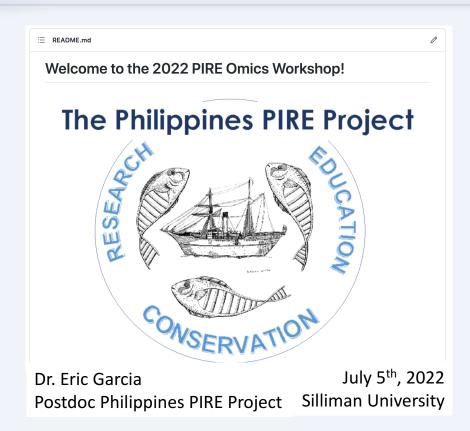


## **Assembly Quality**



1



# **Assembly Quality**

genome

assembly



# **Assembly Quality**

#### **Expected genes**

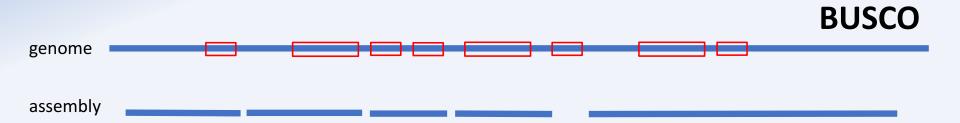


**BUSCO** 

| Importance | Metric | Direction           | Description                                   |
|------------|--------|---------------------|---|
| 1st        | BUSCO  | Bigger is<br>better | % of expected genes observed in your assembly |



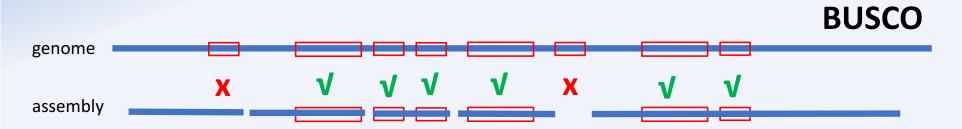
# **Assembly Quality**



| Importance | Metric | Direction           | Description                                   |
|------------|--------|---------------------|---|
| 1st        | BUSCO  | Bigger is<br>better | % of expected genes observed in your assembly |



# **Assembly Quality**



| Importance | Metric | Direction           | Description                                   |
|------------|--------|---------------------|---|
| 1st        | BUSCO  | Bigger is<br>better | % of expected genes observed in your assembly |



# **Assembly Quality**

genome assembly

| Importance | Metric | Direction        | Description  |
|------------|--------|------------------|--|
| 1st        | BUSCO  | Bigger is better | % of expected genes observed in your assembly  |
| 2nd        | N50    | Bigger is better | Lenght of the smaller contig from the set of contigs needed to reach half of your assembly |

**N50** 



# **Assembly Quality**

### **% Genome Size Completeness**



| Importance | Metric                   | Direction        | Description  |
|------------|--------------------------|------------------|--|
| 1st        | BUSCO                    | Bigger is better | % of expected genes observed in your assembly  |
| 2nd        | N50                      | Bigger is better | Lenght of the smaller contig from the set of contigs needed to reach half of your assembly |
| 3rd        | Genome size completeness | Bigger is better | Lenght of assembly divided by estimated genome lenght                                      |



## **Assembly Quality**

### **% Genome Size Completeness**



| Importance | Metric                   | Direction           | Description  |
|------------|--------------------------|---------------------|--|
| 1st        | BUSCO                    | Bigger is<br>better | % of expected genes observed in your assembly  |
| 2nd        | N50                      | Bigger is better    | Lenght of the smaller contig from the set of contigs needed to reach half of your assembly |
| 3rd        | Genome size completeness | Bigger is<br>better | Lenght of assembly divided by estimated genome lenght                                      |



# **Assembly Quality**

genome assembly 1 2 3 4 5

| Importance | Metric                   | Direction         | Description  |
|------------|--------------------------|-------------------|--|
| 1st        | BUSCO                    | Bigger is better  | % of expected genes observed in your assembly  |
| 2nd        | N50                      | Bigger is better  | Lenght of the smaller contig from the set of contigs needed to reach half of your assembly |
| 3rd        | Genome size completeness | Bigger is better  | Lenght of assembly divided by estimated genome lenght                                      |
| 4th        | L50                      | Smaller is better | Number of contigs needed to reach half of your assembly                                    |

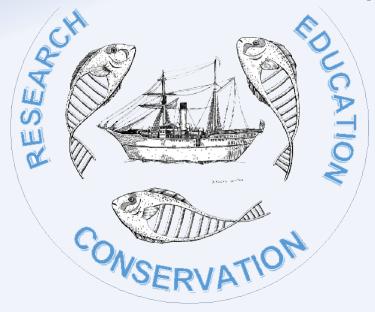


# **Assembly Quality**

genome assembly

### **Largest contig**

| Importance | Metric                   | Direction           | Description  |
|------------|--------------------------|---------------------|--|
| 1st        | BUSCO                    | Bigger is better    | % of expected genes observed in your assembly  |
| 2nd        | N50                      | Bigger is better    | Lenght of the smaller contig from the set of contigs needed to reach half of your assembly |
| 3rd        | Genome size completeness | Bigger is better    | Lenght of assembly divided by estimated genome lenght                                      |
| 4th        | L50                      | Smaller is better   | Number of contigs needed to reach half of your assembly                                    |
| 5th        | Largest contig           | Bigger is<br>better | Lenght of largest contig   |







# **Assembly Quality**

| Importance | Metric                   | Direction         | Description  |
|------------|--------------------------|-------------------|--|
| 1st        | BUSCO                    | Bigger is better  | % of expected genes observed in your assembly  |
| 2nd        | N50                      | Bigger is better  | Lenght of the smaller contig from the set of contigs needed to reach half of your assembly |
| 3rd        | Genome size completeness | Bigger is better  | Lenght of assembly divided by estimated genome lenght                                      |
| 4th        | L50                      | Smaller is better | Number of contigs needed to reach half of your assembly                                    |
| 5th        | Largest contig           | Bigger is better  | Lenght of largest contig   |