

Arief Gusnanto

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,500
citations

687363

13
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

3034
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Sparse modelling of cancer patientsâ€™ survival based on genomic copy number alterations. Journal of Biomedical Informatics, 2022, 128, 104025. | 4.3 | 1 |
| 2 | Prediction of tumour pathological subtype from genomic profile using sparse logistic regression with random effects. Journal of Applied Statistics, 2021, 48, 605-622. | 1.3 | 0 |
| 3 | Use of shared gamma frailty model in analysis of survival data in twins.. Theoretical Biology Forum, 2021, 114, 45-58. | 0.2 | 0 |
| 4 | Properties and approximate p-value calculation of the Cramer test. Journal of Statistical Computation and Simulation, 2020, 90, 1965-1981. | 1.2 | 1 |
| 5 | Geometry-based distance for clustering amino acids. Journal of Applied Statistics, 2020, 47, 1235-1250. | 1.3 | 1 |
| 6 | Method for Automatic Selection of Parameters in Normal Tissue Complication Probability Modeling. International Journal of Radiation Oncology Biology Physics, 2018, 101, 704-712. | 0.8 | 1 |
| 7 | Identification of transcript regulatory patterns in cell differentiation. Bioinformatics, 2017, 33, 3235-3242. | 4.1 | 0 |
| 8 | Classification of form under heterogeneity and non-isotropic errors. Journal of Applied Statistics, 2017, 44, 1495-1508. | 1.3 | 0 |
| 9 | Stratifying tumour subtypes based on copy number alteration profiles using next-generation sequence data. Bioinformatics, 2015, 31, 2713-2720. | 4.1 | 9 |
| 10 | Sparse alternatives to ridge regression: a random effects approach. Journal of Applied Statistics, 2015, 42, 12-26. | 1.3 | 1 |
| 11 | Estimating optimal window size for analysis of low-coverage next-generation sequence data. Bioinformatics, 2014, 30, 1823-1829. | 4.1 | 24 |
| 12 | Partial least squares and logistic regression random-effects estimates for gene selection in supervised classification of gene expression data. Journal of Biomedical Informatics, 2013, 46, 697-709. | 4.3 | 8 |
| 13 | Correcting for cancer genome size and tumour cell content enables better estimation of copy number alterations from next-generation sequence data. Bioinformatics, 2012, 28, 40-47. | 4.1 | 173 |
| 14 | Identification of candidate genes linking systemic inflammation to atherosclerosis; results of a human in vivo LPS infusion study. BMC Medical Genomics, 2011, 4, 64. | 1.5 | 25 |
| 15 | Transcription profiling in human platelets reveals LRRFIP1 as a novel protein regulating platelet function. Blood, 2010, 116, 4646-4656. | 1.4 | 90 |
| 16 | A HaemAtlas: characterizing gene expression in differentiated human blood cells. Blood, 2009, 113, e1-e9. | 1.4 | 215 |
| 17 | Identification of variation in the platelet transcriptome associated with Glycoprotein 6 haplotype. Platelets, 2008, 19, 258-267. | 2.3 | 9 |
| 18 | Robust smooth segmentation approach for array CGH data analysis. Bioinformatics, 2007, 23, 2463-2469. | 4.1 | 35 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Comparative gene expression profiling of in vitro differentiated megakaryocytes and erythroblasts identifies novel activatory and inhibitory platelet membrane proteins. <i>Blood</i> , 2007, 109, 3260-3269. | 1.4 | 153 |
| 20 | Identification of differentially expressed genes and false discovery rate in microarray studies. <i>Current Opinion in Lipidology</i> , 2007, 18, 187-193. | 2.7 | 39 |
| 21 | Improving the power to detect differentially expressed genes in comparative microarray experiments by including information from self-self hybridizations. <i>Computational Biology and Chemistry</i> , 2007, 31, 178-185. | 2.3 | 1 |
| 22 | Multidimensional local false discovery rate for microarray studies. <i>Bioinformatics</i> , 2006, 22, 556-565. | 4.1 | 69 |
| 23 | Fold-Change Estimation of Differentially Expressed Genes using Mixture Mixed-Model. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article26. | 0.6 | 11 |
| 24 | Platelet genomics and proteomics in human health and disease. <i>Journal of Clinical Investigation</i> , 2005, 115, 3370-3377. | 8.2 | 146 |
| 25 | False discovery rate, sensitivity and sample size for microarray studies. <i>Bioinformatics</i> , 2005, 21, 3017-3024. | 4.1 | 410 |
| 26 | A DNA microarray for fission yeast: minimal changes in global gene expression after temperature shift. <i>Yeast</i> , 2004, 21, 25-39. | 1.7 | 39 |
| 27 | DNA ADDUCTS OF BENZO[A]PYRENE- AND DIBENZO[A,L]PYRENE-DIOL EPOXIDES IN HUMAN LUNG EPITHELIAL CELLS: KINETICS OF ADDUCT REMOVAL, EFFECTS ON CELL CYCLE CHECKPOINTS, AND GENE EXPRESSION. <i>Polycyclic Aromatic Compounds</i> , 2004, 24, 549-566. | 2.6 | 9 |
| 28 | Variable selection in random calibration of near-infrared instruments: ridge regression and partial least squares regression settings. <i>Journal of Chemometrics</i> , 2003, 17, 174-185. | 1.3 | 26 |