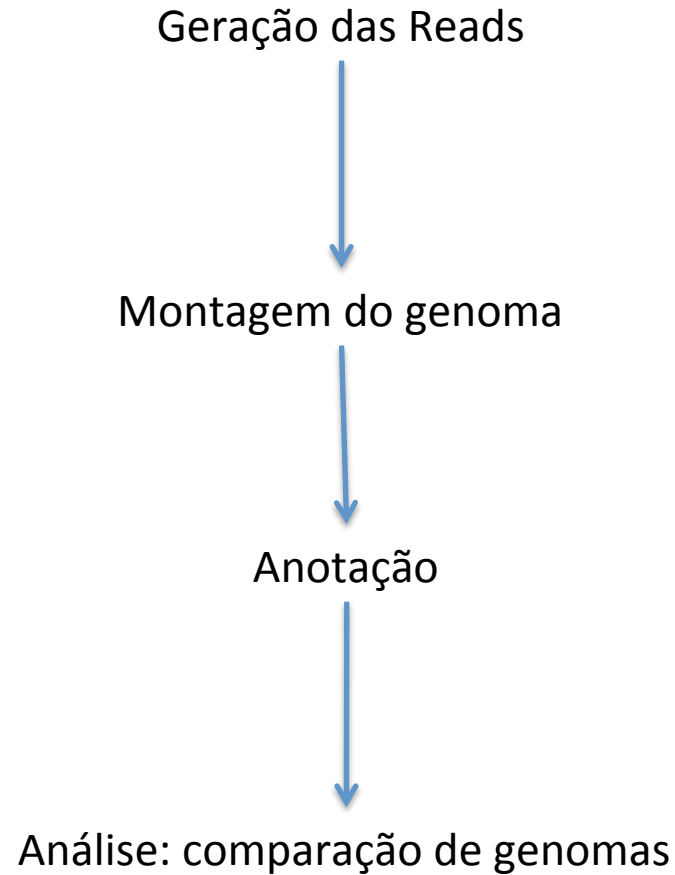


# Introdução a Anotação e Comparação de Genomas

Tiago Mendes

# Sequenciamento de genomas:



# Sequenciamento de genomas:

Geração das Reads



Montagem do genoma

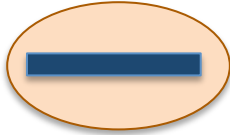


