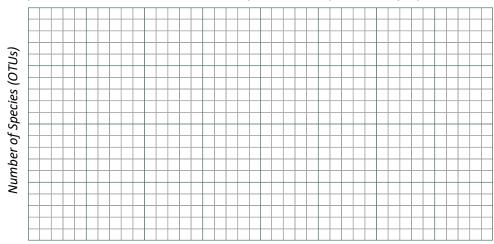
**Overview**: Quantifying diversity within and among samples, whether you are studying plants, insects, or microbes, gives us insight into the ecological processes influencing the community, which might include species interactions, environmental conditions, spatial effects, disturbances, etc.

## **Activity Learning Goals:**

- Quantify alpha and beta diversity of the jellybean "community."
- Describe why observed richness is always lower than estimated richness using the Chao1 method.
- Make a collector's curve and perform rarefaction analysis to make another estimate of total richness, and describe why this is the closest estimate to true richness.

Work in teams of 2 or 3. Each team has a "sample" of 40 jellybeans. Each "sample" represents a different "site" (water sample, soils, etc.) or subset of the entire jellybean community (all the jellybeans in this room). We know that there are 49 flavors, but only 13 colors; we will try to measure this using only our samples.

- 1. Decide on a species definition. <u>Flavor</u> and <u>color</u> are two different definitions of "species" of jellybean, also known as an operational taxonomic unit (OTU).
- 2. **Alpha diversity**. Calculate observed richness (**S**<sub>obs</sub>). You can do this by grouping jellybeans by "species" and counting the number of different groups.
- 3. **Alpha diversity**. Calculate the estimated richness ( $S_{est}$ ) using the *Chao1* estimator, which estimates true richness based on the number of singletons and doubletons in your sample:  $S_{est} = S_{obs} + (F_1^2/2F_2)$   $F_1 = \text{number of species in your sample represented as singletons} = _____
  <math>F_2 = \text{number of species in your sample represented as doubletons} = _____$
- 4. **Alpha diversity**. Rarefaction analysis fits a mathematical curve (a "rarefaction curve") to your observed species to estimate true diversity. To make this estimate, sample one at a time. The first point is plotted x=1 (1 sample) and y=1 (1 OTU). The second point is x=2 (2<sup>nd</sup> sample), and y=1 if it is the same OTU, or y=2 if it is a new OTU. Continue until you have sampled all the jellybeans.



5. **Beta diversity.** To compare diversity among samples, we can use the Jaccard's index (J). J = a / (a + b + c), where a = the number of shared species between two samples, b = number of unique species in sample 1, and c = number of unique species in sample 2. Jaccard's index ranges from 0 (completely different) to 1 (completely similar).

Jellybean Color	Abundance	Jellybean Flavor	Abundance	
Black		BerryBlue		
BlueLight		Blueberry		
BlueDark		BubbleGum		
Brown		ButteredPopcorn		
GreenLight		Cantaloupe		
GreenDark		Cappucino		
MixedSpeckled		CaramelCorn		
Orange		Chocolate Pudding		
Pink		Cinnamon		
Purple		Coconut		
Red		CottonCandy		
White		CreamSoda		
Yellow		CrushedPineapple		
	+			
	+	DrPepper FrenchVanilla		
Total abundance (N)				
		GreenApple		
		IslandPunch		
		JuicyPear		
		Kiwi		
		SunkistLemon		
		LemonDrop		
		LemonLime		
		Licorice		
		SunkistLime		
		Mango		
		Margarita		
		MixedBerry		
		SunkistOrange		
		OrangeSherbert		
		Peach		
		PinaColada		
		SunkistPinkGrapefruit		
		Plum		
		Pomegranate		
		Raspberry		
		RedApple		
		RootBeer	+	
		SizzlingCinnamon		
		SourCherry	+	
		StrawberryCheesecake	+	
		StrawberryCneesecake	+	
		StrawbornyDaquiri	+	
		StrawberryJam	+	
		SunkistTangerine	+	
		ToastedMarshmallow		
		TopBanana	1	
		TuttiFrutti		
		VeryCherry		
		Watermelon		
		WildBlackberry		
		Total abundance (N)		