Main Points

1) Introduction to estimating species richness

-- estimating species richness with the Shannon diversity index

-- the influence of abundance (sampling effort) on species richness

2) Species accumulation and species rarefaction

-- sample- and individual-based assessment

3) Review for Test 1

Thursday 1 Oct = Test 1 (bring a calculator); test material is through Thursday 24 September

Tuesday 6 Oct = Q/A session for HW #2

Thursday 8 Oct = debate #1: single vs multi-species conservation. For non-debaters, remember to print out and bring "different group evaluation" handout from website. For debaters, Jake encourages you to set up a meeting to discuss outline of ideas.

Jake will send HW #2 out by the end of the day.

Pre-reading: Tuesday 6 Oct = Stoner et al.

Terms: species richness, species evenness, Shannon diversity index, accumulation curve, rarefaction curve

Group Debates (105 pts for debate, 15 pts for each eval)

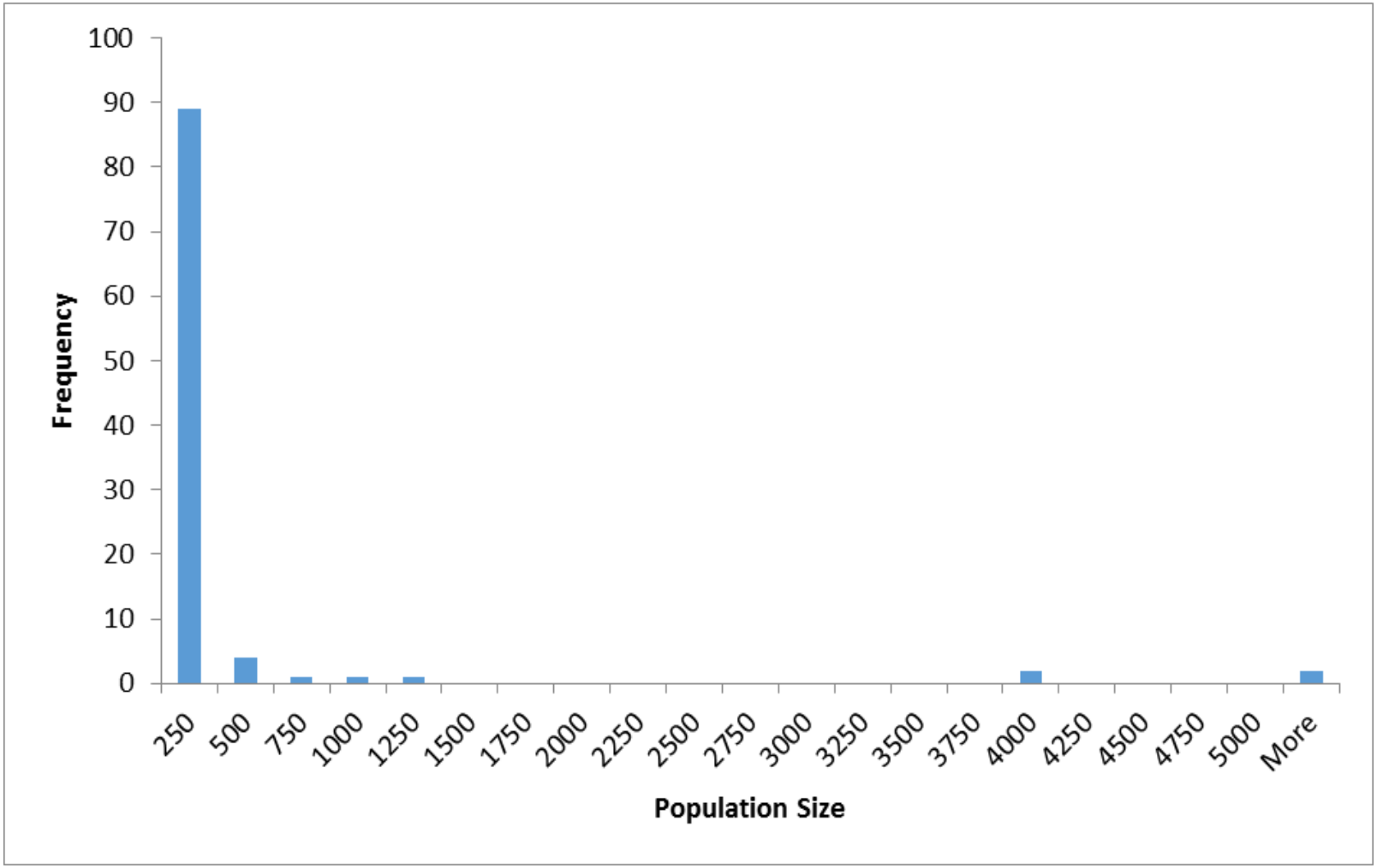
Single- vs Multi-Species Conservation
Single Species: Lauren, Kody, Cheyenne
Multi-Species: Marissa V., Tracey, Marissa D.

Pros and Cons of Consumptive Use of Wildlife
Pros: Martha, Ashtyn, Rebecca
Cons: Brent, Ina, Aubrey

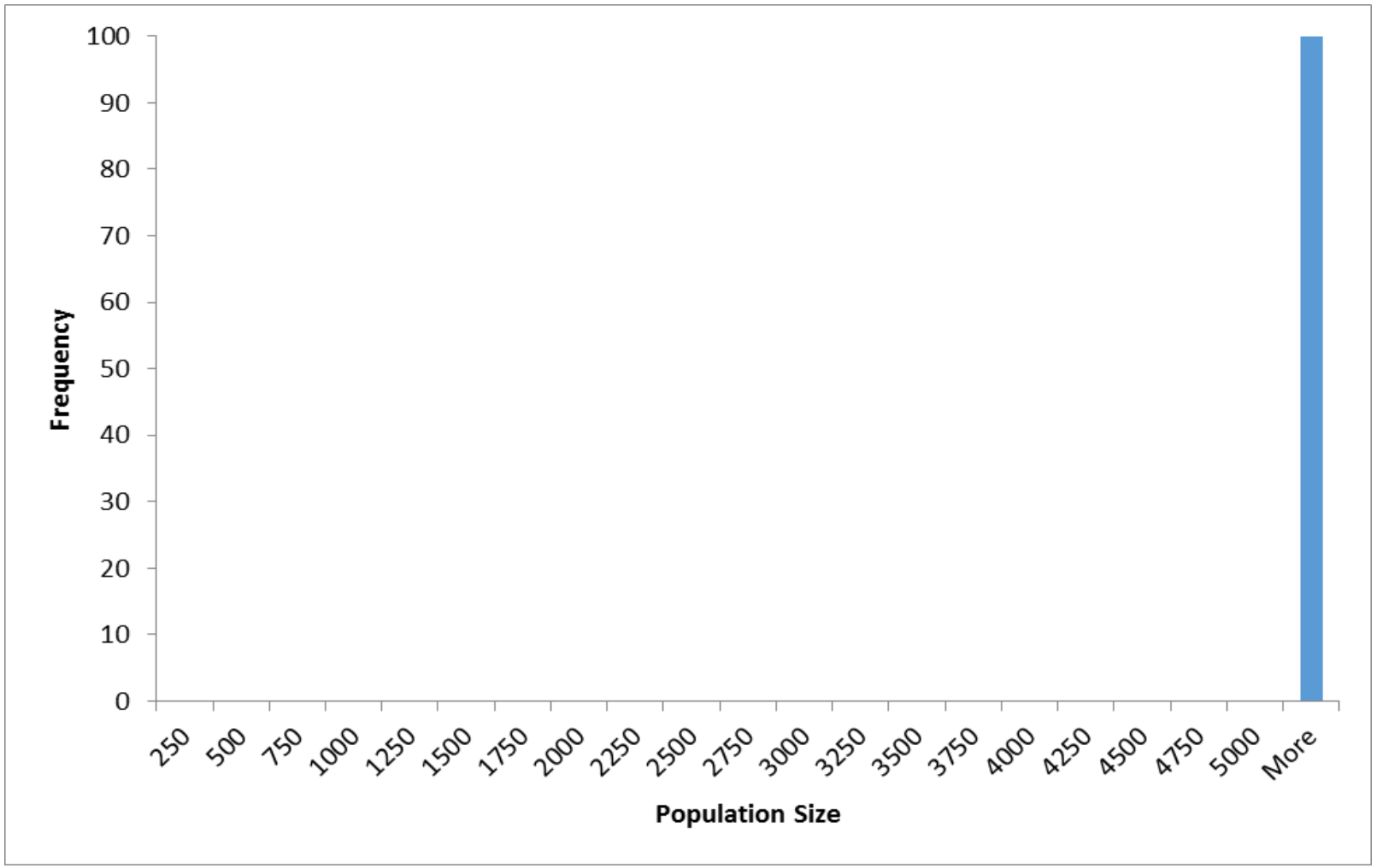
Pros and Cons of Climate Change Mitigation
Pros: Bonnie, Bryce, Joey
Cons: Quentin, Chelsea, Kayla