Anotação

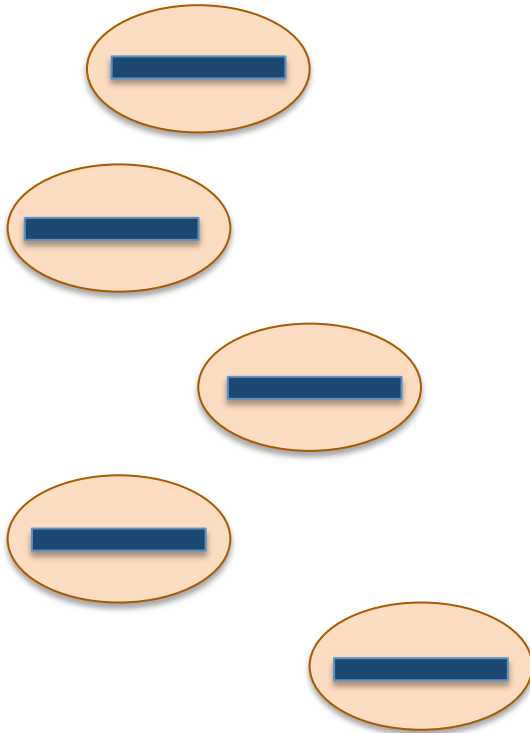


Análise: comparação de genomas

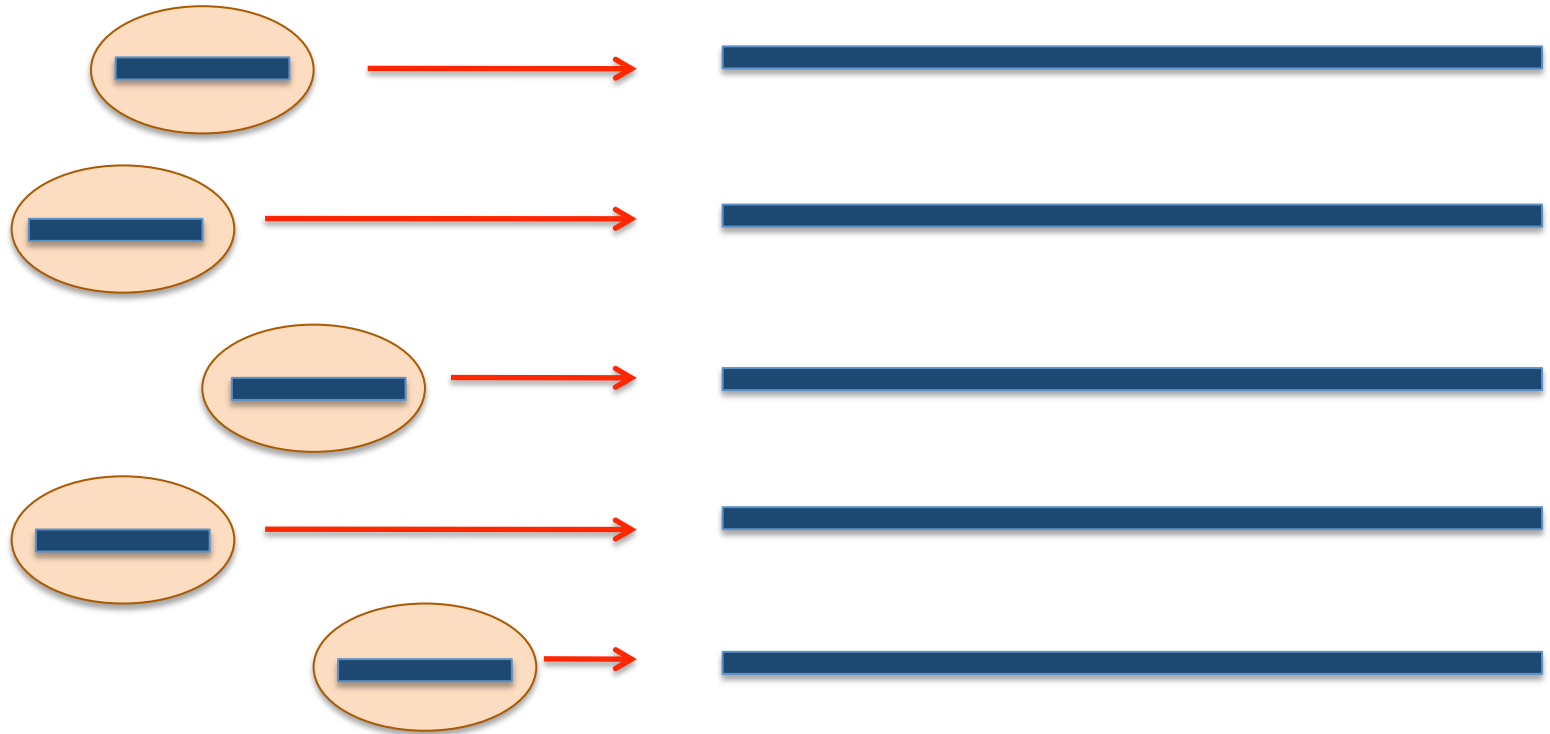
# Geração de reads:



# Geração de reads:



# Geração de reads:



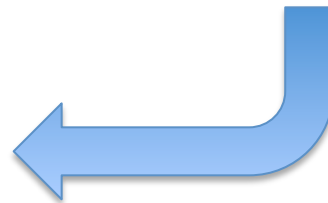
# Geração de reads:



