Metagenomics, Day 3, Morning: Sampling & Presence/Absence

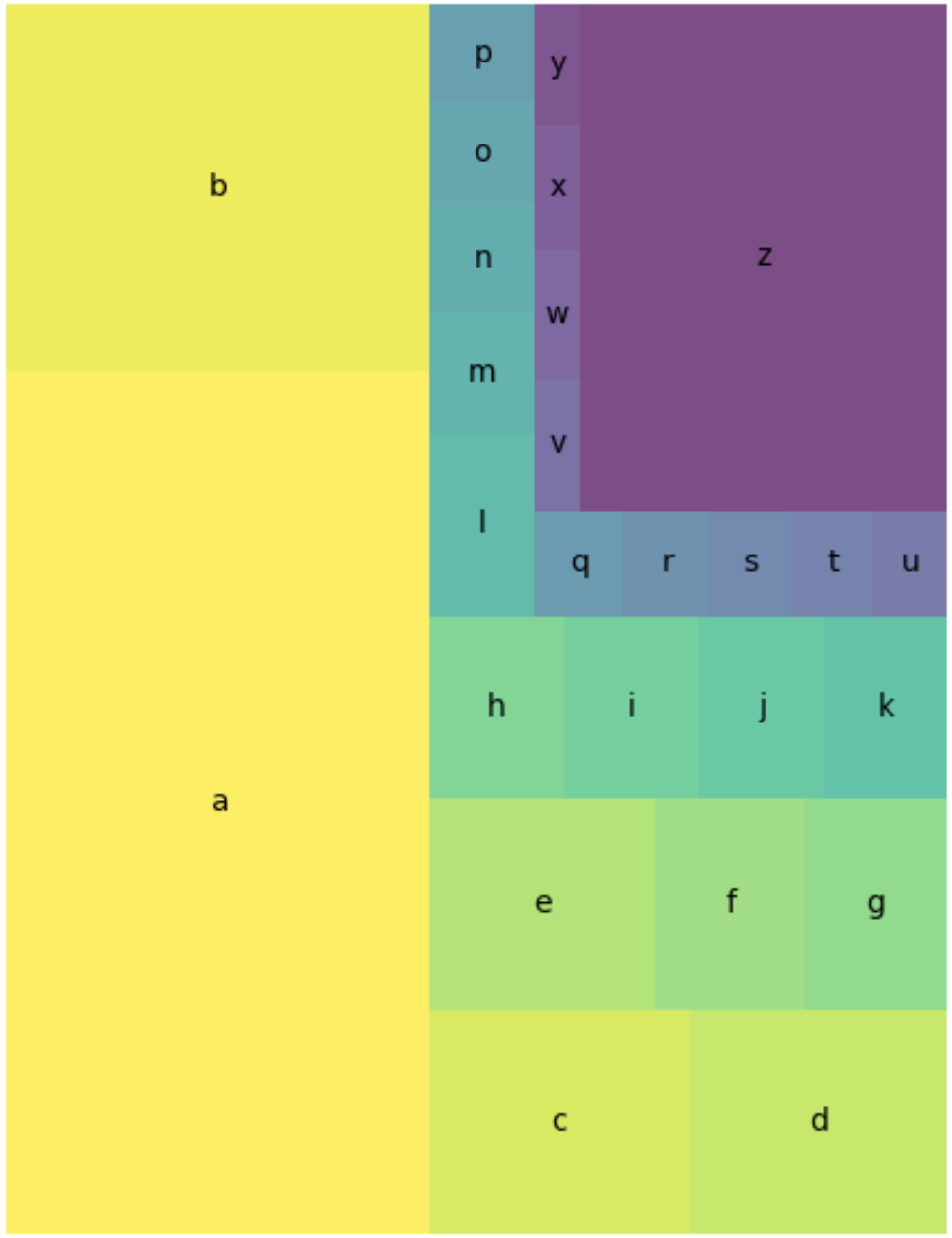
Titus Brown

July 17, 2025

STAMPS 2025

This is an proportional representation of the content of a metagenome, as estimated by sourmash.

The sizes are ”accurate” in that they are visually proportional.



