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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:
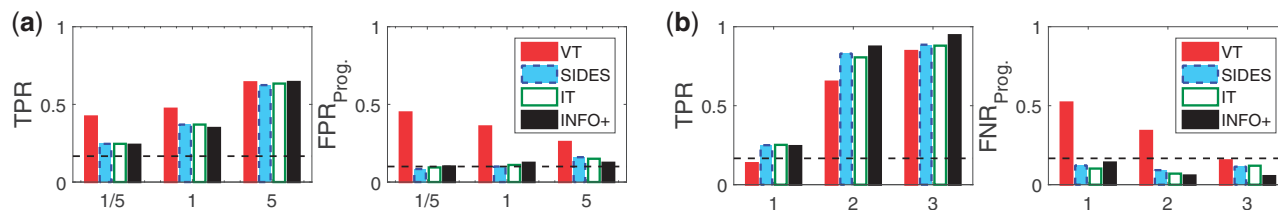

Fig. 2. When biomarkers have both prognostic/predictive strength (M-1) VT achieves higher TPR, otherwise (M-2) the gains in TPR are vanishing. In terms of $FNR_{Prog.}$, VT always has very high error rate on selecting *solely* prognostic biomarkers as predictive, and it performs worse than random selection. This is the average $TPR/FNR_{Prog.}$ over 200 simulated datasets for three different values of the predictive strength θ: 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 $TPR/FNR_{Prog.}$ 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.