I1 -- HIO -- Agg CDF > Sample CDF -- LG

I2 -- LIO --Agg CDF > Sample CDF -- DG

I3 -- HIO -- Sample CDF > Agg CDF -- DR

I4 -- LIO --Agg CDF > Sample CDF -- G

I5 -- HIO --Agg CDF > Sample CDF -- LG

I6 -- LIO -- Sample CDF > Agg CDF -- DR

I7 -- HIO -- Agg CDF > Sample CDF -- LG

I8 -- LIO --Agg CDF > Sample CDF -- DG

I9 -- HIO -- Sample CDF > Agg CDF -- LR

I10 -- LIO --Agg CDF > Sample CDF - G
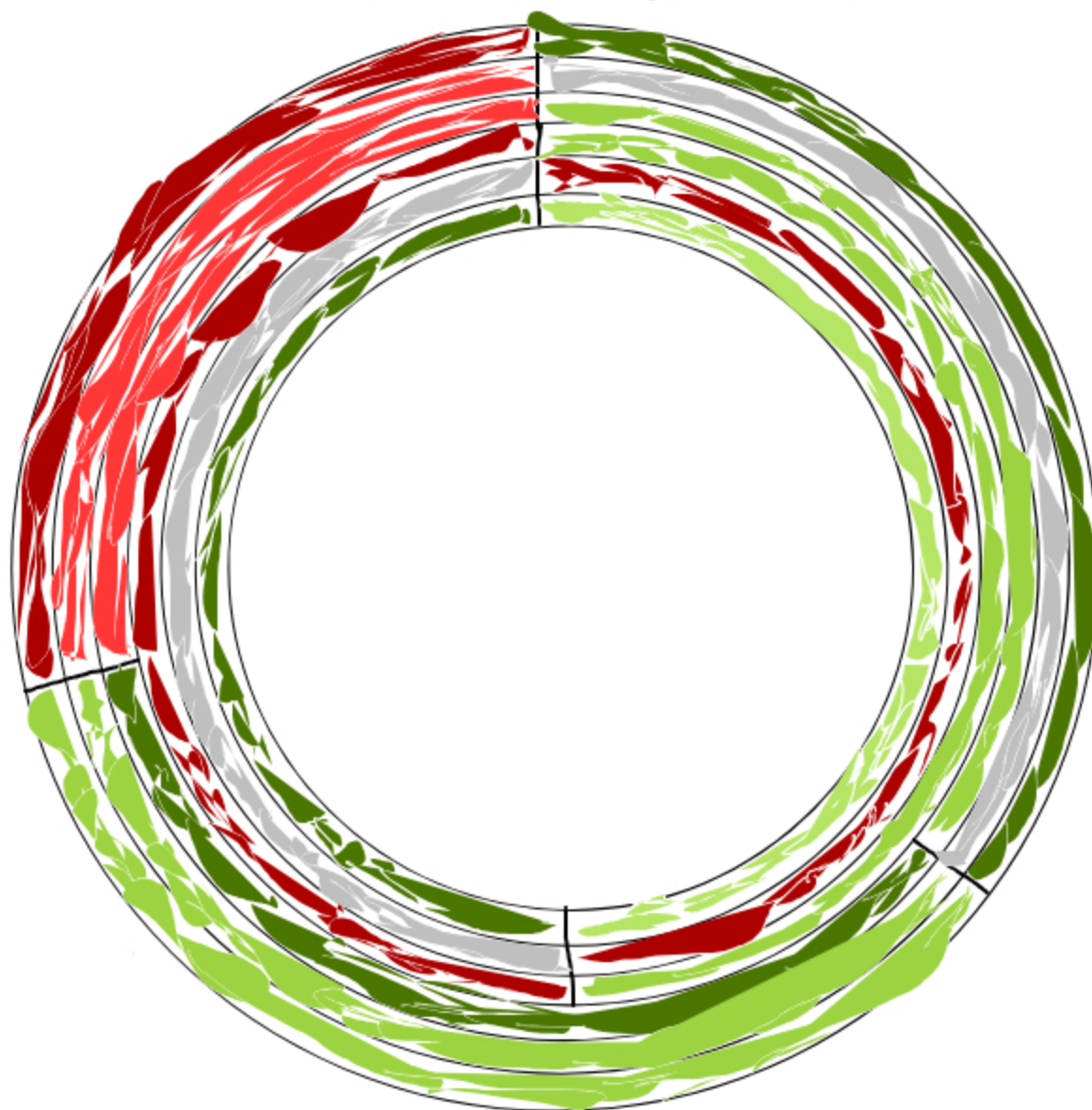
I11 -- HIO -- Agg CDF > Sample CDF -- LG

I12 -- LIO -- Sample CDF > Agg CDF -- LR

I13 -- HIO -- Agg CDF > Sample CDF -- DG

I14 -- LIO -- Agg CDF > Sample CDF -- LG

I15 -- HIO -- Sample CDF > Agg CDF-- DR

Weights of indicators are not apparent.
Can give viewers the wrong idea about size. For instance, the outermost arcs will cover
the most area and make the graph look more red

We don't know if indicators are LIO or HIO.
Spatiality is preserved somewhat.

Scenario:
I1 thru I15 are indicator organisms.

i1&i2 are phylums, i3&i4 are classes, i5&i6 are
orders, i7-i9 are families, i10-i12 are genuses, i13-
i15 are species.

Every odd numbered indicator is high indicator
organism. Every even numbered indicator is low
indicator organism. 3rd, 6th, 9th, 12th and 15th
indicators have "more" CDF for sample
compared to aggregate.

If dark green, agg CDF is very high compared to
sample CDF
If light green, agg CDF is somewhat high
compared to sample CDF
If grey, no big difference.
if light red, sample CDF is somewhat high
compared to agg CDF
if dark red, agg CDF is very high compared to
sample CDF

The more green this figure is, the less a sample is
"close" to the disease aggregate.
The more red, the higher the chance a sample is
"close" to the disease aggregate.