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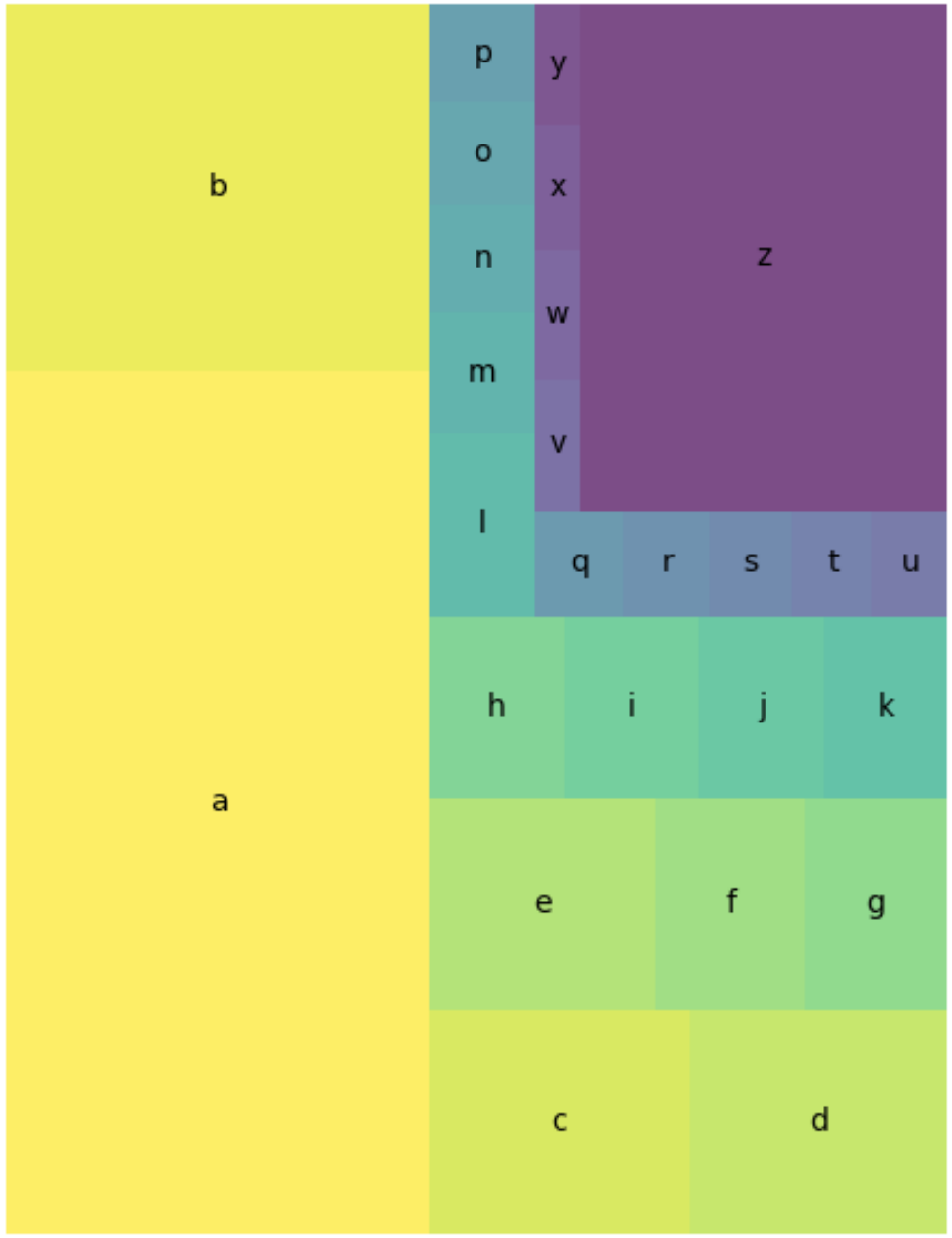
w: s__Faecousia sp022781505 (0.5%)
x: s__Limivicinus sp946061515 (0.5%)
y: s__UBA7173 sp001701135 (0.5%)
z: remaining taxa (16.1%)

The size of each box is, essentially:

size of genome
x
abundance of genome

(The actual bp numbers are available, too; ask me when we get to the command line!)



