

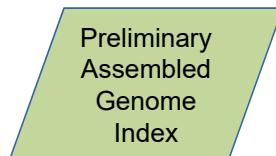


- **Make an index of the preliminary assembled genome.**
- **This is necessary to use the assembly in the next step.**

Make a samtools  
compatible index.

Preliminary assembled  
genome

```
samtools faidx prelim_assembly.fasta
```



Continue with  
the "polish  
errors" section