Leveraging Big Data -Bibliometric Intelligence for Editors

Elizabeth Caley

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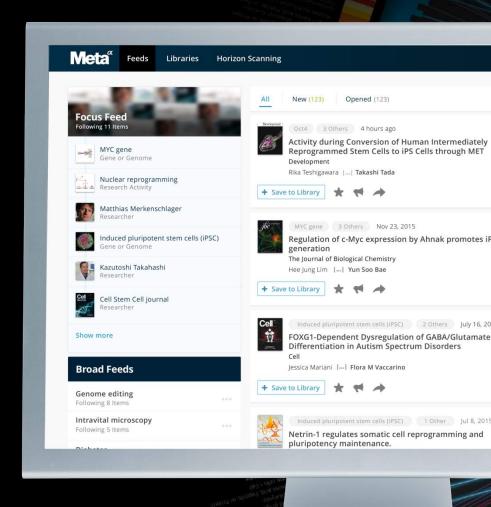




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What's the topic?

How well does the topic fit my journal?

Who authored it?

What is their publication history?

Choi et al.
Functional impacts of amino acid variants
Page 1

Abstract

As next generation sequencing projects generate massive genome-wide sequence variation data, bioinformatics tools are being developed to provide computational predictions on the disease phenotypes. Different classes of sequence variations at the nucleotide level are involved in human diseases, including substitutions, insertions, deletions, frameshifts, and nonsense mutations. Frameshifts and non-sense mutations are likely to cause a negative effect on interest among related sequences, an approach that is not directly applicable to insertions or deletions. Here, we introduce a versatile alignment-based score as a new metric to predict the damaging effects of variations not limited to single amino acid substitutions but also in-frame insertions, deletions and multiple amino acid substitutions. This alignment-based score measures the change in sequence similarity of a query sequence to a protein sequence (n=21,662) from common polymorphisms (n=37,022) for UniProt human protein variations, and also in separating deleterious variants (n=15,179) from neutral variants (n=17,891) for UniProt non-human protein variations. In our approach, the area under the receiver operating characteristic curve (AUC) for the human and non-human protein variation datasets is ~0.85. effects of protein sequence variations including single or multiple amino acid substitutions, and

Are the findings novel?

How does it rank against other submissions?

Is this a highly citable paper?

Who could review it?



Evaluates over 400 characteristics of the manuscript

Projected Citation
Count

23

Choi et al mino acid variant Page :

Abstract

Journal

Matches

Journal Matching Score

81%

As next generation sequencing

cational predictions on the

data, bioinformatics tools are being o

Authoritation for the series of the series o

functional effects of sequence variations and narrow down the search of casual variants for

olved in human diseases, including substitutions, insertions, deletions, frameshifts, and non-

se mutations. Frameshifts and non-sense mutations are likely to cause a negative effect on

tein function. Existing prediction tools primarily focus on studying the deleterious effects of

ngle aming acid substitutions through examining aming acid conservation at the position of

deletions. Here we introduce a receptile eligenment based score on a new matrix to receipt the

damaging effects of variations not limited to single amino acid substitutions but also in-fram

insertions, deletions and multiple amino acid substitutions. This alignment based ecora-

The same of the sa

results showed that the scoring scheme performs well in separating disease-associated variants

(11-21,002) from common polymorphisms (11-31,022) for other total and protest variations, and

also in separating deleterious variants (n=15.179) from neutral variants (n=17.891) for UniProt

on-human protein variations. In our approach, the area under the receiver operating

aracteristic curve (AUC) for the human and non-human protein variation datasets is ~0.8

also observed that the alignment-based score correlates with the deleteriousness of a

quence variation. In summary, we have developed a new algorithm, PROVEAN (Protein

and an end of the provided a generalized approach to product the relief of

effects of protein sequence variations including single or multiple amino acid substitutions, and

Forecasted Impact Score

0.81

Top

10%

Manuscript
Ranking





New Editor Assignments - Stacey Middle Lavelle, PhD, MDd

Contents: These are submissions that have been Assigned to the Editor. They require one of the following: another Editor assignment, Reviewer invitations, or Decision. Use prows to change the sort order.