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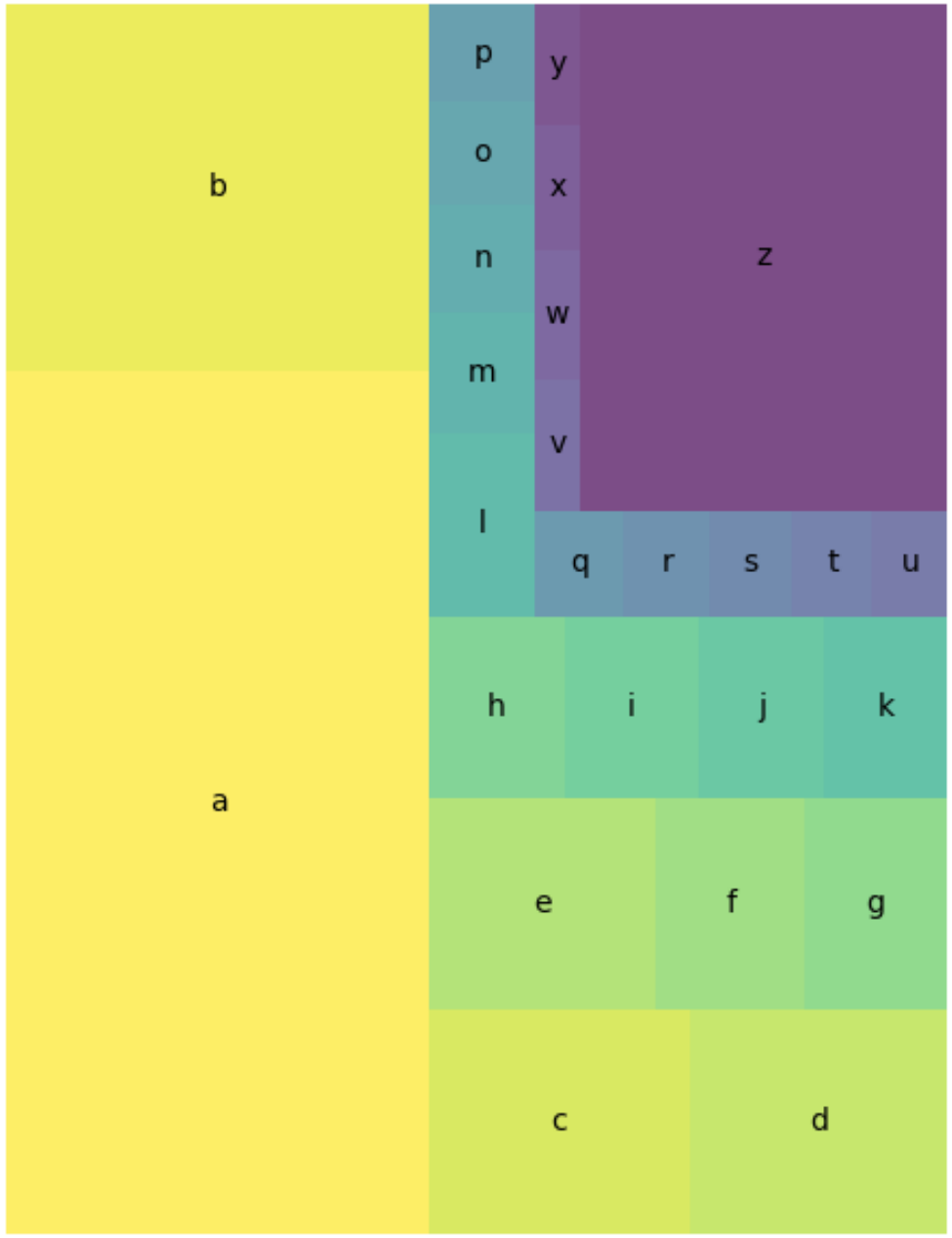
Think of this as a *dartboard*, and of sequencing as throwing a dart at this map.

Throwing more darts is sequencing more deeply.



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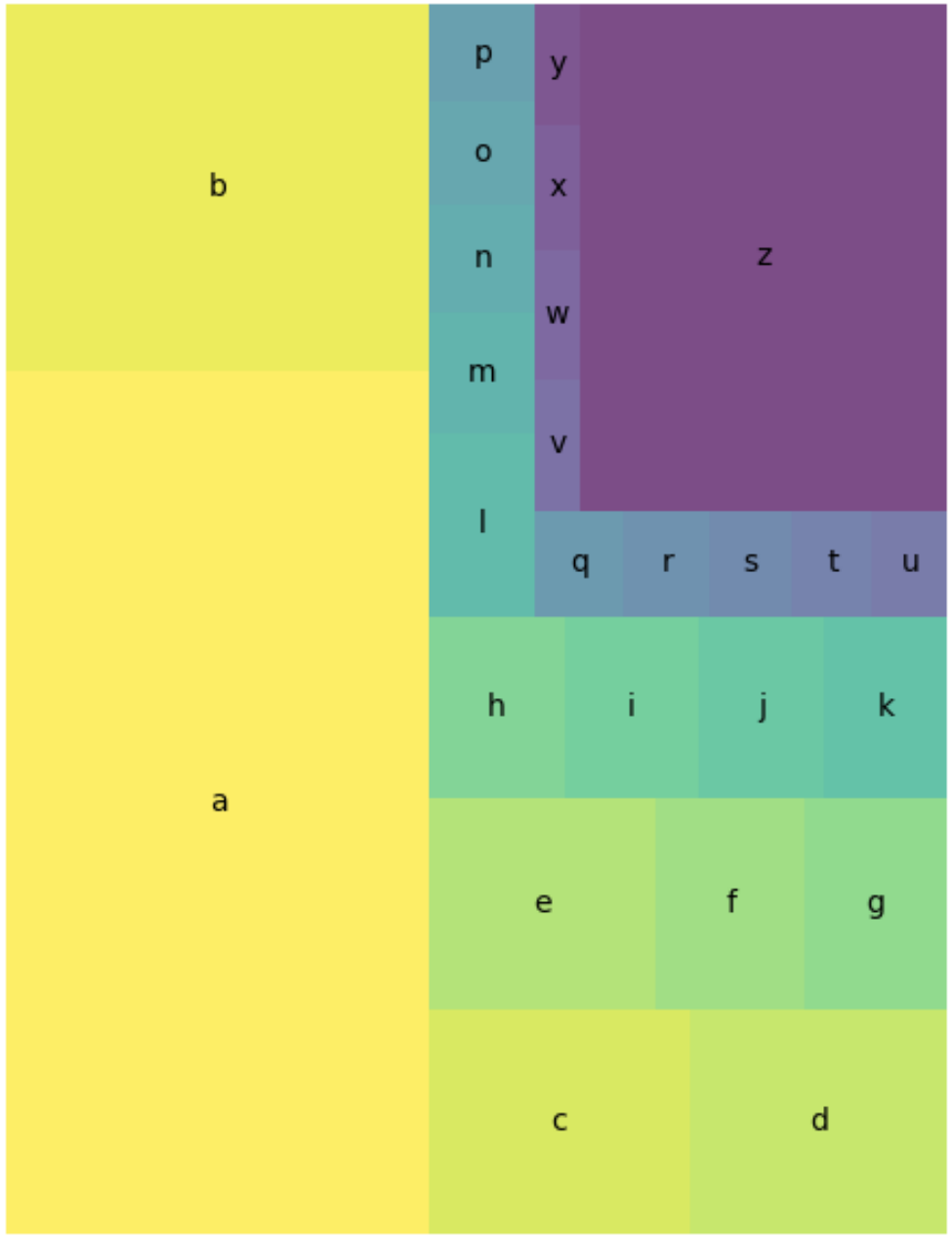
Q1: What will you mostly get if you throw twice as many darts at this dart board?



