

**Reference:**

*SplicePort - An interactive splice-site analysis tool*

Rezarta Islamaj Dogan, Lise Getoor, W. John Wilbur and Stephen M. Mount  
Nucleic Acids Research, 2007, doi:10.1093/nar/gkm407

*Features Generated for Computational Splice-Site Prediction Correspond to Functional Elements*

Rezarta Islamaj Dogan, Lise Getoor, W. John Wilbur and Stephen M. Mount  
BMC Bioinformatics, 2007. [BMC-link](#)

**WEB:** [www.spliceport.org](http://www.spliceport.org)

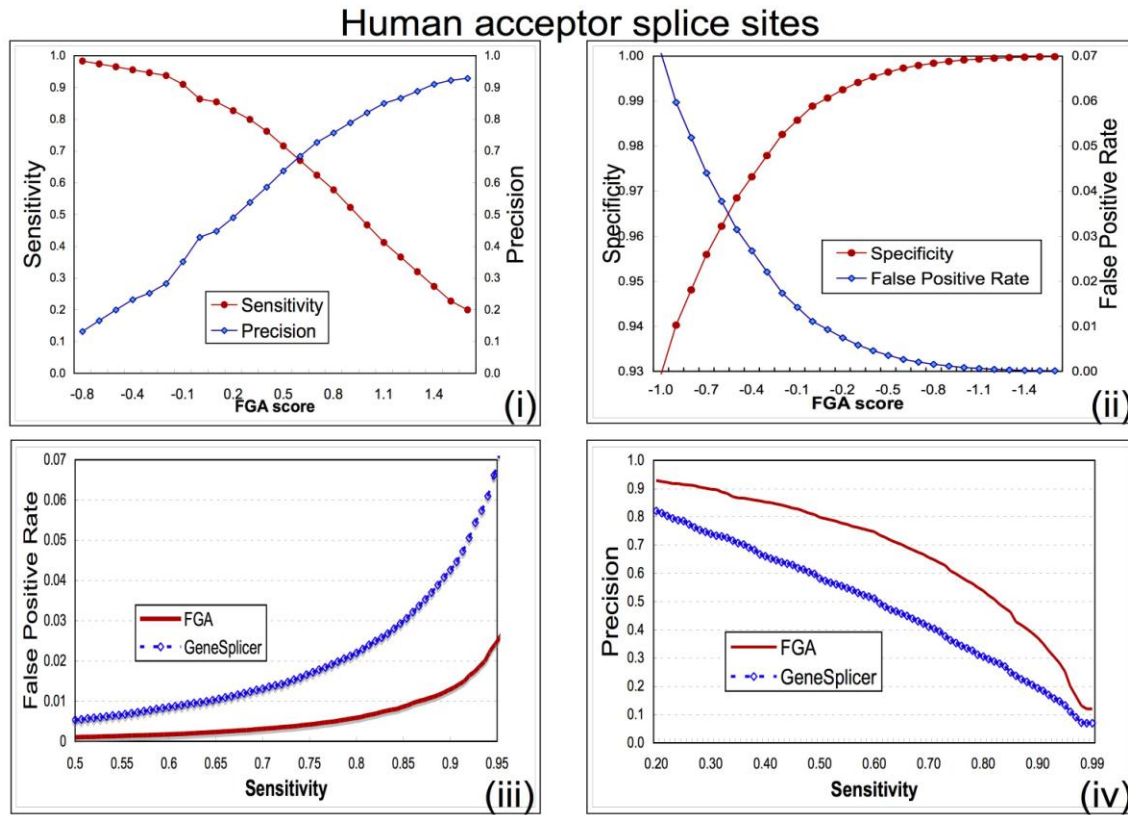


Figure 1. Splice-site predictor for human acceptor sites.