Conservation in Protected Areas vs Human-Occupied Landscapes
Protected Areas: Rachel, Emily, Grace, Lydia
Human-Occupied Landscapes: Karissa, Deo, Courtney, Victoria

HW #1 3a, variation in lambdas



HW #1 3b, no variation in lambdas



Estimating species richness

- **<u>species richness</u> = the number of species in a region, site, or sample.**

sagebrush-steppe (richness = 2)

forest/woodland (richness = 6)

Estimating species richness

- **<u>species evenness</u> = the degree to which individuals are divided equally among species.**

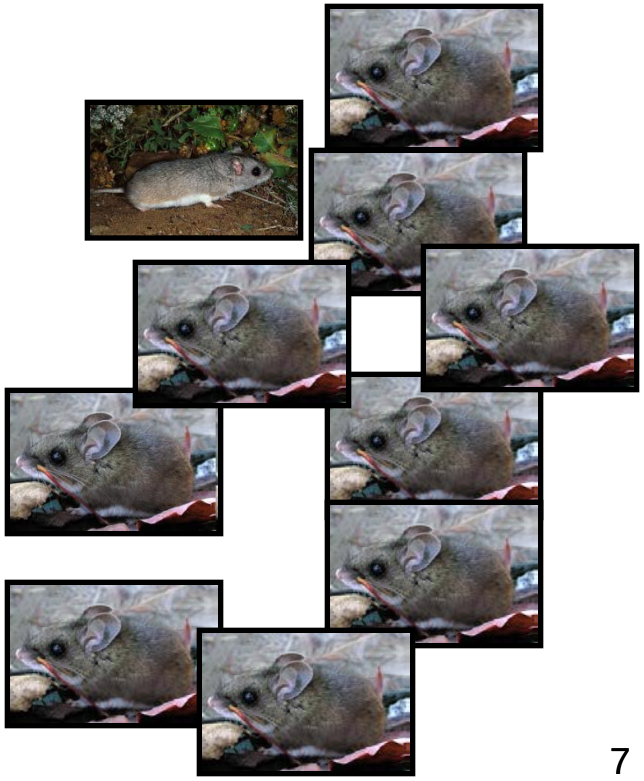
sagebrush-steppe

forest/woodland

Estimating species richness

- **<u>species diversity (Shannon)</u> = an index combining species richness and species evenness.**

sagebrush-steppe



Estimating species richness

- **<u>species diversity (Shannon)</u> = an index combining species richness and species evenness.**

$$H = -\sum_{i=1}^{S} (p_i * \ln (p_i))$$

$$H_{max} = \ln (S)$$

S = total number of species sampled

p_i = relative abundance of species i

sagebrush-steppe

Estimating species richness

- **<u>species diversity (Shannon)</u> = an index combining species richness and species evenness.**

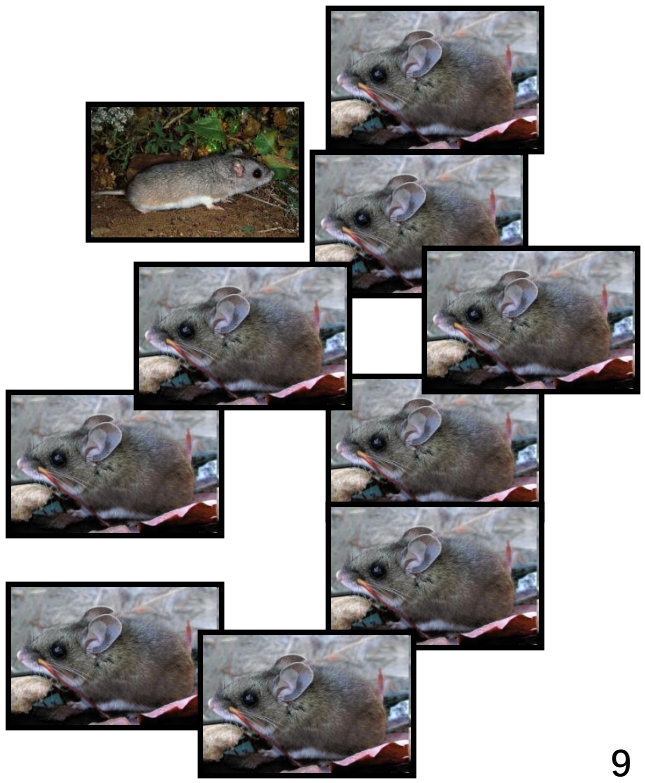
$$H = -\sum_{i=1}^{S} (p_i * \ln (p_i))$$

$$H_{max} = \ln (S)$$

$$H = -\Sigma\ (0.9 * -0.11) + (0.1 * -2.30) = 0.33$$

$$J = H/H_{max} = 0.48$$

sagebrush-steppe



Estimating species richness

- **<u>species diversity (Shannon)</u> = an index combining species richness and species evenness.**

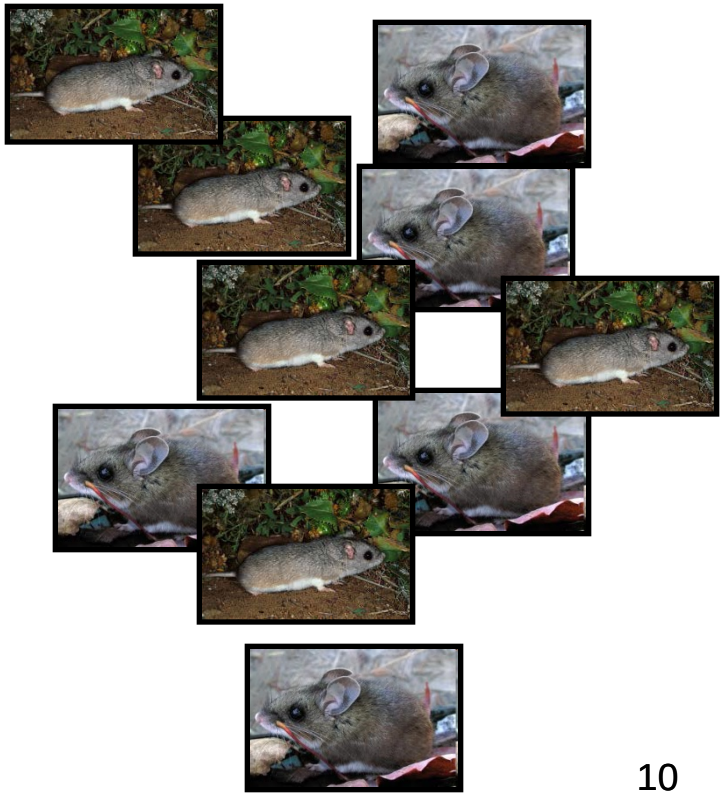
$$H = -\sum_{i=1}^{S} (p_i * \ln (p_i))$$

