach. Bioinformatics, 2020, 36, i326-i334. | 4.1 | 6 |
| 27 | Fast Construction of Near Parsimonious Hybridization Networks for Multiple Phylogenetic Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 565-570. | 3.0 | 5 |
| 28 | InvBFM: finding genomic inversions from high-throughput sequence data based on feature mining. BMC Genomics, 2020, 21, 173. | 2.8 | 4 |
| 29 | A new recombination lower bound and the minimum perfect phylogenetic forest problem. Journal of Combinatorial Optimization, 2008, 16, 229-247. | 1.3 | 3 |
| 30 | HPV-EM: an accurate HPV detection and genotyping EM algorithm. Scientific Reports, 2020, 10, 14340. | 3.3 | 3 |
| 31 | Identifying interacting SNPs with parallel fish-agent based logic regression. , 2011, , . |  | 2 |
| 32 | Concod: Accurate consensus-based approach of calling deletions from high-throughput sequencing data. , 2016, , . |  | 2 |
| 33 | GAPPadder: A sensitive approach for closing gaps on draft genomes with short sequence reads. , 2017, , . |  | 1 |
| 34 | An improved approach for reconstructing consensus repeats from short sequence reads. BMC Genomics, 2018, 19, 566. | 2.8 | 1 |
| 35 | Workshop: Calling Structural Variation with low-coverage sequencing data by mapping to focal region. , 2012, , . |  | 0 |
| 36 | An SVM-based approach for discovering splicing junctions with RNA-Seq. , 2014, , . |  | 0 |