Docket #: S22-041

Reconfiguration of Tabular Data for Discovery of Deep Interaction Features and its Applications in Analysis of Multidimensional Data

Stanford scientists have developed a high-performance informatics framework for deep learning analyses of high dimensional (HD) omics data.

High dimensional (HD) data is commonplace in biomedicine and industry today. With this wave of large omic (genomic, proteomic, among others) datasets, novel analysis techniques, including dimensionality reduction, discriminant analysis, Bayesian classification, decision trees, and neural networks, have been developed to extract and understand important information contained in HD data. However, HD data contain multi-level information with complex relationships, and its maximal exploitation is challenging. Current methods attempt to make sense of HD data by embedding them directly onto a low dimension without explicitly considering the underlying biological characteristics of the dataset.

Stanford scientists, therefore, developed a method called genomap that transforms HD data into an ordered format that allows maximization of information of specific omics data interactions, like gene-gene interactions and enables deep exploration of the resulting information by advanced signal processing techniques such as multidimensional convolution filtering. They tested this approach on various gene expression datasets and showed that it vastly improves the performance of analyses compared to existing methods.

Stage of Development
Prototype

Applications

- Tabular HD data analysis for various applications including industrial product development and scientific research in drug discovery, genomic analysis, data classification and clustering, sensor data analysis, disease detection, marketing and finance data analysis, social media, telecommunication, etc.

Advantages

- First of its kind
- Transforms tabular data into a configured data format.
- Uses image processing techniques on tabular data for extracting high level information.
- Applicable to a wide variety of HD data.

Publications

- Md Tauhidul Islam and Lei Xing (2023). Cartography of Genomic Interactions Enables Deep Analysis of Single-Cell Expression Data. Nature Communications, 14, 679.

Patents

- Published Application: 20240249799

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