$$H_{max} = \ln (S)$$

$$H = - \Sigma (0.5 * -0.69) + (0.5 * -0.69) = 0.69$$

$$J = H/H_{max} = 1.0$$

sagebrush-steppe



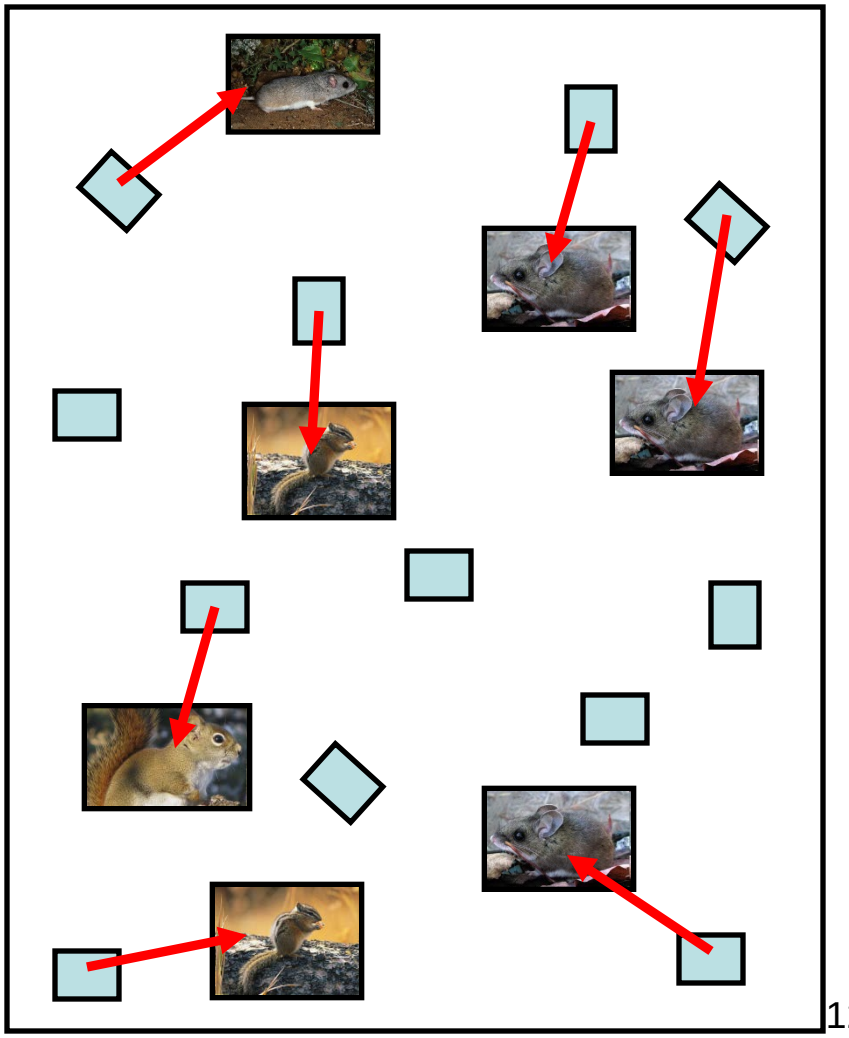
Accumulation curves: what they are, why they're used

- **<u>species accumulation curve</u> = graph depicting the total number of species sampled during data collection as additional individuals/samples are added to the total of previously-sampled individuals/samples.**

- **used primarily to visualize how species are added (or accumulated) with increasing individuals/samples.**

Sample- vs individual-based species richness

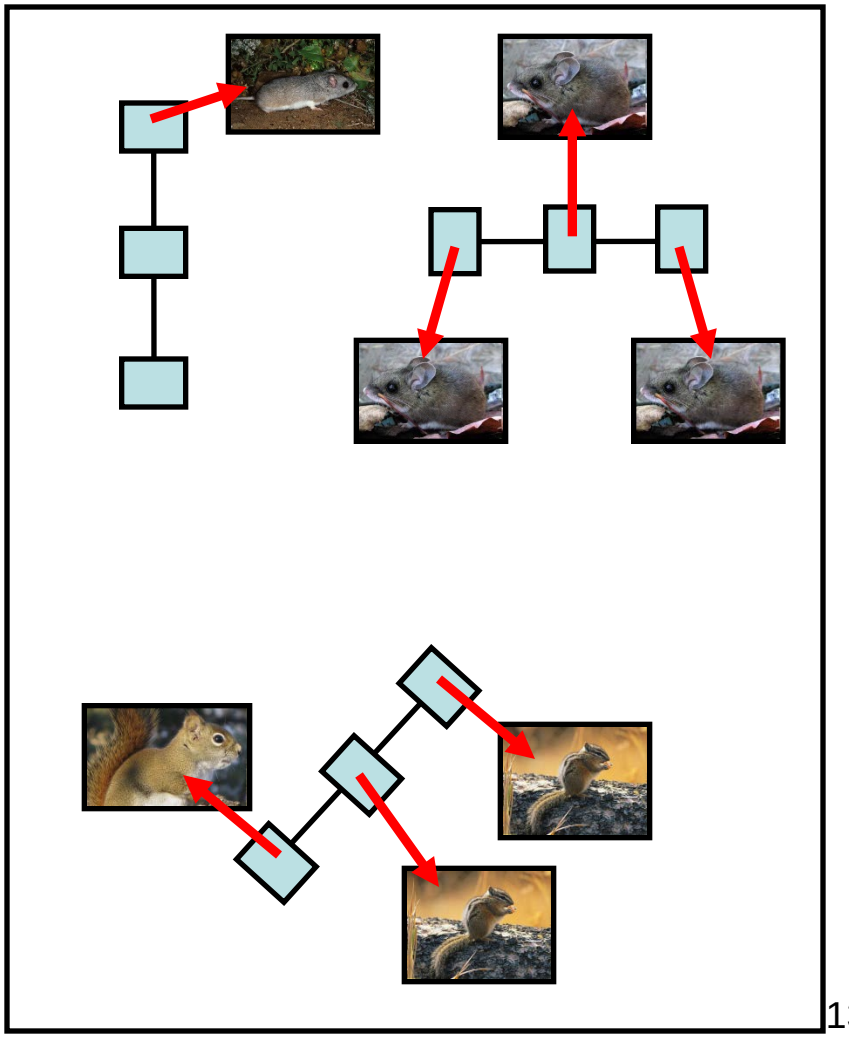
- **<u>Individual-based assessment</u> examines a predetermined number of individuals (e.g., n = 7 small mammals) to assess richness**