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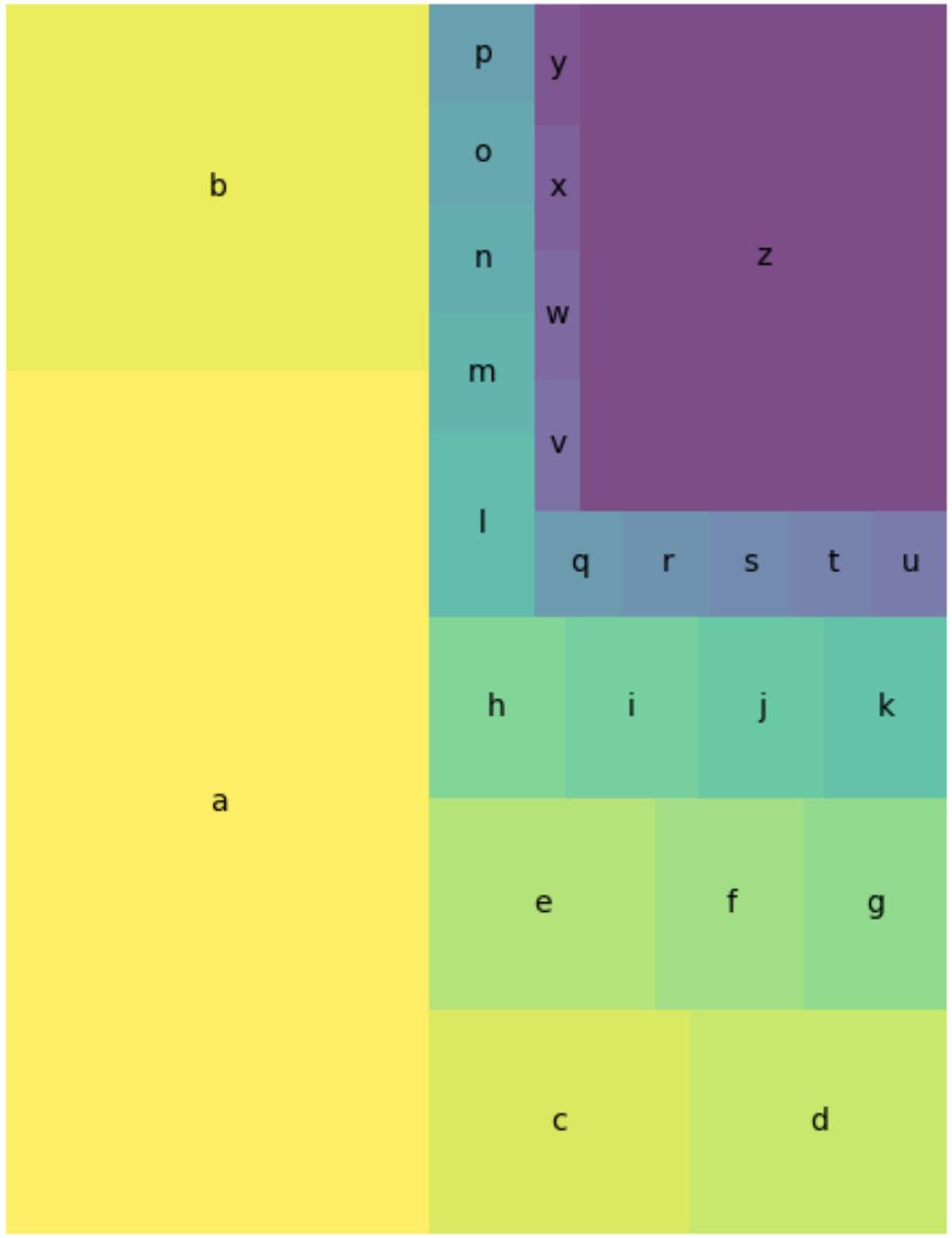
Q2: What happens to the abundances (not displayed ;) if you throw twice as many darts at this dart board?



