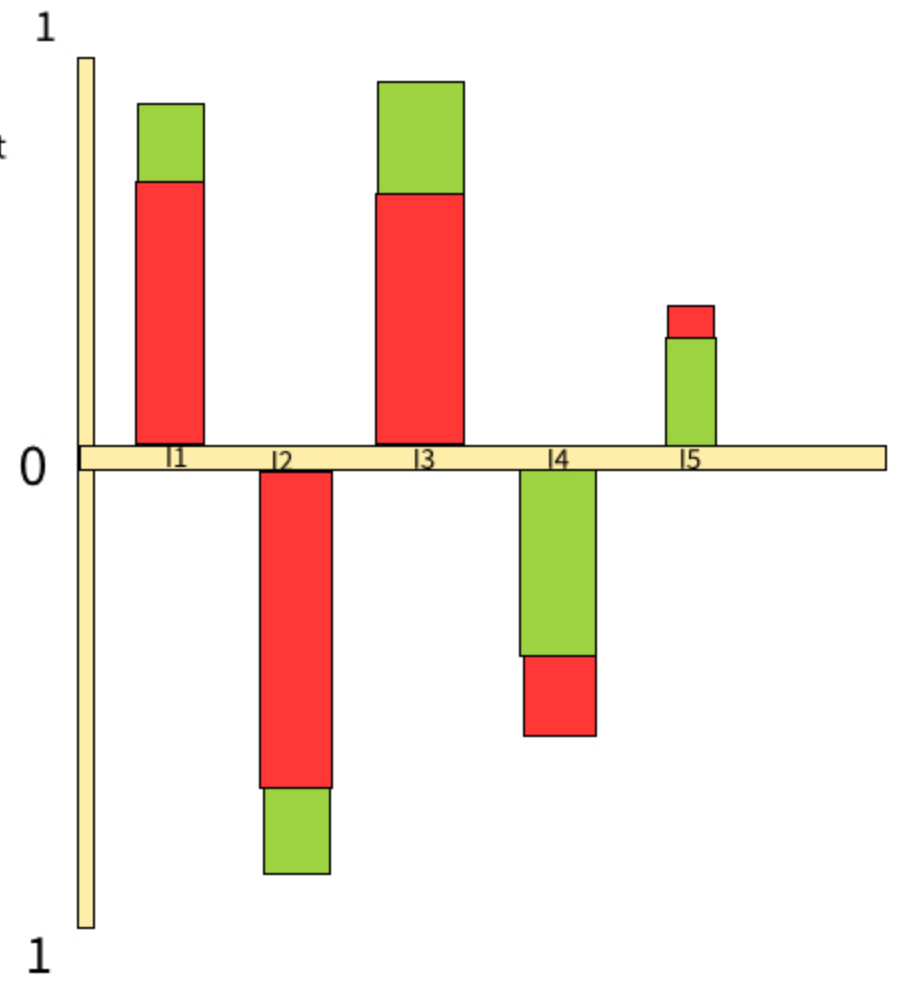


Y-axis shows CDF values. It is 1 on both directions. However, the upper quadrant is for High Indicator Organisms(HIO) and the lower quadrant is for Low Indicator Organisms(LIO).



Positives:
Literature weight is shown in order. If we wanted, width of each bar can correspond to literature weight(It is the same size here).
LIO and HIO are properly differentiated.

Negatives:
What if we have 300 indicators? This would be infeasible.
Spatial context is not preserved(that is, where an indicator lies on the hierarchy). We don't know which order of the hierarchy the indicator is from.

X-axis shows indicators. Indicators are arranged on the x-axis from highest to lowest literature weight.

Each indicator will have two bars. One for sample CDF and the other for aggregate CDF. Additionally, sample CDF will be shown in red and aggregate CDF will be shown in green.

Scenario:
I1, I3 and I5 are high indicator organisms.
I2 and I4 are low indicator organisms.

I1 has most literature weight and I5 has least literature weight.

I1 I2 and I3 have "less" sample CDF compared to aggregate CDF. I4 and I5 have "more" sample CDF than aggregate CDF.

If a sample has "more" CDF than aggregate for many indicators, that is bad because the sample is approaching CDF levels which means that the sample may be prone to a disease.