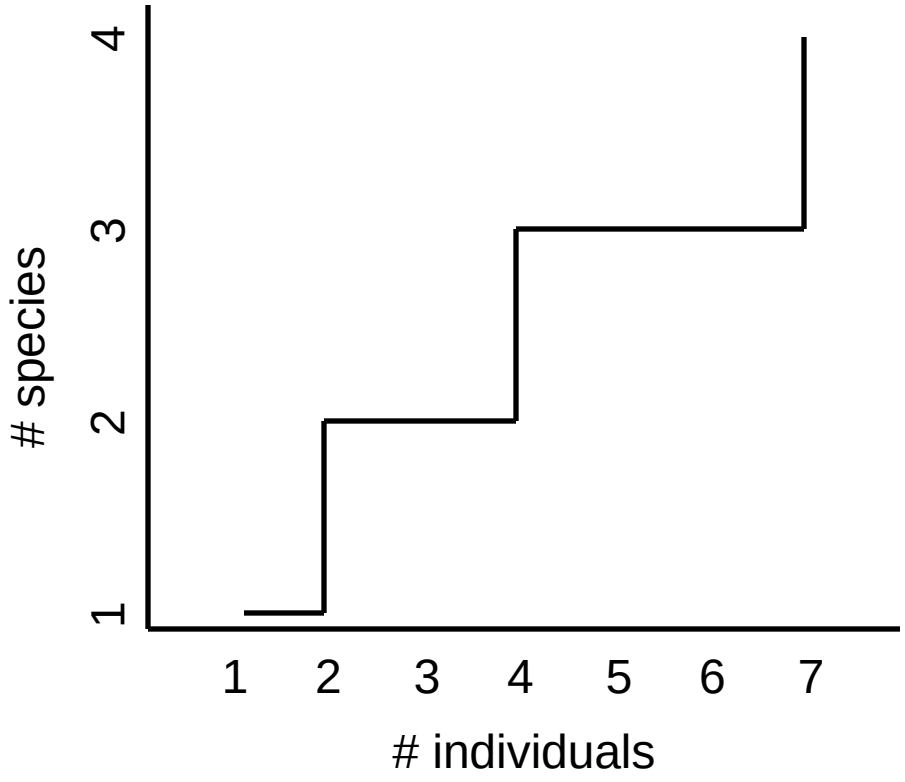
Sample- vs individual-based species richness

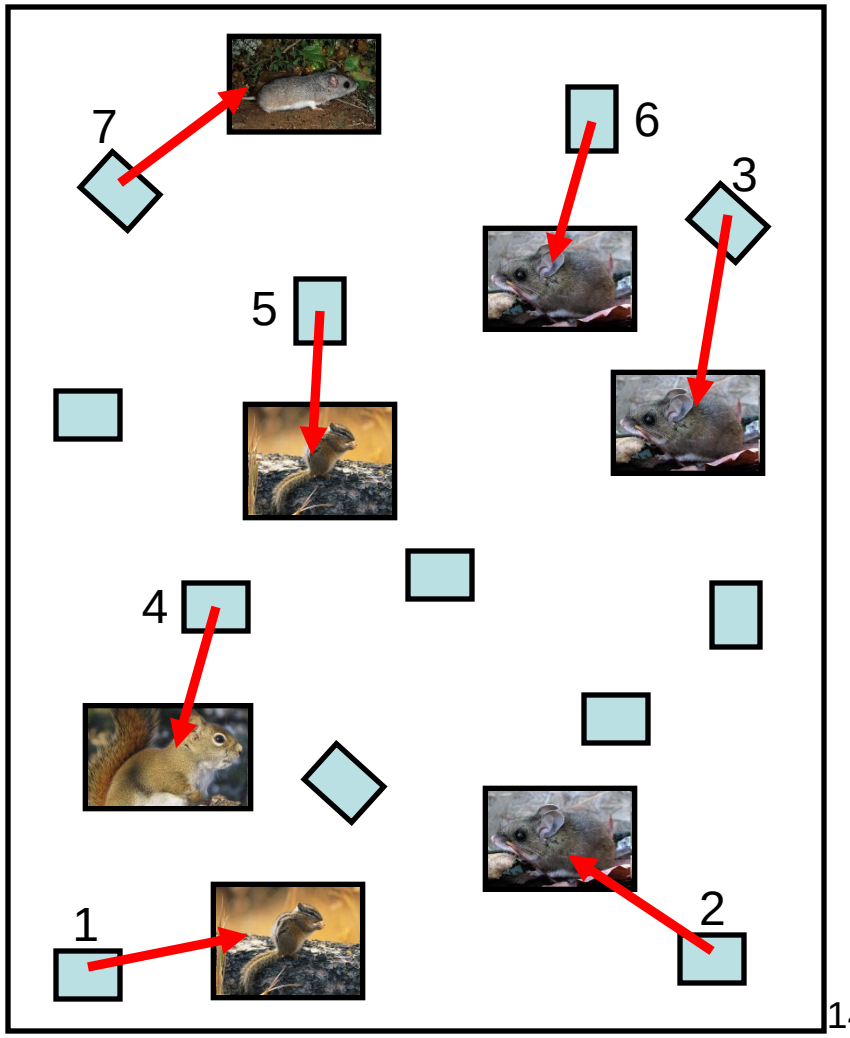
- **Individual-based assessment** examines a predetermined number of individuals (e.g., n = 7 small mammals) to assess richness

- **Sample-based assessment uses replicate samples (e.g., n = 3 transects) to assess richness**