Part (i) depicts the sensitivity,  $TP/(TP+FN)$ , and Positive Predictive Value,  $TP/(TP+FP)$ , also known as precision, vs. FGA score for the human acceptor splice sites. Part (ii) depicts specificity,  $TN/(TN+FP)$ , and False Positive Rate,  $FP/(TN+FP)$ , vs. FGA score. Figures (iii) and (iv) show the False Positive Rate vs. Sensitivity and Precision, vs. Sensitivity. In Figures (iii) and (iv) FGA results are compared with those of GeneSplicer. These results show that FGA produces fewer false positives and higher precision for every sensitivity threshold. These differences are highly statistically significant.

## Human donor splice sites

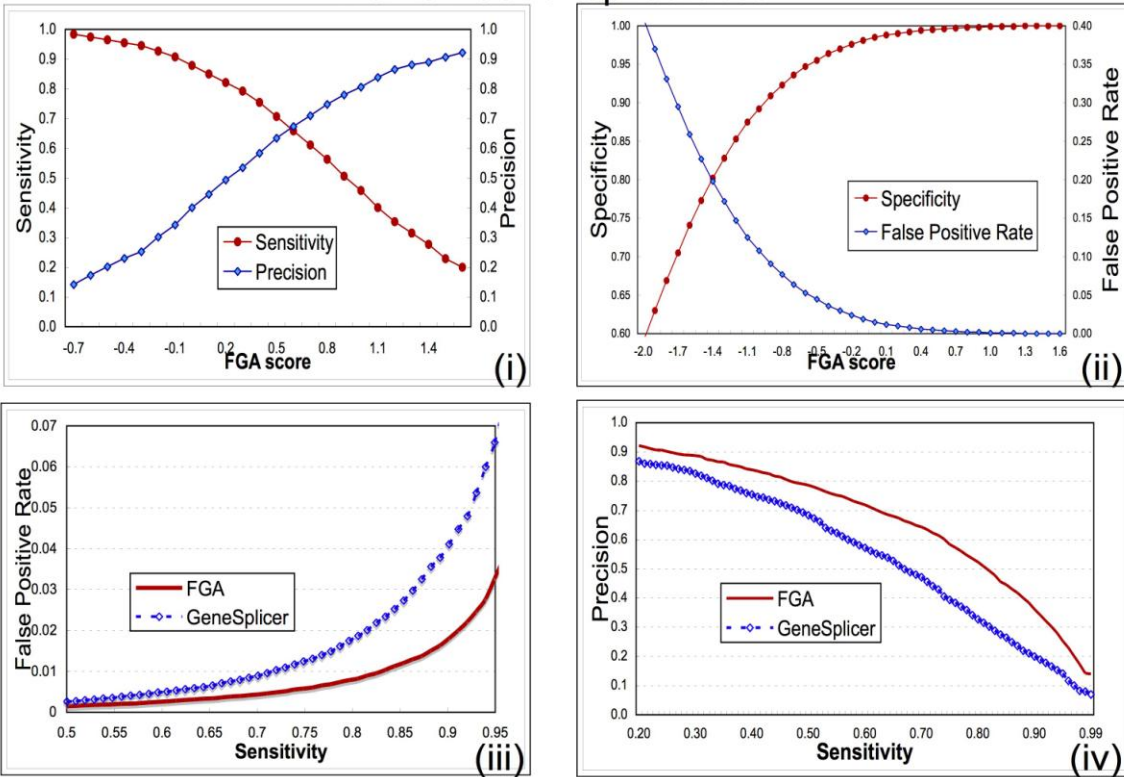


Figure 2. Splice-site predictor for human donor sites.

Part (i) depicts the sensitivity,  $TP/(TP+FN)$ , and Positive Predictive Value,  $TP/(TP+FP)$ , also known as precision, vs. FGA score for the human donor splice sites. Part (ii) depicts specificity,  $TN/(TN+FP)$ , and False Positive Rate,  $FP/(TN+FP)$ , vs. FGA score. Figures (iii) and (iv) show the False Positive Rate vs. Sensitivity and Precision, vs. Sensitivity. In Figures (iii) and (iv) FGA results are compared with those of GeneSplicer. These results show that FGA produces fewer false positives and higher precision for every sensitivity threshold. These differences are highly statistically significant.