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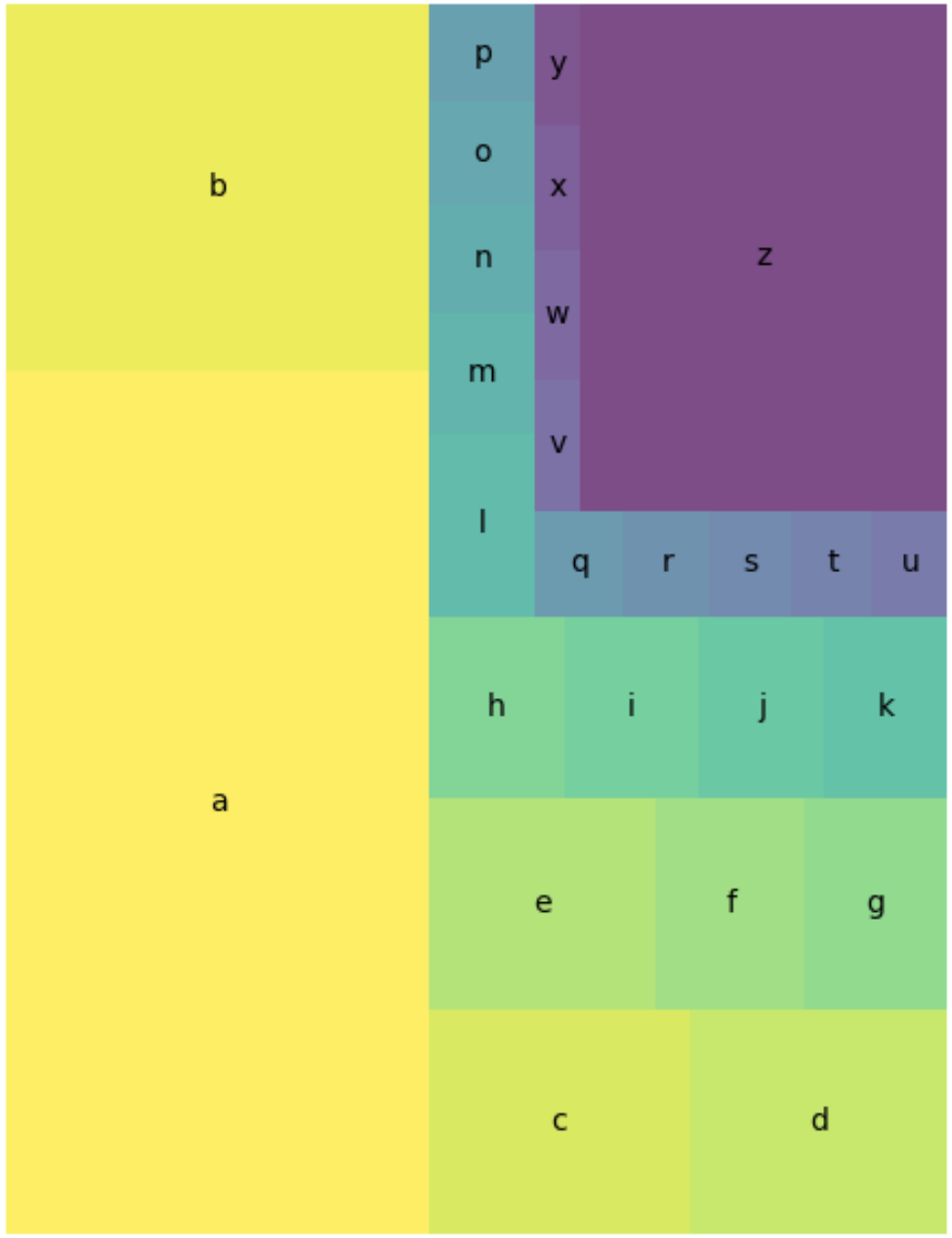
Let’s suppose you can select darts with different size tips.

Q3: How does this change your dart throwing strategy?



