

Paul J Kennedy

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

2,640
citations

471371

17
h-index

233338

45
g-index

89
all docs

89
docs citations

89
times ranked

3311
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 1 | Deep Learning Techniques for Medical Image Segmentation: Achievements and Challenges. Journal of Digital Imaging, 2019, 32, 582-596. | 1.6 | 972 |
| 2 | Training deep neural networks on imbalanced data sets. , 2016, , . | | 240 |
| 3 | An evaluation of document clustering and topic modelling in two online social networks: Twitter and Reddit. Information Processing and Management, 2020, 57, 102034. | 5.4 | 164 |
| 4 | Long non-coding RNAs harboring miRNA seed regions are enriched in prostate cancer exosomes. Scientific Reports, 2016, 6, 24922. | 1.6 | 144 |
| 5 | A review of the infection, genetics, and evolution of Neospora caninum: From the past to the present. Infection, Genetics and Evolution, 2013, 13, 133-150. | 1.0 | 111 |
| 6 | Relational autoencoder for feature extraction. , 2017, , . | | 94 |
| 7 | Machine learning and applications in microbiology. FEMS Microbiology Reviews, 2021, 45, . | 3.9 | 81 |
| 8 | A combined convolutional and recurrent neural network for enhanced glaucoma detection. Scientific Reports, 2021, 11, 1945. | 1.6 | 71 |
| 9 | A balanced iterative random forest for gene selection from microarray data. BMC Bioinformatics, 2013, 14, 261. | 1.2 | 70 |
| 10 | <i>Vacceed</i>: a high-throughput <i>in silico</i> vaccine candidate discovery pipeline for eukaryotic pathogens based on reverse vaccinology. Bioinformatics, 2014, 30, 2381-2383. | 1.8 | 60 |
| 11 | A novel strategy for classifying the output from an in silicovaccine discovery pipeline for eukaryotic pathogens using machine learning algorithms. BMC Bioinformatics, 2013, 14, 315. | 1.2 | 38 |
| 12 | Ensemble Feature Learning of Genomic Data Using Support Vector Machine. PLoS ONE, 2016, 11, e0157330. | 1.1 | 36 |
| 13 | Evaluating High-Throughput Ab Initio Gene Finders to Discover Proteins Encoded in Eukaryotic Pathogen Genomes Missed by Laboratory Techniques. PLoS ONE, 2012, 7, e50609. | 1.1 | 33 |
| 14 | The Curse of Dimensionality: A Blessing to Personalized Medicine. Journal of Clinical Oncology, 2010, 28, e723-e724. | 0.8 | 29 |
| 15 | A guide to in silico vaccine discovery for eukaryotic pathogens. Briefings in Bioinformatics, 2013, 14, 753-774. | 3.2 | 29 |
| 16 | Discovering a vaccine against neosporosis using computers: is it feasible?. Trends in Parasitology, 2014, 30, 401-411. | 1.5 | 28 |
| 17 | Multi-Label Feature Selection using Correlation Information. , 2017, , . | | 27 |
| 18 | Dual Implicit Mining-Based Latent Friend Recommendation. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2020, 50, 1663-1678. | 5.9 | 26 |

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|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | Enhancing In Silico Protein-Based Vaccine Discovery for Eukaryotic Pathogens Using Predicted Peptide-MHC Binding and Peptide Conservation Scores. PLoS ONE, 2014, 9, e115745. | 1.1 | 25 |
| 20 | Correlated Multi-label Classification with Incomplete Label Space and Class Imbalance. ACM Transactions on Intelligent Systems and Technology, 2019, 10, 1-26. | 2.9 | 20 |
| 21 | Identification of lung cancer miRNA-miRNA co-regulation networks through a progressive data refining approach. Journal of Theoretical Biology, 2015, 380, 271-279. | 0.8 | 18 |
| 22 | A Cost-Sensitive Learning Strategy for Feature Extraction from Imbalanced Data. Lecture Notes in Computer Science, 2016, , 78-86. | 1.0 | 18 |
| 23 | A Gene-Based Positive Selection Detection Approach to Identify Vaccine Candidates Using Toxoplasma gondii as a Test Case Protozoan Pathogen. Frontiers in Genetics, 2018, 9, 332. | 1.1 | 17 |
| 24 | Atrous Convolution for Binary Semantic Segmentation of Lung Nodule. , 2019, , . | | 15 |
| 25 | Synthetic CT images for semi-sequential detection and segmentation of lung nodules. Applied Intelligence, 2021, 51, 1616-1628. | 3.3 | 15 |
| 26 | Feature Selection of Imbalanced Gene Expression Microarray Data. , 2011, , . | | 14 |
| 27 | Visual Analytics of Complex Genomics Data to Guide Effective Treatment Decisions. Journal of Imaging, 2016, 2, 29. | 1.7 | 13 |
| 28 | On the application of reverse vaccinology to parasitic diseases: a perspective on feature selection and ranking of vaccine candidates. International Journal for Parasitology, 2017, 47, 779-790. | 1.3 | 13 |
| 29 | Case-Based Retrieval Framework for Gene Expression Data. Cancer Informatics, 2015, 14, CIN.S22371. | 0.9 | 12 |
| 30 | Convolutional Deep Belief Network with Feature Encoding for Classification of Neuroblastoma Histological Images. Journal of Pathology Informatics, 2018, 9, 17. | 0.8 | 12 |
| 31 | Improving the gene structure annotation of the apicomplexan parasite Neospora caninum fulfils a vital requirement towards an in silico-derived vaccine. International Journal for Parasitology, 2015, 45, 305-318. | 1.3 | 11 |
| 32 | Discovering influential authors in heterogeneous academic networks by a co-ranking method. , 2013, , . | | 10 |
| 33 | Dynamic island model based on spectral clustering in genetic algorithm. , 2017, , . | | 10 |
| 34 | Review of Innovative Immersive Technologies for Healthcare Applications. Innovations in Digital Health Diagnostics and Biomarkers, 2022, 2, 27-39. | 0.5 | 10 |
| 35 | Using Artificial Intelligence to Build with Unprocessed Rock. Key Engineering Materials, 0, 517, 939-945. | 0.4 | 9 |
| 36 | DBNorm: normalizing high-density oligonucleotide microarray data based on distributions. BMC Bioinformatics, 2017, 18, 527. | 1.2 | 9 |