# Geração de reads:

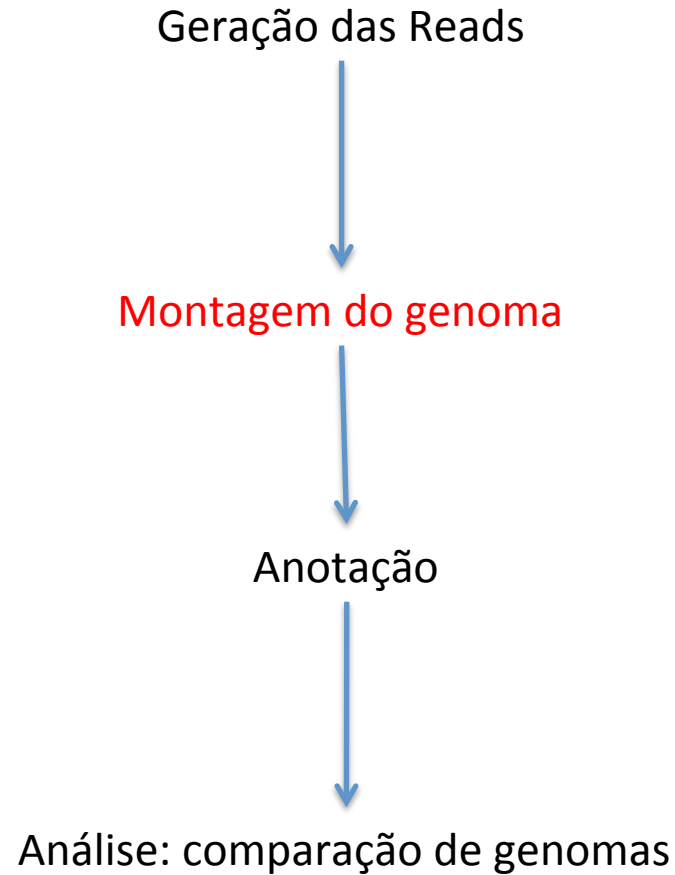


SEQUENCIAMENTO





# Sequenciamento de genomas:



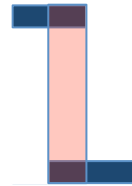
# Montagem do genoma:



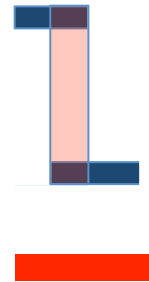
# Montagem do genoma:



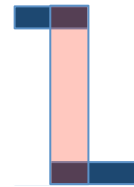
# Montagem do genoma:



# Montagem do genoma:



# Montagem do genoma:



Aligned reads

```
ACGCGATTCAGGTTACCACG
GCGATTCAGGTTACCACGCG
GATTCAGGTTACCACGCGTA
TTCAGGTTACCACGCGTAGC
CAGGTTACCACGCGTAGCGC
GGTTACCACGCGTAGCGCAT
TTACCACGCGTAGCGCATT
ACCACGCGTAGCGCATTACA
CACGCGTAGCGCATTACACA
CGCGTAGCGCATTACACAGA
CGTAGCGCATTACACAGATT
TAGCGCATTACACAGATTAG
```

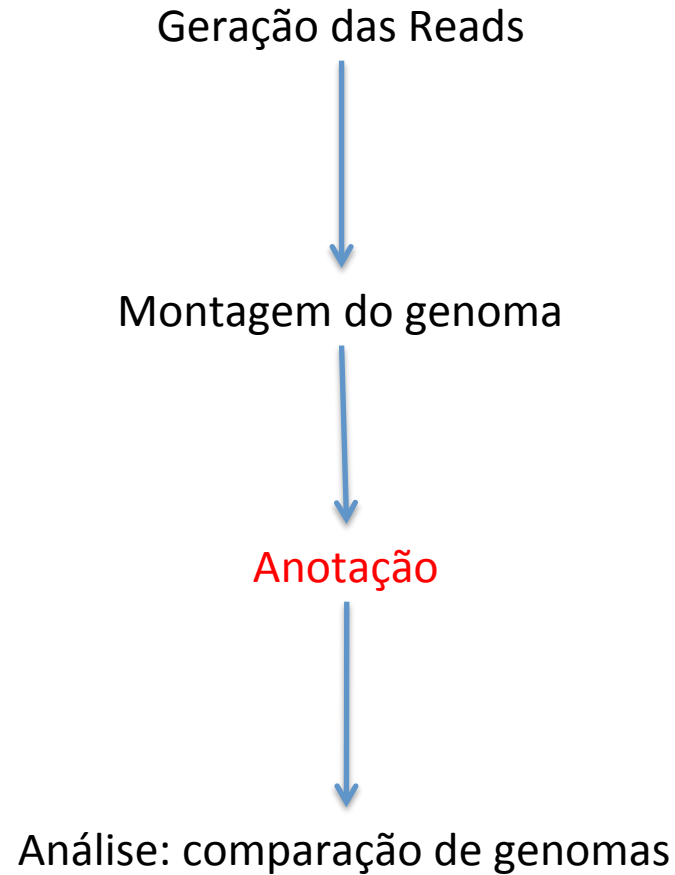
Consensus contig

```
ACGCGATTCAGGTTACCACGCGTAGCGCATTACACAGATTAG
```

# Montagem do genoma:



# Sequenciamento de genomas:





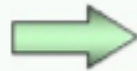




# Anotação:

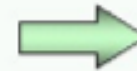
Anotação de  
**NUCLEOTÍDEOS**

Onde estão os genes?



