

Abstract Submitted  
for the MAR05 Meeting of  
The American Physical Society

**Quantifying optimal accuracy of local primary sequence bioinformatics methods**<sup>1</sup> DANIEL AALBERTS, ERIC DAUB, JESSE DILL, Williams College — Traditional bioinformatics methods scan primary sequences for local patterns. It is important to assess how accurate local primary sequence methods can be. We study the problem of donor pre-mRNA splice site recognition, where the sequence overlaps between real and decoy data sets can be quantified, exposing the intrinsic limitations of the performance of local primary sequence methods. We assess the accuracy of local primary sequence methods generally by studying how they scale with dataset size and demonstrate that our new Primary Sequence Ranking methods have superior performance. Our Primary Sequence Ranking analysis tools are available at <http://rna.williams.edu/>

<sup>1</sup>Supported by NIH grant GM068485

Daniel Aalberts  
Williams College

Date submitted: 01 Dec 2004

Electronic form version 1.4