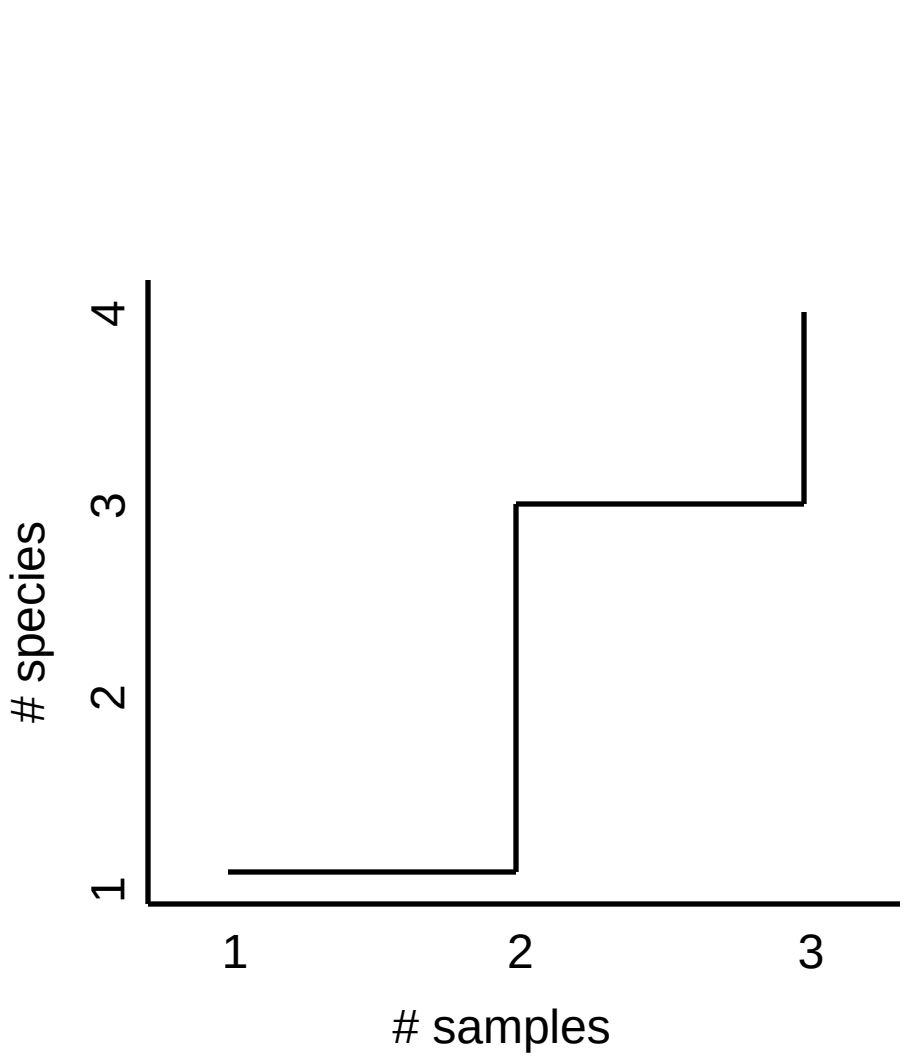


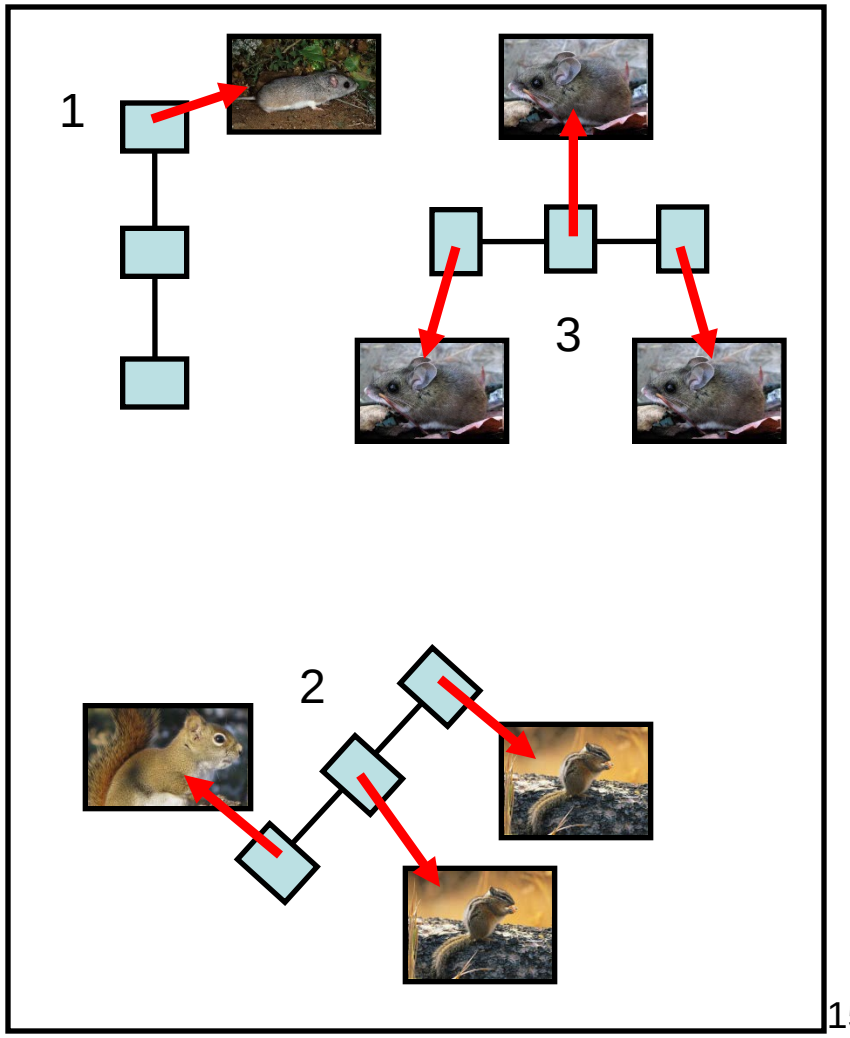
Individual-based accumulation curve





Sample-based accumulation curve





The problem of unequal effort

<u>sagebrush-steppe</u>
2 transects *
10 traps/transect *
3 nights = 60 trap-nights

= 19 individuals of 2 species

<u>forest/woodland</u>
4 transects *
10 traps/transect *
3 nights = 120 trap-nights

= 36 individuals of 6 species

The problem of unequal effort

- **generally, the number of individuals sampled at a site is correlated positively with the number of species.**

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- **generally, the number of individuals sampled at a site also is correlated positively with sampling effort.**

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The problem of unequal effort

- **generally, the number of species sampled at a site is correlated positively with the number of individuals.**

- **generally, the number of individuals sampled at a site also is correlated positively with sampling effort.**

- **so, the number of species we sample at a site should be partly determined by our sampling effort.**

The problem of unequal effort

- **we can account for the influence of unequal effort on the number of species through <u>rarefaction</u>.**

<u>forest/woodland</u>
4 transects *
10 traps/transect *
3 nights = 120 trap-nights

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Rarefaction curves: what they are, why they're used

- **<u>species rarefaction curve</u> = graph produced by repeatedly resampling the total number of individuals/samples, and plotting the average number of species represented by 1, 2, … N individuals/samples.**

Rarefaction curves: what they are, why they're used

- **<u>species rarefaction curve</u> = graph produced by repeatedly resampling the total number of individuals/samples, and plotting the average number of species represented by 1, 2, … N individuals/samples.**

- **this generates the expected number of species in a subset of n individuals/samples drawn at random from a larger total of N individuals/samples.**

Rarefaction curves: what they are, why they're used

- **species rarefaction curve = graph produced by repeatedly resampling the total number of individuals/sites, and plotting the average number of species represented by 1, 2, … N individuals/samples.**

- **this generates the expected number of species in a subset of n individuals/samples drawn at random from a larger total of N individuals/samples.**

- **used to compare species richness among communities where sampling effort differs.**

Rarefaction curves: what they are, why they're used

Community 1
7 individuals
4 species

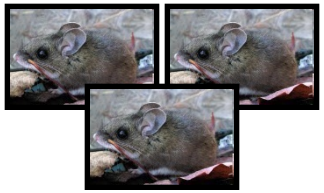
Community 2
3 individuals
2 species

Random Communities

RC1 =

RC2 =

RC3 =



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RC50 (or 100, or 1000, or whatevs)

Rarefaction curves: what they are, why they're used

Community 1
7 individuals
4 species

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3 individuals
2 species

Random Communities

RC1 =

RC2 =

RC3 =

.

.

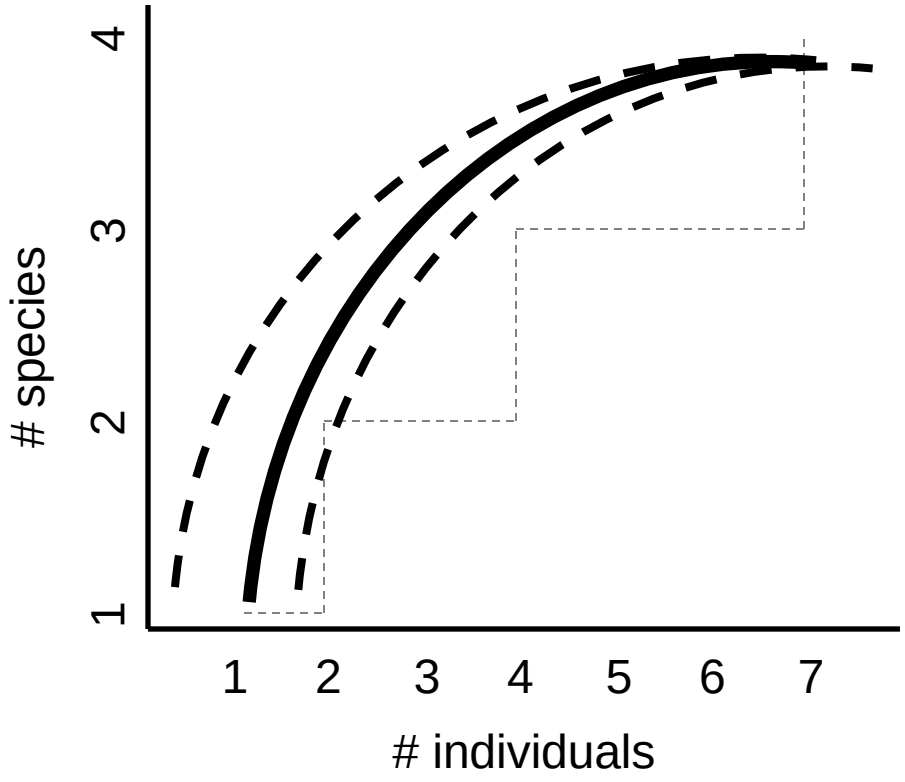
.

