

What environment did we just sequence?

A group of scientists just sequenced some bacteria from 4 environments (plant roots, soil, pre-term infants human guts, term infants human guts). Unfortunately, someone didn't write down which barcode was used for any of the environments!! Now we must figure out which environment was which by looking at the unique bacterial community in each bag. Also, we only have the sequence for the **reverse complement** and our database is in the forward direction. So, we also need to figure out the sequence of the forward direction before we proceed.

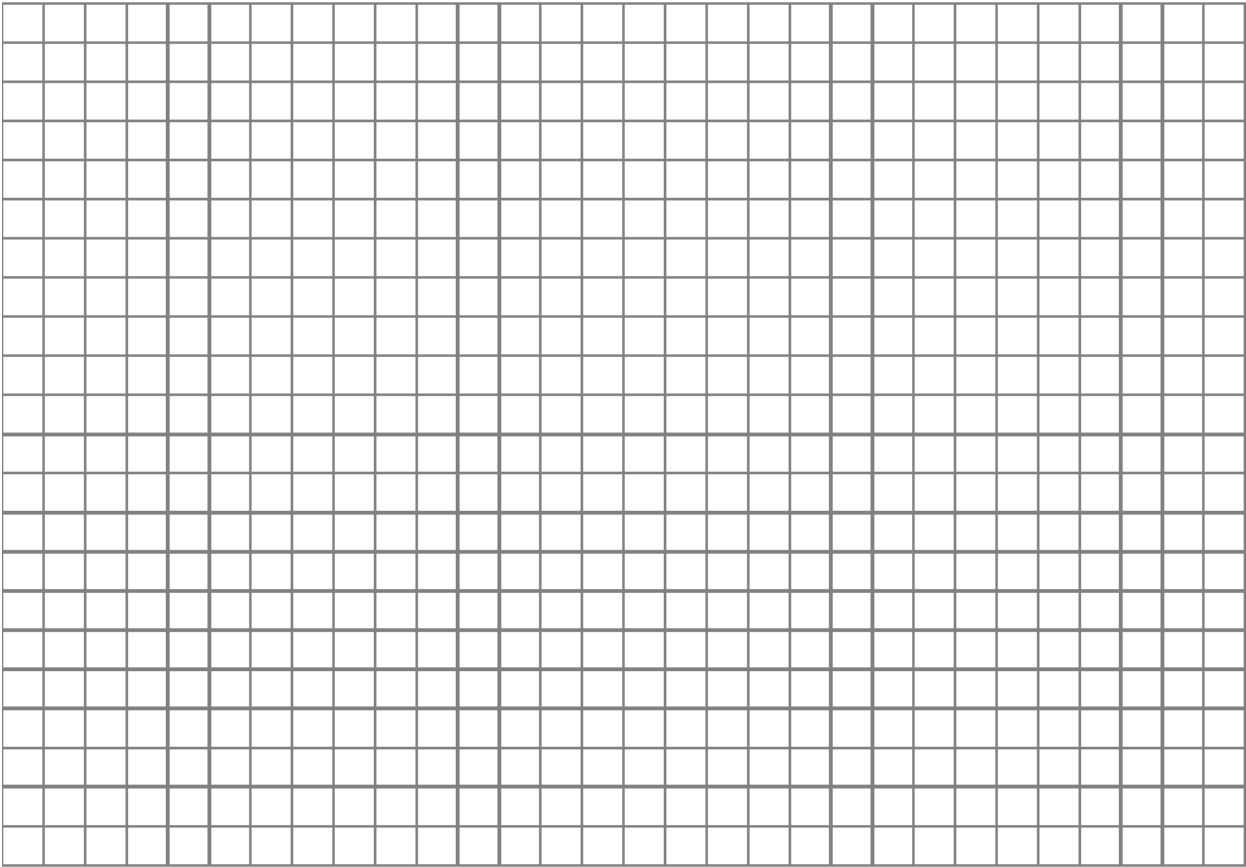
You will have a total of 6 bags. One bag has all the information you need about each environment. In another bag, you have the sequence for the bacteria IDs. In 4 different bags labeled 1-4, you have the bacterial communities. Let's start figuring out which environment we sequenced!