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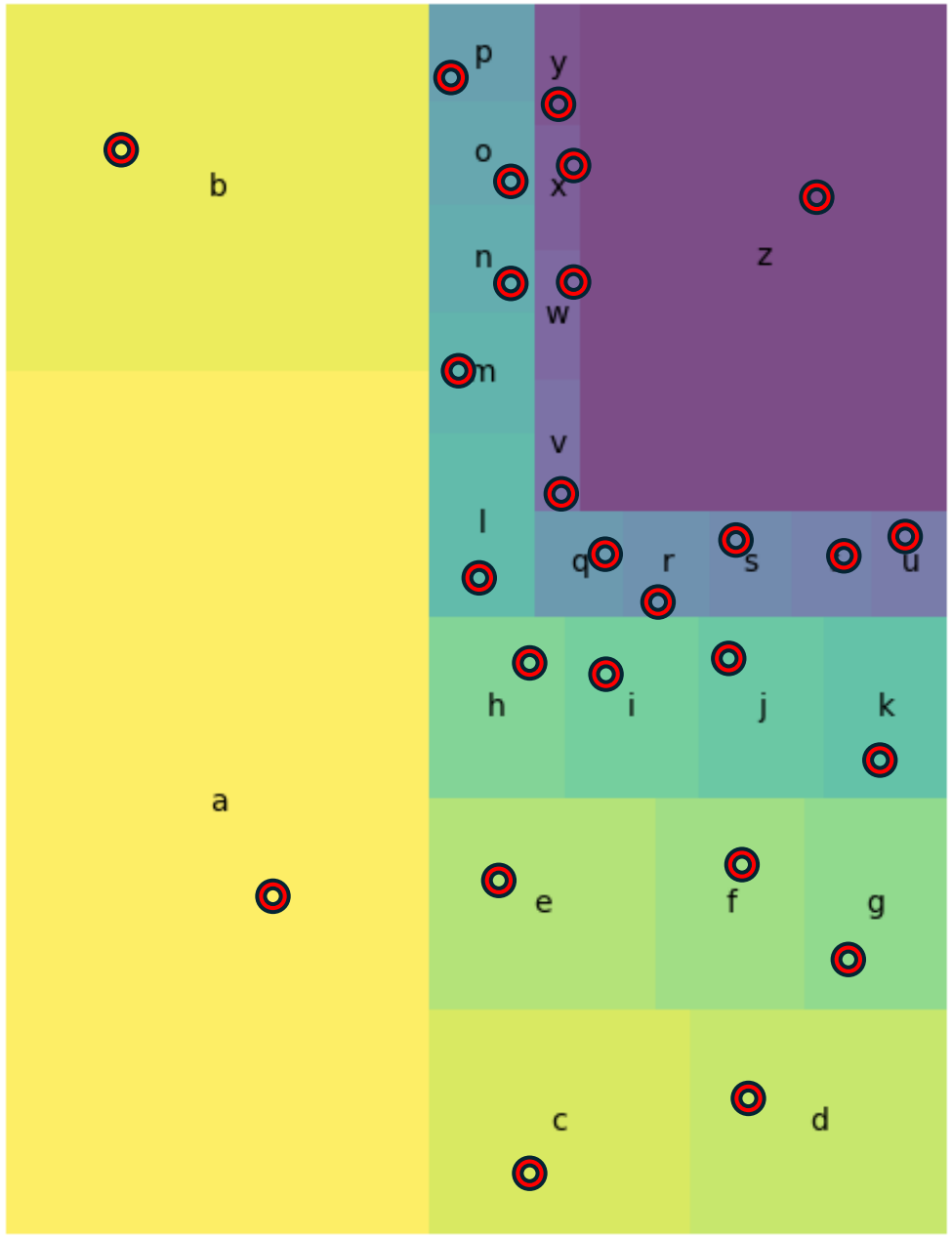
(linkage & sequencing read length)

Now let's change the darts to be strongly magnetic, so that they ONLY hit the red circles.

Q4: How does ***this*** change your dart throwing strategy?

(This is a 16S/amplicon analogy ☺)



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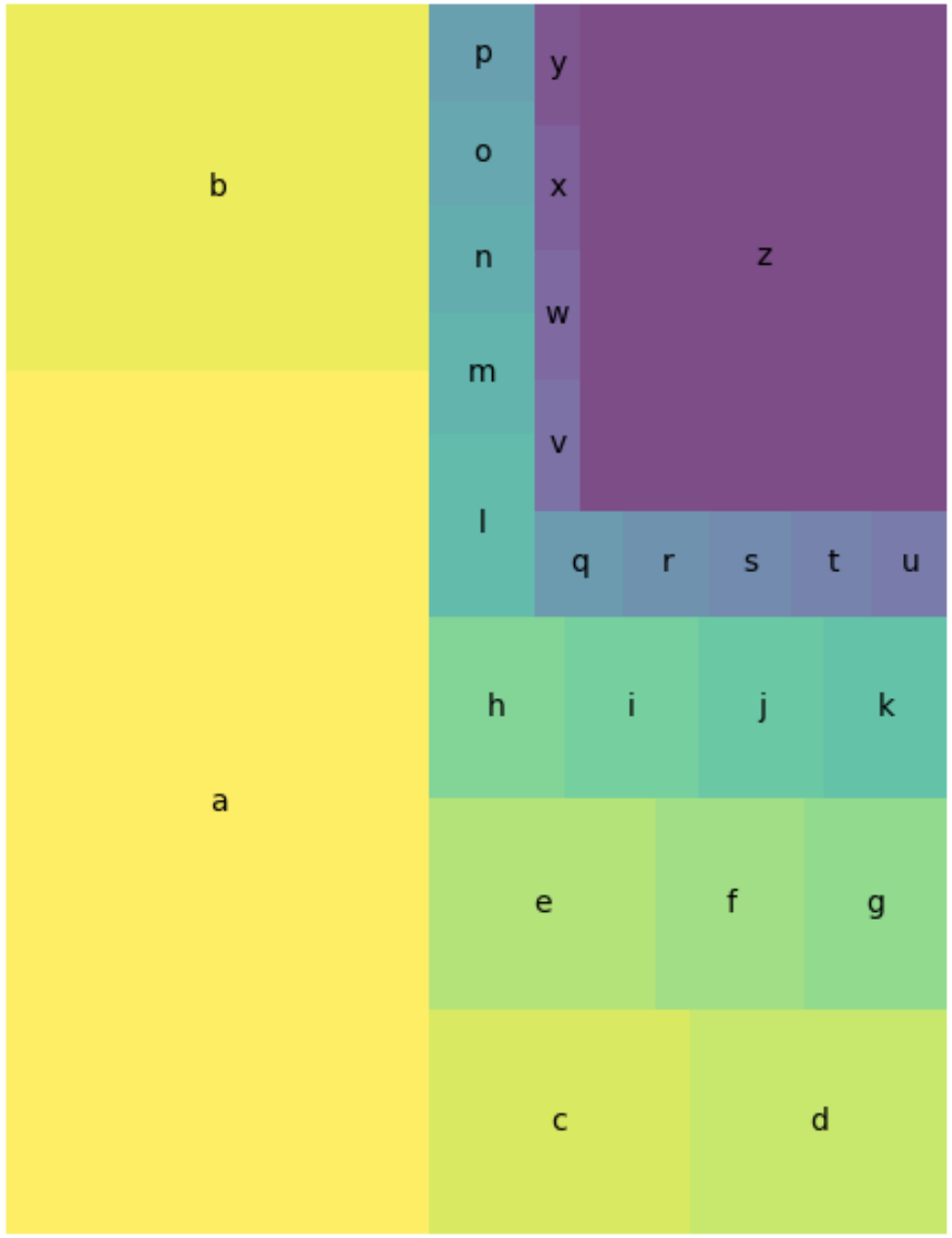
Q5: what is the unclassified stuff?

