

Machine Learning In the Genome Browser

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Extended Abstract

A new era of predictive deep learning in bioinformatics is well underway, with significant advances in data-rich areas such as protein structure prediction and functional genomics. There is a proliferation of new techniques, which in turn presents a challenge of how to integrate and interpret the output of these novel tools. The genome browser, with its idea of stackable annotation tracks, offers one integrative paradigm. I'll review some recent advances in ML for computational biology, focusing (though not exclusively) on our lab's contributions. I'll demonstrate how we have begun to incorporate these insights into JBrowse, our dynamic-HTML genome browser, and its annotation editor Apollo. I will focus on syntenic, protein and protein-coding gene structure, and regulatory variant interpretation as three examples of how ML can be integrated within the genome browser using current methods.