Corrigendum

Distinguishing prognostic and predictive biomarkers: an information theoretic approach

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The author wishes to apologize for a mistake in Figure 2 in the above manuscript. The figure appears correctly below:

![Figure 2](image-url)

**Fig. 2.** When biomarkers have both prognostic/predictive strength (M-1) VT achieves higher TPR, otherwise (M-2) the gains in TPR are vanishing. In terms of FNR\textsubscript{Prog}, VT always has very high error rate on selecting solely prognostic biomarkers as predictive, and it performs worse than random selection. This is the average TPR/FNR\textsubscript{Prog} over 200 simulated datasets for three different values of the predictive strength \( \delta \): 1/5 means a strongly prognostic signal, 1 means equal strength between prognostic and predictive signals, and 5 means a strongly predictive signal. The sample size is 2000, and the dimensionality \( p = 30 \) biomarkers. Dashed lines show the TPR/FNR\textsubscript{Prog} if we were ranking the biomarkers at random. (a) M-1: Biomarkers can be both prognostic and predictive. (b) M-2: Biomarkers are solely either prognostic or predictive.

The paper has been corrected online.