Page: 1 of 1 (1 total submissions)

Display 10 vesults per page.

tion 🛕		Manuscript Number ▲▼	Article Type ▲▼	Section/ Category ▲▼	l	Author Name ▲▼	Initial Date Submitted ▲▼	Status Date ▲V	Curren Status
View Submission Predictive Bibliometrics Results Details File Inventory Assign Editor Set Final Disposition Submit Editor's Decision and Cor Send E-mail	Prec (/%) mm ()	dictive Bibliome) = Article Trajed = Predictive Bib	Communication trics Status Summary: tory Score/Publicatio	n Match% process	test test	Stacey Middle Lavelle, PhD, MDd & !#	May 10 2016 2:13:50:097PM	May 10 2016 2:20:25:877PM	With Editor

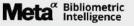
Page: 1 of 1 (1 total submissions)

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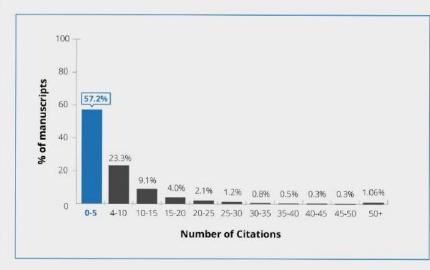
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Predictive Analytics

The major research areas identified in this manuscript are:



Chronic Lymphocytic Leukaemia Refractory



Alemtuzuma



Therapy-related Myelodysplastic Syndrome



ludarabine



Clinical Trial



Hematopoie



equencing



Acute Myeloid Leukemia Pathway



DNA Damage



ytopenia

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Recommended Reviewers

Recommended Reviewers is an intelligently curated list of active researchers who would be best suited to review the manuscript, based on the topics identified in the manuscript. By comparing the topics within this manuscript to the five-year publication history of over seven million authors, the following active researchers (and their most relevant paper) have been recommended to review this manuscript.



Cheng-Hwai Tzeng

Clinicopathologic features and outcome of acute erythroid leukemia based on 2008 revised World Health Organization classification Leukemia & Lymphoma



Gail J Roboz

Targeted Deletion of Autophagy Genes Atg5 Or Atg7 in The Chondrocytes Promotes Caspase– Dependent Cell Death And Leads To Mild Growth Retardation Journal of Bone and Mineral Research



Detlef Haase

New comprehensive cytogenetic scoring system for primary myelodysplastic syndromes (MDS) and oligoblastic acute myeloid leukemia after MDS derived from an international database merge

Journal of Clinical Oncology : Official Journal of the American Society of Clinical Oncology



Richard J B Wells

Initial transfusion intensity predicts survival in myelodysplastic syndrome Leukemio & Lymphoma



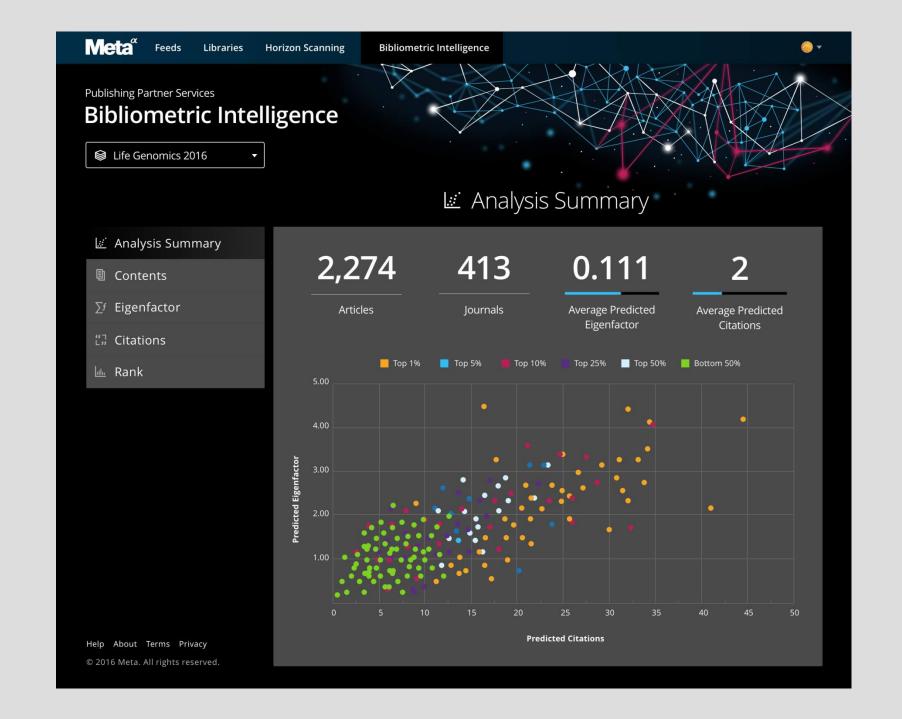
luan Gad

Correlation of chromosome karyotype with dyshaematopoiesis and reticulin in myelodysplastic syndrome
Zhongguo shi yan xue ye xue za zhi

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International Journal of Occupational Medicine and Environmental Health 2015;28(1) http://dx.doi.org/10.2478/s13382-014-032-6

NON-COMMUNICABLE DISEASES IN THE ASIA-PACIFIC REGION: PREVALENCE, RISK FACTORS AND COMMUNITY-BASED PREVENTION

WAH-YUN LOW, Yew-Kong Lee and ALEXANDER LOURDES SAMY

University of Malaya, Kuala Lumpur, Malaysia Faculty of Medicine

Diabetes

NCD

CVD

sion. Strategies to combat NCDs in the Asia Pacific region are as follows: population-based dietary salt reduction, pleath education, psychological interventions, i.e., cognitive behavioral therapy and motivational-interviewing, taxation and bans on tobacco-related advertisements, implementing smoke-free zones and surveillance by the World Health Organization.