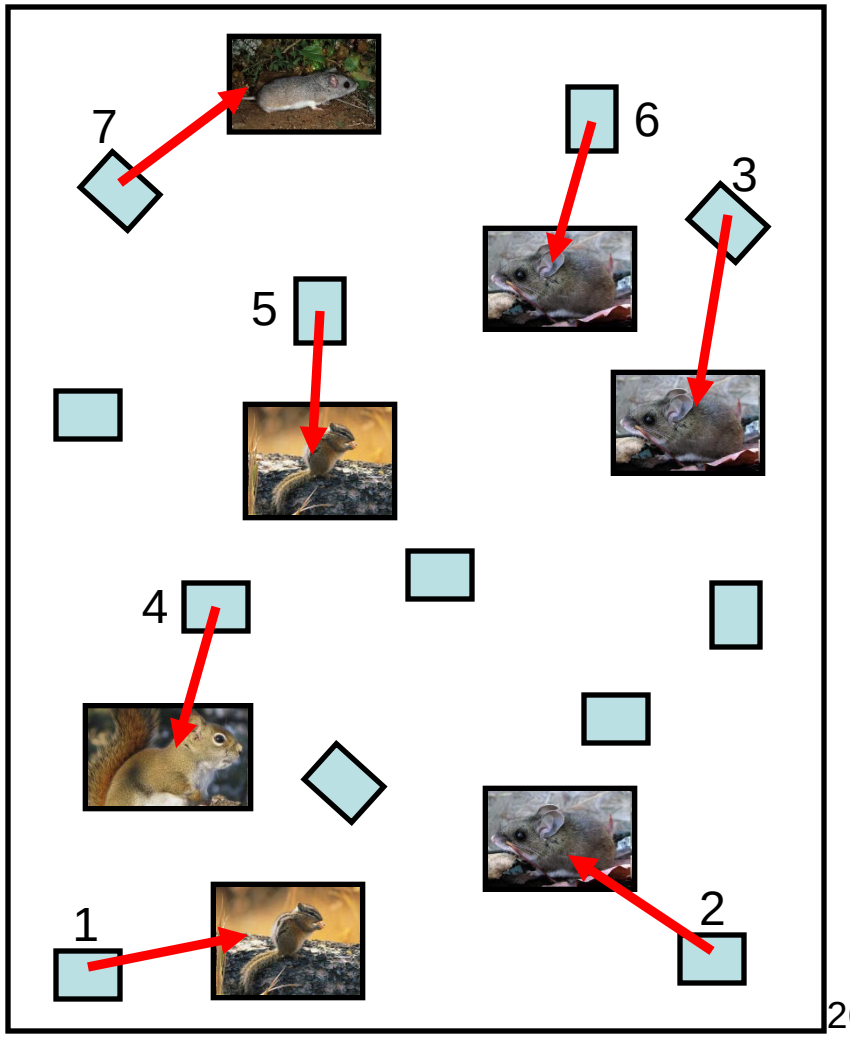
RC50 (or 100, or 1000, or whatevs)

- we are randomly drawing n individuals from the total of N individuals many times, then calculate a diversity index (e.g., Shannon, Simpson).

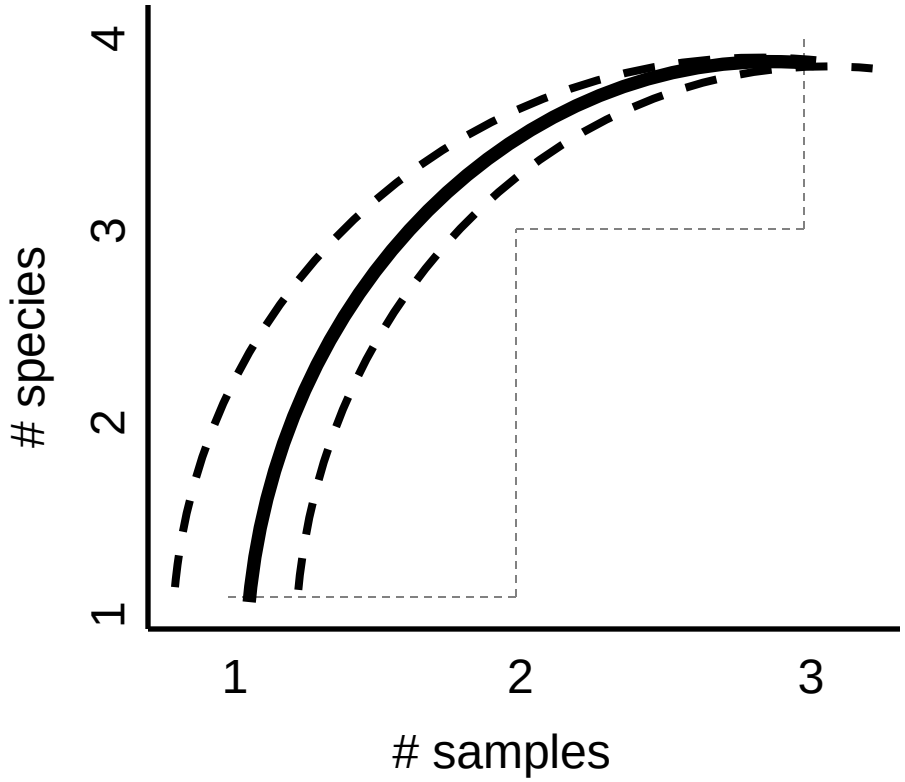
- because the diversity index is a mean calculated from the random communities, we also have a variance

