Combi Seminar

Wednesday, 10.28.20 | 1:30 | held remotely
https://depts.washington.edu/gsrestrc/remote.htm

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“Deep profiling of human transcriptome to understand cancer and Alzheimer's disease”

Modern machine learning (ML) models can accurately predict patient progress, an individual's phenotype, or molecular events such as transcription factor binding. However, they do not explain why selected features make sense or why a particular prediction was made. For example, a model may predict that a patient will get chronic kidney disease, which can lead to kidney failure. The lack of explanations about which features drove the prediction – e.g., high systolic blood pressure, high BMI, or others – hinders medical professionals in making diagnoses and decisions on appropriate clinical actions. Our lab seeks to develop approaches based on explainable artificial intelligence (AI) and machine learning (ML) for biology and medicine.

https://suinlee.cs.washington.edu/

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Combi website at http://www.gs.washington.edu/news/combi.htm

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