Control measures must focus on prevention and strengthening inter-sectorial collaboration.

Non-communicable diseases (NCDs), Urbanization, Hypertension, Obesity, Community-based prevention,

Non-communicable diseases (NCDs) are the pivotal cause of disease burden and mortality in the Asia Pacific region, claiming 55% of total life in the South East Asia region each year and 75% in the Western Pacific region [1,2]. The Asia Pacific region is experiencing a rapid increase in NCD-related deaths; the World Health Organization estimates that the highest worldwide increment in total

mortality in a 10-year time frame (2005-2015) will be observed in the South-Fast Asia and Western Pacific regions with 21% increase in the South-East Asia region [3] and 12.3 million deaths in the Western Pacific region [2]. This increase in NCDs presents a major barrier to global development, specifically to the achievement of the Millennium Development Goals [4] in low-and-middle in-

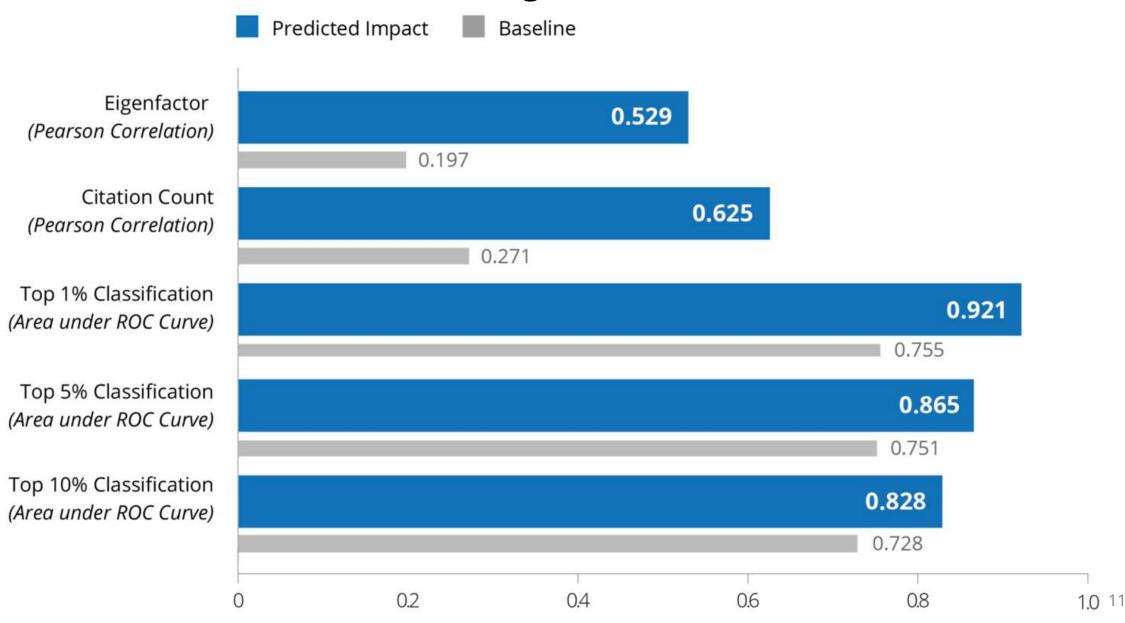
s paper was presented at the 6th ICOH International Conference on Work Environment and Cardiovascular Diseases; 2013 Mar 27-30; Tokyo, Japan. Received May 9, 2014. Accepted: September 3, 2014.

Corresponding author: W.-Y. Low, Faculty of Medicine, University of Malaya, 50603 Kuala Lumpur, Malaysia (e-mail: lowws/s/um/eda.m/s/).

Bibliometric Intelligence

Over 1M Biomedical manuscripts analyzed over 3 years Examines over 400 characteristics

Bibliometric Intelligence Performance



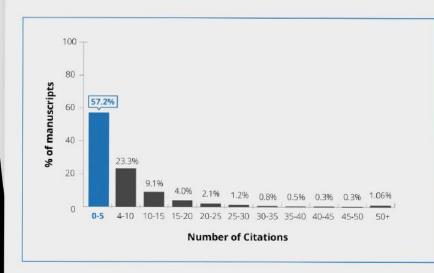
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