First let's figure out the reverse complement for each bacterium and assign each one a different color:

| Reverse Complement | DNA | Bacteria | Color |
|--------------------|-----|----------|-------|
| CGTAGC | | | |
| CGATCC | | | |
| GCTATG | | | |
| TGACGG | | | |
| TGAGTA | | | |
| TAGCTA | | | |
| TGAATC | | | |
| CGATTG | | | |
| CAGTCT | | | |

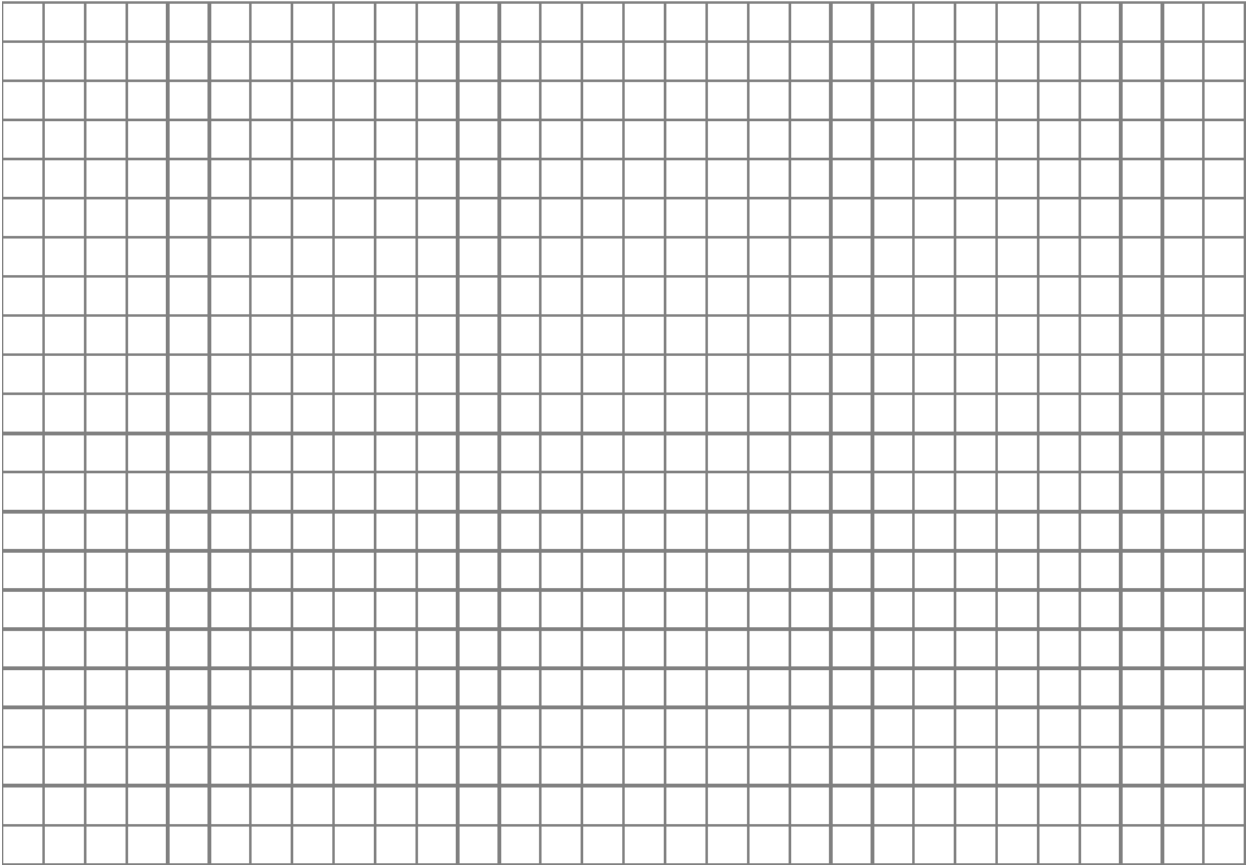
Environment 1 is: _____

| DNA | Bacteria | How many? | Relative Abundance? |
|-----|----------|-----------|---------------------|
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| | | | |
| | | | |



