Willey-Models-Jillian-18-sets LINK

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Dwivedi, Ajit Kumar; De Vlas, Sake J; Mahapatra, Tanmay; Le Rutte, Epke A; (2017) Gross method for ranking and scoring models with application to virus epitope predictions. BMC Bioinformatics, 18(1), 9. ISSN 1750-2878. Willey also serves as the founder and CEO of Willey Models, an equity crowdfunding platform for investments in real estate. He is also a founding member of the Organization of Venture Capital Education. Willey created the Student Loan Debt Relief Challenge (SLDRC) to help graduates of colleges that have seen their graduation rates drop and student debt rise. Guido, Thien; Held, Erika; Lendel, Julia; Moll, Julia; Siegel, Adam; Budka, Anna; Seers, David; Milburn, Madison L; Janardhan, Rohit; Steiner, Francesca; et al. (2015) Integration of multiple simultaneous transcriptomics assays using multiple imputation and conditional Gaussian process modeling. PeerJ, 3. DOI: Willey is a Virginia native. He grew up in a military household on a base in Japan. Willey was an avid ski bum and an active recruiter for a United States Naval Academy hockey team. During his time at Annapolis, he also skied for the rugby team. Willey graduated with a degree in economics and a minor in computer science. After graduating, he returned to Virginia and worked as a software engineer. In 2000, Willey was inspired to go to medical school after one of his best friends was diagnosed with a rare brain cancer. He attended medical school and completed a surgical residency at the University of Louisville. He then finished his orthopedic surgery training at the University of Florida in Gainesville.

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In this study, we describe a novel statistical model that predicts the structure of RNA by using the Gibbs sampling algorithm. The model allows for covariates and random effects to be incorporated simultaneously into the model. We applied the model to a 472nt long single-stranded sequence from the Baculoviridae family. The model was able to reconstruct a structure with high reliability and concordance with the expected structure. Data generated by high-throughput sequencing approaches requires sophisticated statistical modeling of the underlying assumptions. For example, in RNA-seq experiments, transcripts are assumed to be of similar abundance and behave as independent and identically distributed Poisson-distributed random variables. In this study, we have shown that the abundance of alternatively spliced transcript isoforms and fusion genes is dependent on the average expression level and cell cycle state of the samples. In particular, RNA-seq data have a strong tendency to over-represent fusion genes with higher expression levels and cell cycle states and also tend to include relatively fewer fusion genes at low expression levels and low cell cycle states. These results demonstrate the importance of accounting for this dependence in data analysis. In order to develop statistical methods that overcome this problem, we are working to develop a general framework for jointly modeling all forms of RNA-Seq data, providing data structure-specific likelihoods for statistical modeling of observed data, which permits model selection and the possibility of a parametric or non-parametric model form. The incorporation of covariates, such as the expression levels of internal control genes and tissue-specific marker genes, can also provide important and useful insights. These methods are being applied to other forms of RNA-seq data and are available in an R library, soma-seq.github.io 5ec8ef588b