

Histone modification. Molecular Function Meta

Bibliometric Intelligence

Elizabeth Caley
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Abstract

As next generation sequencing projects generate massive genome-wide sequence variation data, bioinformatics tools are being developed to provide computational predictions on the functional effects of sequence variations and narrow down the search of casual variants for 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 protein function. Existing prediction tools primarily focus on studying the deleterious effects of single amino acid substitutions through examining amino acid conservation at the position of 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 homolog before and after the introduction of an amino acid variation to the query sequence. Our results showed that the scoring scheme performs well in separating disease-associated variants (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. We also observed that the alignment-based score correlates with the deleteriousness of a sequence variation. In summary, we have developed a new algorithm, PROVEAN (Protein Variation Effect Analyzer), which provides a generalized approach to predict the functional effects of protein sequence variations including single or multiple amino acid substitutions, and

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REVIEW PAPER

International Journal of Occupational Medicine and Environmental Health 2015;28(1) http://dx.doi.org/10.2478/s13382-014-0326-

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, health 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-East 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-

This paper was presented at the 6th ICOH International Conference on Work Emironment and Cardiovascular Diseases; 2013 Mar 27–30; Tokyo, Japan. Received: May 9, 2014. Accepted: Sptember 3, 2014. Occupation of the Corresponding authors: Wei T. Lon, Feating of Medicine, University of Malaya, 59003 Kunla Lumpur, Malaysia (e-mail: lowsy@um.edu.my).

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