(What *could* it be?)



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The size of each box is, essentially:

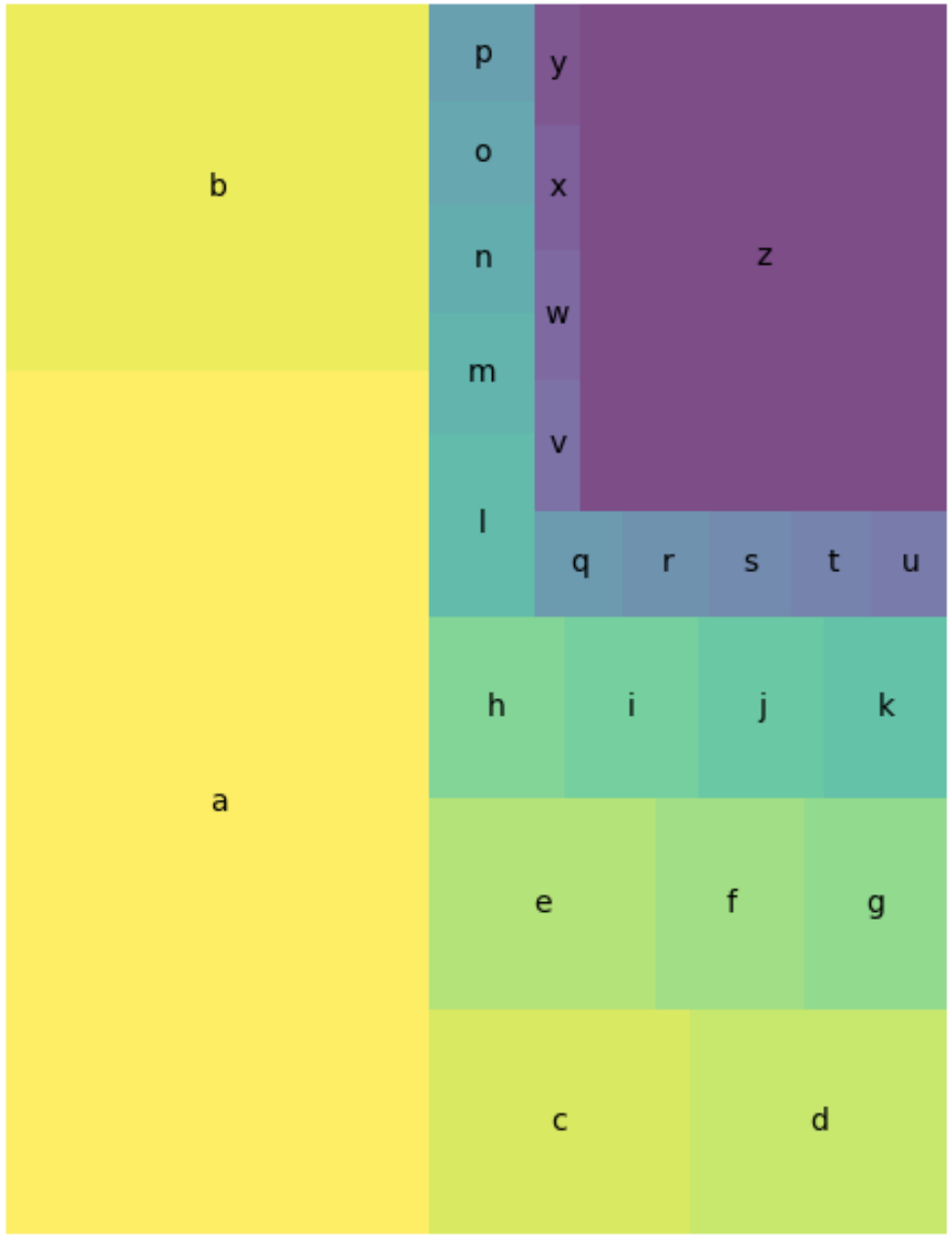
size of genome x abundance of genome

Bacteria: ~5 million base pairs.

Eukaryotes: 100 million-5 billion base pairs (20-1000x bigger)

Viruses: 10,000-50,000 base pairs. (100x *smaller)*