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|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | Virtual reality for the observation of oncology models (VROOM): immersive analytics for oncology patient cohorts. <i>Scientific Reports</i> , 2022, 12, . | 1.6 | 9 |
| 38 | Computer Aided Classification of Neuroblastoma Histological Images Using Scale Invariant Feature Transform with Feature Encoding. <i>Diagnostics</i> , 2018, 8, 56. | 1.3 | 8 |
| 39 | Identifying Brain Abnormalities with Schizophrenia Based on a Hybrid Feature Selection Technology. <i>Applied Sciences (Switzerland)</i> , 2019, 9, 2148. | 1.3 | 8 |
| 40 | Applying Machine Learning to Predict the Exportome of Bovine and Canine Babesia Species That Cause Babesiosis. <i>Pathogens</i> , 2021, 10, 660. | 1.2 | 7 |
| 41 | Extracting and Explaining Biological Knowledge in Microarray Data. <i>Lecture Notes in Computer Science</i> , 2004, , 699-703. | 1.0 | 6 |
| 42 | Non-parametric and integrated framework for segmenting and counting neuroblastic cells within neuroblastoma tumor images. <i>Medical and Biological Engineering and Computing</i> , 2013, 51, 645-655. | 1.6 | 6 |
| 43 | ABC-sampling for Balancing Imbalanced Datasets Based on Artificial Bee Colony Algorithm. , 2015, , . | | 6 |
| 44 | Segmenting Neuroblastoma Tumor Images and Splitting Overlapping Cells Using Shortest Paths between Cell Contour Convex Regions. <i>Lecture Notes in Computer Science</i> , 2013, , 171-175. | 1.0 | 6 |
| 45 | Unsupervised Domain-Adaptation-Based Tensor Feature Learning With Structure Preservation. <i>IEEE Transactions on Artificial Intelligence</i> , 2022, 3, 370-380. | 3.4 | 6 |
| 46 | Variance-based Feature Selection for Classification of Cancer Subtypes Using Gene Expression Data. , 2018, , . | | 5 |
| 47 | Design of airport security screening using queueing theory augmented with particle swarm optimisation. <i>Service Oriented Computing and Applications</i> , 2020, 14, 119-133. | 1.3 | 5 |
| 48 | Track Shape, Resulting Dynamics and Injury Rates of Greyhounds. , 2018, , . | | 5 |
| 49 | A framework for high dimensional data reduction in the microarray domain. , 2010, , . | | 4 |
| 50 | Predicting Protein Therapeutic Candidates for Bovine Babesiosis Using Secondary Structure Properties and Machine Learning. <i>Frontiers in Genetics</i> , 2021, 12, 716132. | 1.1 | 4 |
| 51 | Knowledge Discovery in Biomedical Data Facilitated by Domain Ontologies. , 2007, , 189-201. | | 4 |
| 52 | Fuzzy logic based modelling and analysis of network traffic. , 2008, , . | | 3 |
| 53 | Determining the Number of Clusters in Co-authorship Networks Using Social Network Theory. , 2012, , . | | 3 |
| 54 | The Core Mouse Response to Infection by <i>Neospora Caninum</i> Defined by Gene Set Enrichment Analyses. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9954. | 1.0 | 3 |