Anotação de  
**PROTEÍNAS**

Quais são os genes?



Anotação de  
**PROCESSOS**

Como os genes interagem?

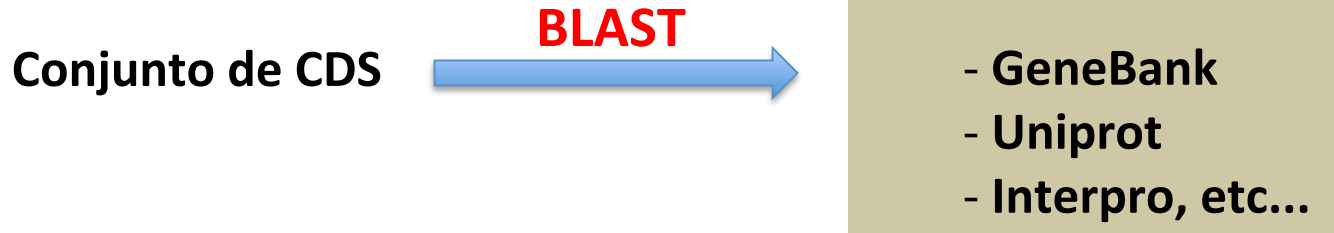
# Anotação:

## 1- Anotação de nucleotídeos:

TCTACCGCAAACAACACCGT **Regiões reguladoras** GAGAGAGAGGGGGGGGTGAGGAGTTGGTA  
T  
GCTTTCCCTACCTGTGCGTCTACCATTGGCAGTGTAGTCCTCTGAGATGCCTCATTGGCGGTACTCTGACCTC  
GCTTTTCCT **CDS** ACTTCTGCTCTGGTTGTGGCGGTAGGCTAGGGGAGGGAGG  
GGGAGGGGGGACGGCGGTGTTCTGCCTCCCCCTTTGCTTGTGGAGATGCAGGCATGTTTTGCATGTGCT  
GAGGACAACGATGTACACTGGGCTGCAACCTGGAAGTGTGGGGCAGAGAGAGAGGGCTCGAGGAATGGAG  
CATGGAGGCTCATGGAGAGGTCTTGTGGTGCCTTTGATGTGGTGG **tRNA** CTACT  
CGCCAGCGAGCCTCTCCTTTCCCGCATGCGTGTGGCTCTTCTCTTCTCTTCCGGTCTCGGCTCTTCTC  
AGGGCAGCGCCAACCAGCCGCAAAAACAAAGCGAGGCACAGAGGAGGAGTACTCACGACACGAGTAATG  
CCGAAGCAGGTCATTTTCATGCAGCAAACATGCCCGGCAGGAGAAACGCCATGGCGCTGTCCGCCGACTGC  
AGGTGTGCCTATGGCGAGCGCCCCCTCCCCCTCACTGAGCG **rRNA** GCACCATC  
GCCACGCGT **Padrões específicos** TTGGGCTCTTTCGTCCTCTCAACCTTCACGACATTTGCGCCTCC  
GTCTCCTGCCTCGCACACTCCCTCACCTCCTCCCTCCTTTCTCTTCCCTTCCCTTCCCTTCGACGCCGGC  
GCCACGCGCACACAGGCACAGGGACAGACACACCTATGGACAGCGTGCTCGTGTGCAAACATGTGGCAGA  
CTCTGCGGCAGCGATATCGTCTTCAGCCCACATCCCTCGCAGCCTTCTGGAGTCCAACGCACGGTGTCTGA  
AGTCTCCGACGGCGGCGCTACACC **Elementos repetitivos** CGAAACCAACAGCCTCTGCATCTTCC  
AAAACCTCGTCGACAGGAATCACTCGCTCGTGGTCTTCCCTCGACAAGACGCAGCGGCTGCTCCTCTTCT  
ACGTGAACCGCCCCTGCGTCTGGTGGGCGCAACCAGAACCTCTTCCAGGA

