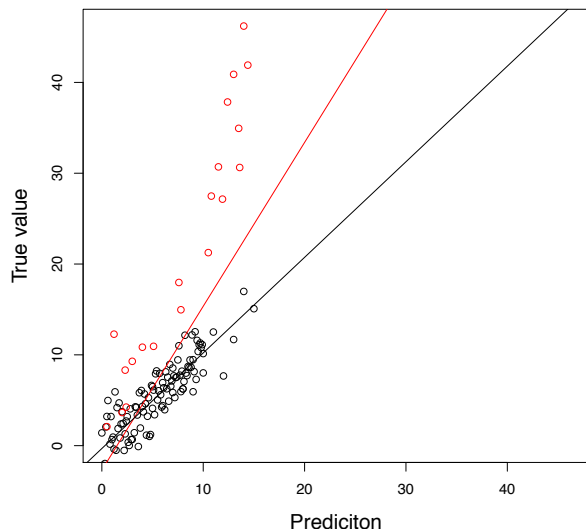


1. Train CR model (red line) using all the data points.



Black line: true model.
Red dots: cancer-specific regions.
Black dots: cancer-independent regions.

1. Perform the hypothesis testing for each region by taking the prediction of CR model as the background.
2. Remove the region with small p-value.
3. Re-train CR model(blue line) using the remaining regions.

1. Take the blue line as the final CR model.
2. Re-perform hypothesis testing for each region by taking the prediction from blue line as background.
3. Output the regions with small p-values.