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|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | Community detection on heterogeneous networks by multiple semantic-path clustering. , 2014, , . | | 3 |
| 56 | Supervised context-aware non-negative matrix factorization to handle high-dimensional high-correlated imbalanced biomedical data. , 2017, , . | | 3 |
| 57 | Two-Dimensional Immersive Cohort Analysis Supporting Personalised Medical Treatment. , 2019, , . | | 3 |
| 58 | Static and Dynamic Selection Thresholds Governing the Accumulation of Information in Genetic Algorithms Using Ranked Populations. Evolutionary Computation, 2010, 18, 229-254. | 2.3 | 2 |
| 59 | Cellular quantitative analysis of neuroblastoma tumor and splitting overlapping cells. BMC Bioinformatics, 2014, 15, 272. | 1.2 | 2 |
| 60 | Balanced Supervised Non-Negative Matrix Factorization for Childhood Leukaemia Patients. , 2016, , . | | 2 |
| 61 | Chemical Named Entity Recognition with Deep Contextualized Neural Embeddings. , 2019, , . | | 2 |
| 62 | Sparse Feature Learning Using Ensemble Model for Highly-Correlated High-Dimensional Data. Lecture Notes in Computer Science, 2018, , 423-434. | 1.0 | 2 |
| 63 | Compilation of parasitic immunogenic proteins from 30Âyears of published research using machine learning and natural language processing. Scientific Reports, 2022, 12, . | 1.6 | 2 |
| 64 | Using Field of Research Codes to Discover Research Groups from Co-authorship Networks. , 2012, , . | | 1 |
| 65 | Determining cellularity status of tumors based on histopathology using hybrid image segmentation. , 2012, , . | | 1 |
| 66 | Redesign of Data Analytics Major: Challenges and Lessons Learned. Procedia, Social and Behavioral Sciences, 2014, 116, 1373-1377. | 0.5 | 1 |
| 67 | A Simple Spring-Loaded Inverted Pendulum (SLIP) Model of a Bio-Inspired Quadrupedal Robot Over Compliant Terrains. , 2018, , . | | 1 |
| 68 | The Untapped Social Impact of Artificial Intelligence for Breast Cancer Screening in Developing Countries: A Critical Commentary of DeepMind. Innovations in Digital Health Diagnostics and Biomarkers, 2021, 1, 29-32. | 0.5 | 1 |
| 69 | The Effect of Mutation on the Accumulation of Information in a Genetic Algorithm. Lecture Notes in Computer Science, 2005, , 360-368. | 1.0 | 1 |
| 70 | Robust Simulation of Lamprey Tracking. Lecture Notes in Computer Science, 2006, , 641-650. | 1.0 | 1 |
| 71 | Integrative Visual Data Mining of Biomedical Data: Investigating Cases in Chronic Fatigue Syndrome and Acute Lymphoblastic Leukaemia. Lecture Notes in Computer Science, 2008, , 367-388. | 1.0 | 1 |
| 72 | Automated Quantitative and Qualitative Analysis of Whole Neuroblastoma Tumour Images for Prognosis. , 2014, , . | | 1 |

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|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 73 | A Review and Comparison of Service E-Contract Architecture Metamodels. Lecture Notes in Computer Science, 2015, , 583-595. | 1.0 | 1 |
| 74 | Classification of Neuroblastoma Histopathological Images Using Machine Learning. Lecture Notes in Computer Science, 2020, , 3-14. | 1.0 | 1 |
| 75 | Fast simulation of animal locomotion: lamprey swimming. , 2006, , 247-256. | | 1 |
| 76 | Computational Antigen Discovery for Eukaryotic Pathogens Using Vacceed. Methods in Molecular Biology, 2021, 2183, 29-42. | 0.4 | 1 |
| 77 | SMCKAT, a Sequential Multi-Dimensional CNV Kernel-Based Association Test. Life, 2021, 11, 1302. | 1.1 | 1 |
| 78 | MCKAT: a multi-dimensional copy number variant kernel association test. BMC Bioinformatics, 2021, 22, 588. | 1.2 | 1 |
| 79 | Entropy profiles of ranked and random populations. , 2010, , . | | 0 |
| 80 | HMXT-GP. , 2011, , . | | 0 |
| 81 | Queue Formation Augmented with Particle Swarm Optimisation to Improve Waiting Time in Airport Security Screening. Advances in Intelligent Systems and Computing, 2019, , 923-935. | 0.5 | 0 |
| 82 | Feature prioritisation on big genomic data for analysing gene-gene interactions. International Journal of Bioinformatics Research and Applications, 2021, 17, 158. | 0.1 | 0 |
| 83 | NARGES: Prediction Model for Informed Routing in a Communications Network. Lecture Notes in Computer Science, 2013, , 327-338. | 1.0 | 0 |
| 84 | The Effect of In-Domain Word Embeddings for Chemical Named Entity Recognition. Communications in Computer and Information Science, 2020, , 54-68. | 0.4 | 0 |
| 85 | Transfer learning approaches to recognize X-ray Covidâ€™19 images. , 2021, , . | | 0 |
| 86 | Knowledge Discovery in Biomedical Data Facilitated by Domain Ontologies. , 0, , 2096-2108. | | 0 |