Q6: what would viruses look like on here?



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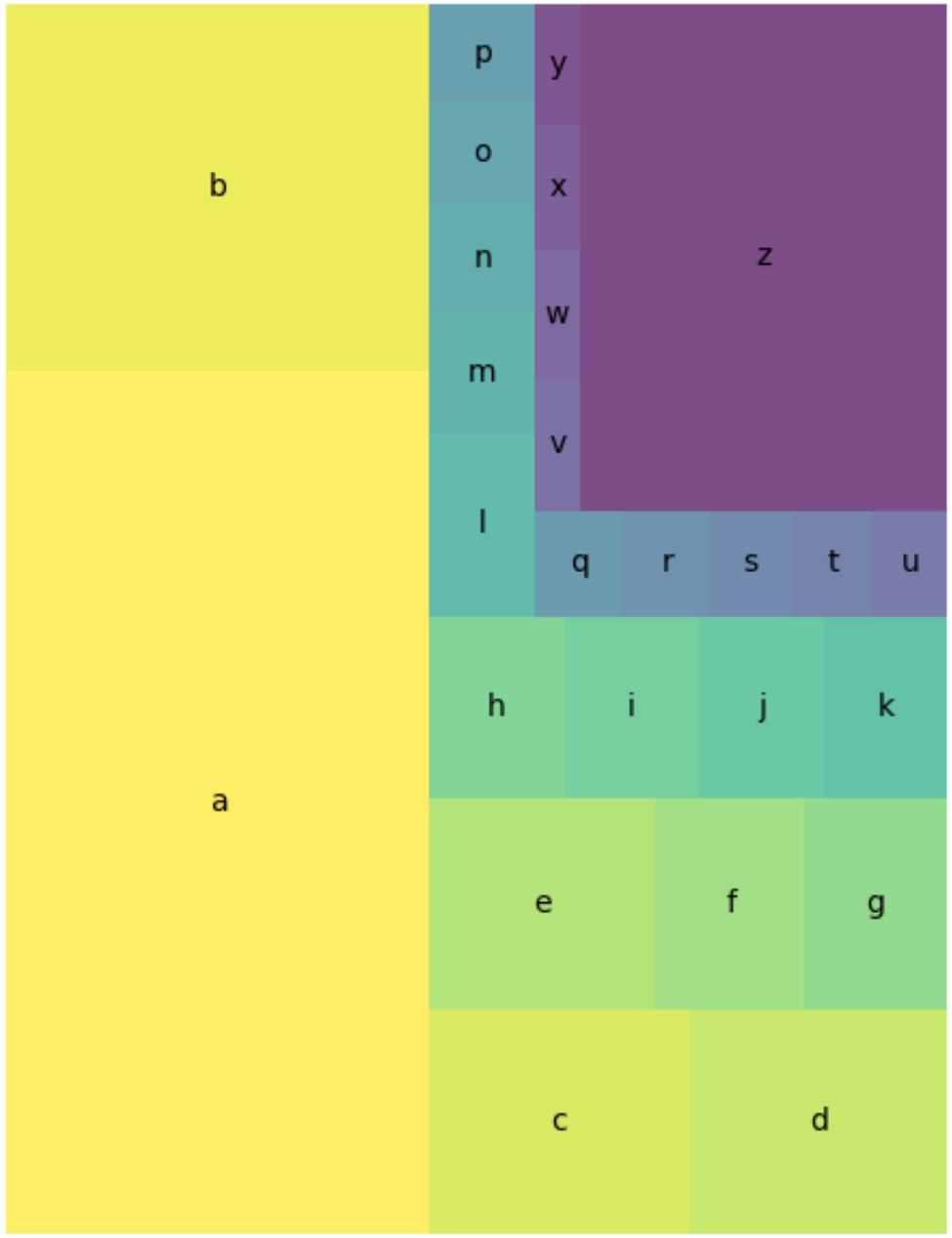
Q7: What would rarefaction be doing in this situation?

(We'll talk about this more on Monday… stats day!)



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