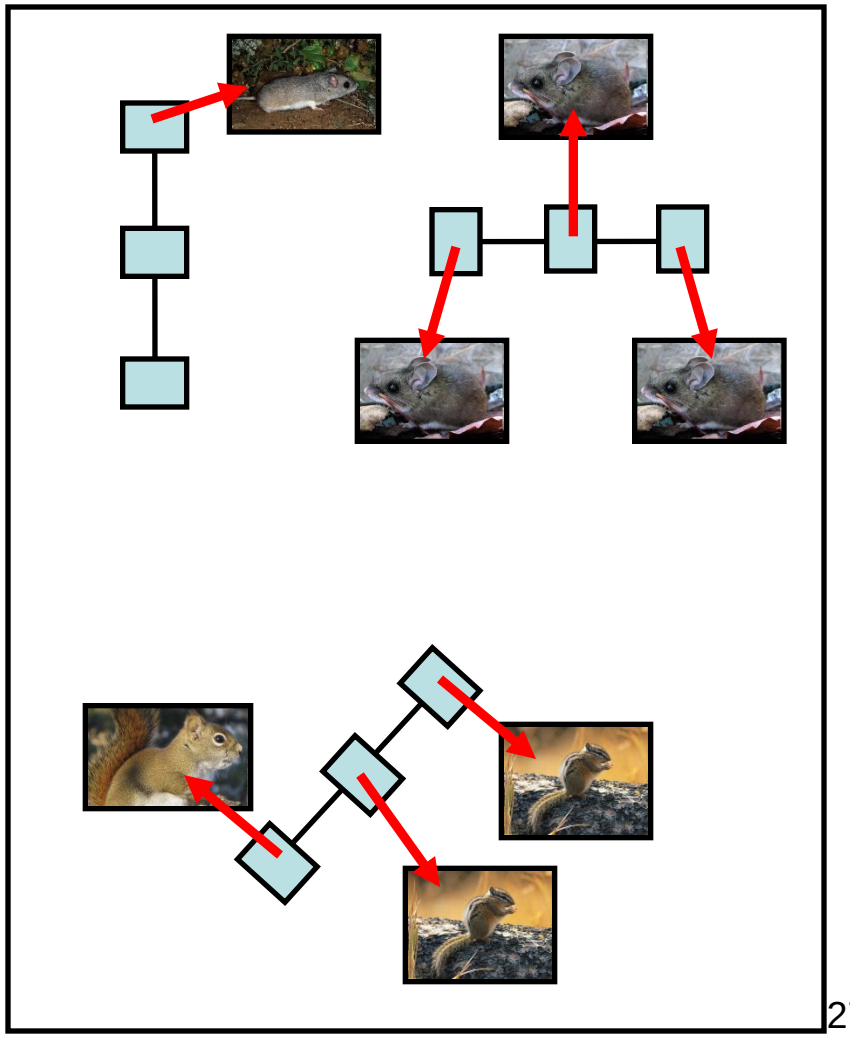
Individual-based rarefaction curve





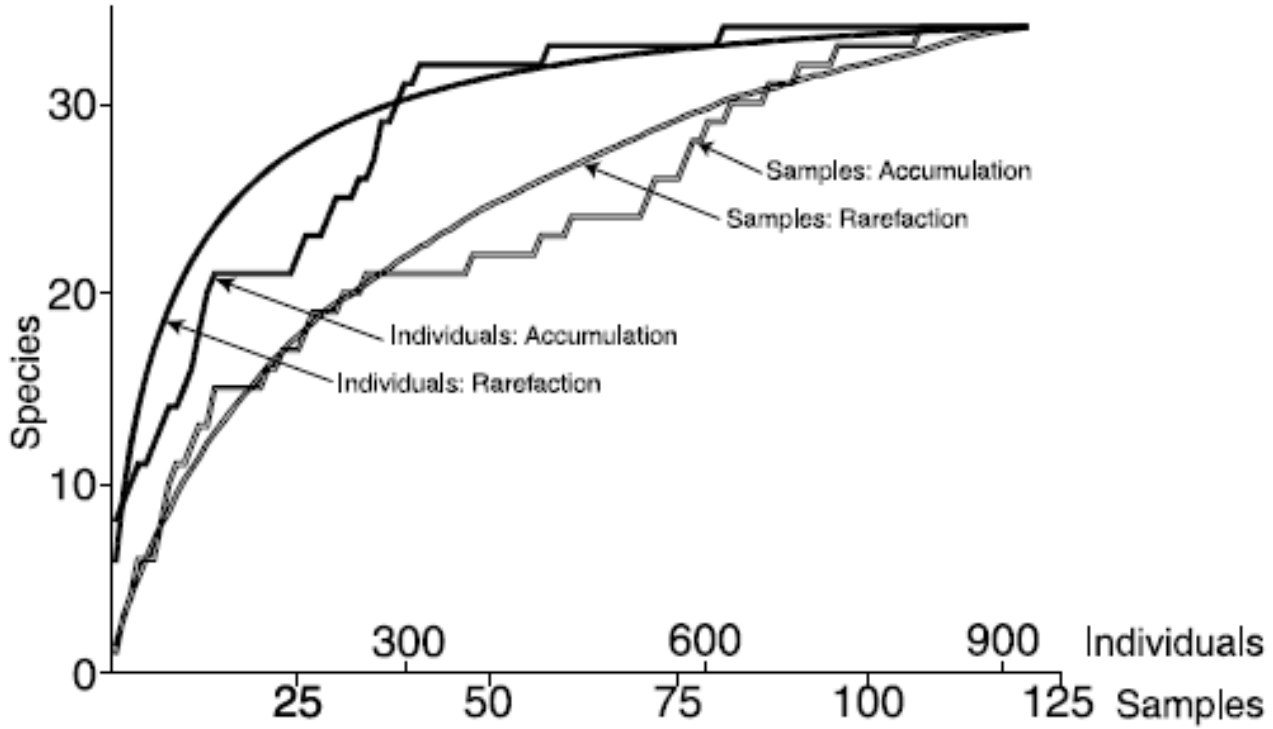
Sample-based rarefaction curve





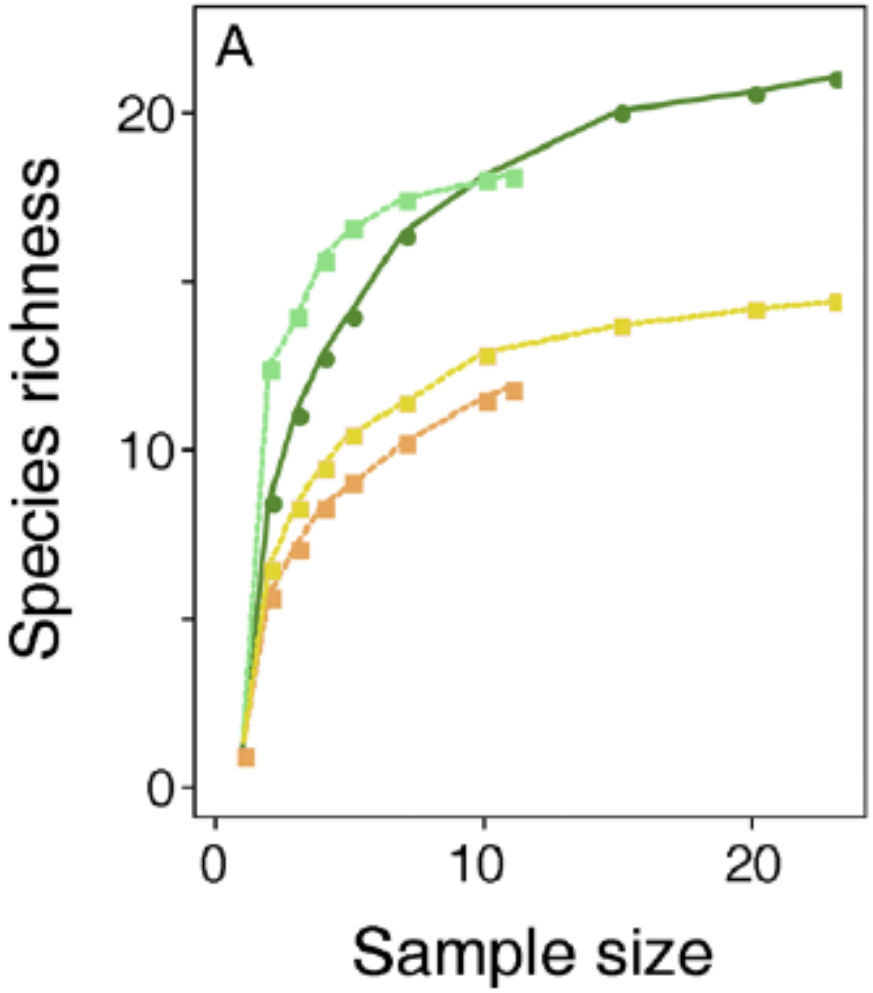
Discussion Q: If we plot individual-based accumulation and rarefaction curves, and sample-based accumulation and rarefaction curves, the sample-based curves are always "under" the individual-based curves. What does this mean? Why is this happening?