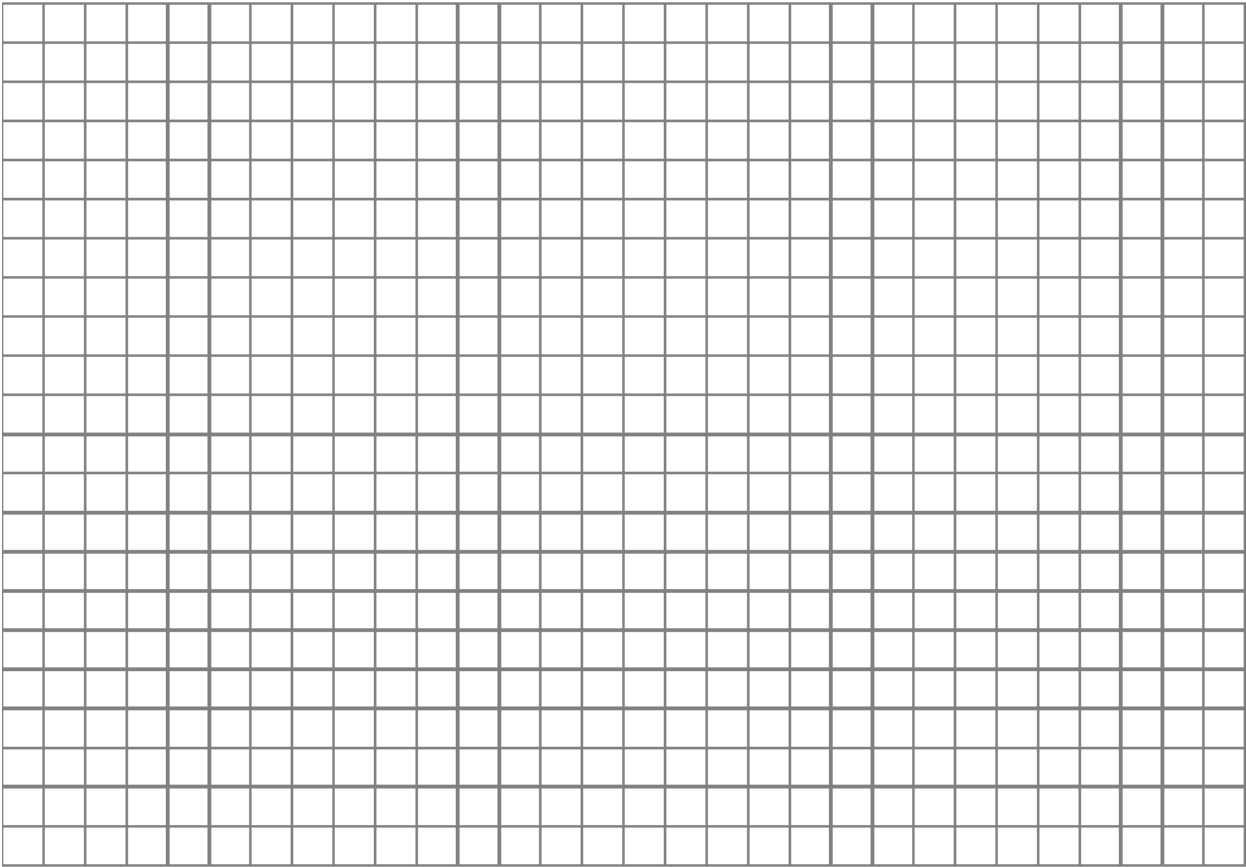
Environment 2 is: _____

| DNA | Bacteria | How many? | Relative Abundance? |
|-----|----------|-----------|---------------------|
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |



Environment 3 is: _____

| DNA | Bacteria | How many? | Relative Abundance? |
|-----|----------|-----------|---------------------|
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| | | | |
| | | | |
| | | | |
| | | | |



Environment 4 is: _____

| DNA | Bacteria | How many? | Relative Abundance? |
|-----|----------|-----------|---------------------|
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