Hint: think to the mammal example, where certain species were <u>only</u> sampled on certain transects.



Gotelli and Colwell. 2001.

Sample-based rarefaction curve

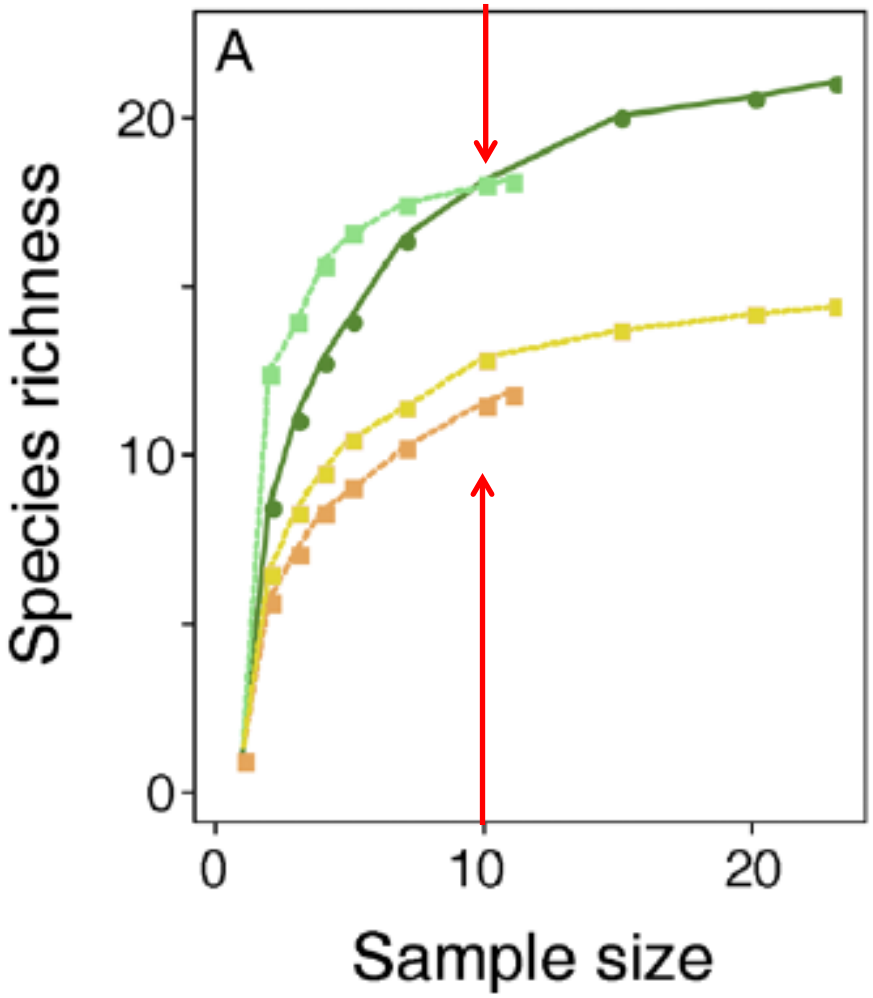


-- compare between sites, treatments, etc for a given sample size (or number of individuals)

High wildlife
Low-wildlife pastoral
Low-wildlife experiment
Low-wildlife agricultural

Young et al. 2014.

Sample-based rarefaction curve



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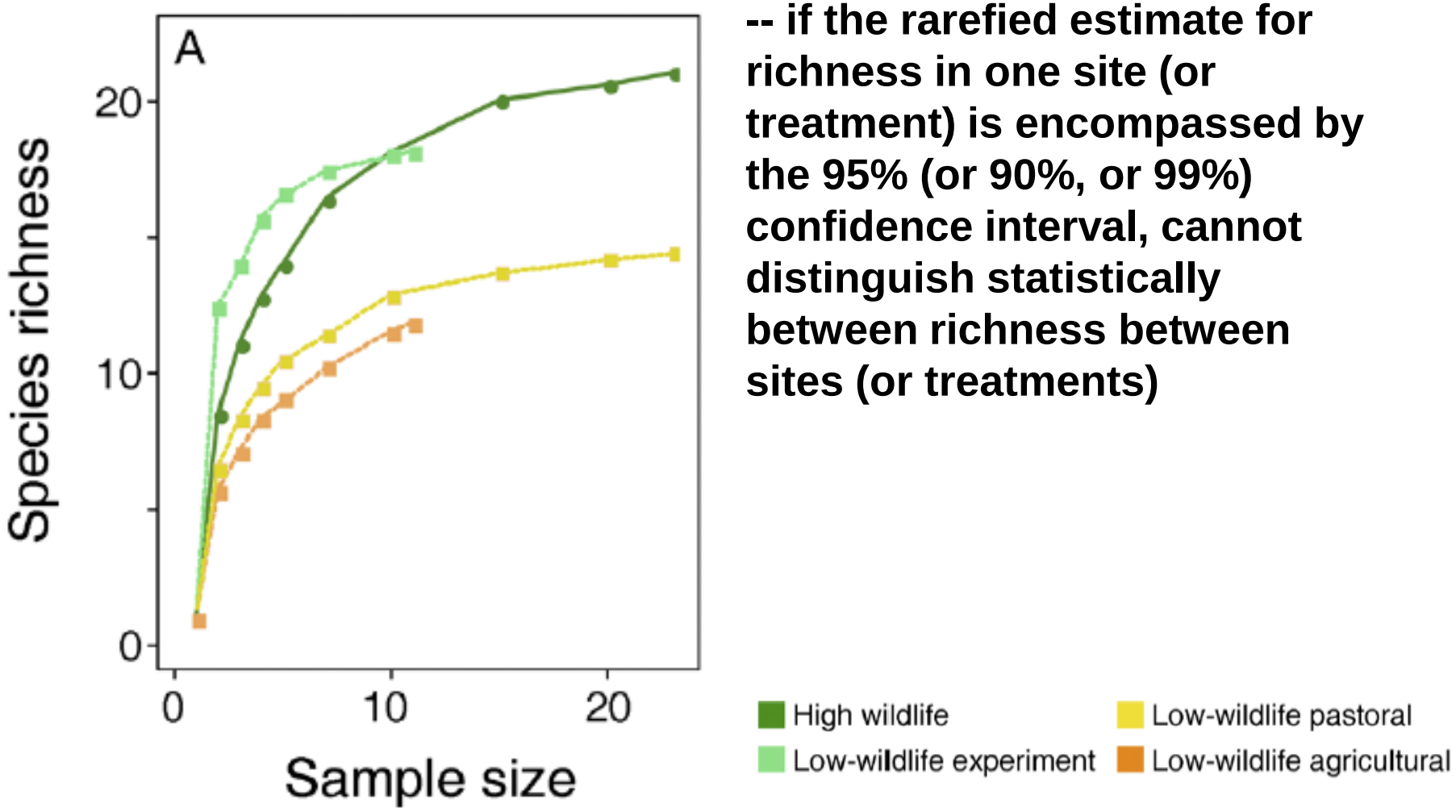
Sample-based rarefaction curve



-- if the rarefied estimate for richness in one site (or treatment) is encompassed by the 95% (or 90%, or 99%) confidence interval, cannot distinguish statistically between richness between sites (or treatments)

Young et al. 2014.