# Anotação:

## 2- Anotação de proteínas



- Proteína nomeadas
- Proteína hipotética conservada
- Proteína hipotética

# Anotação:

## 3- Anotação de processos:

Proteínas anotadas



- 1 – Processo biológico
- 2 – Função molecular
- 3 – Componentes celulares



# Anotação:

```
graph TD; A[Anotação] --> B[Anotação automática]; B --> C[Anotação manual e curadoria];
```

## Anotação automática

Glimmer  
GeneScan  
RBSfinder  
tRNAscan  
GeneMark  
Repet Masker  
BLAST

## Anotação manual e curadoria



# Sequenciamento de genomas:

Geração das Reads



Montagem do genoma

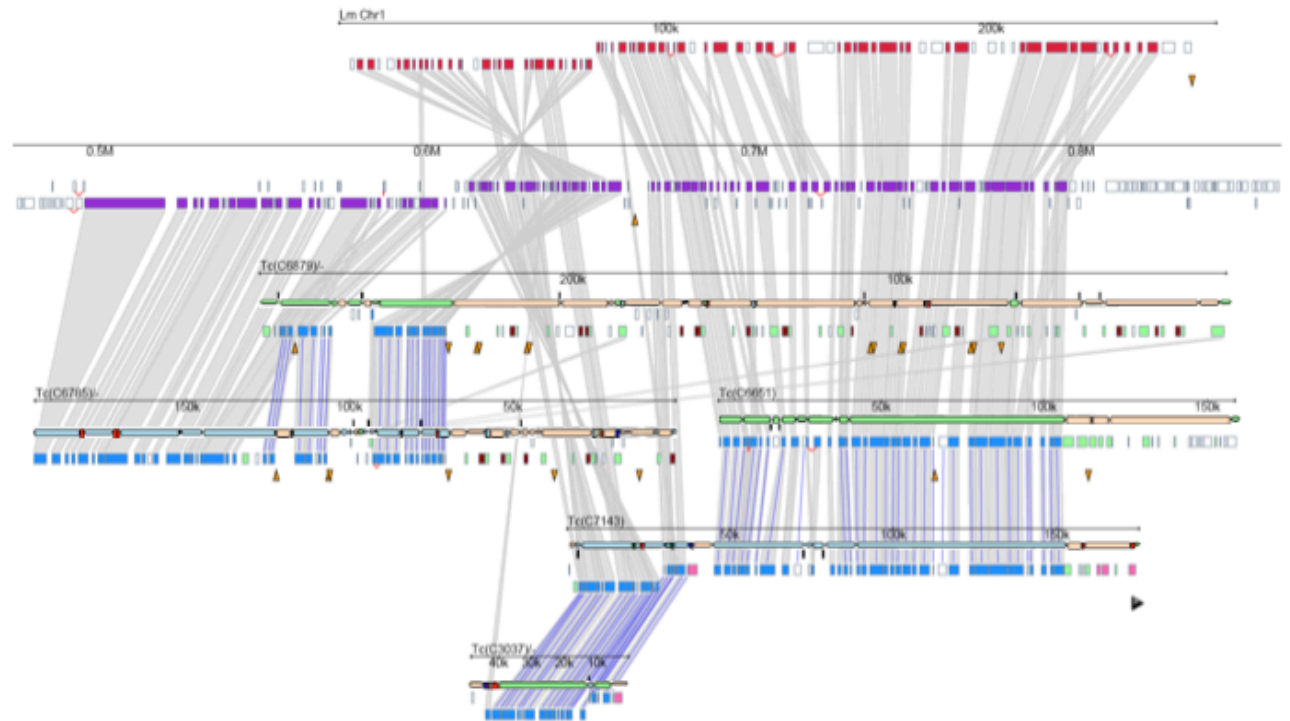
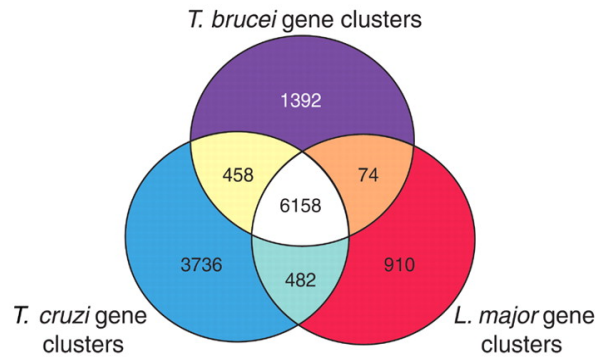


Anotação



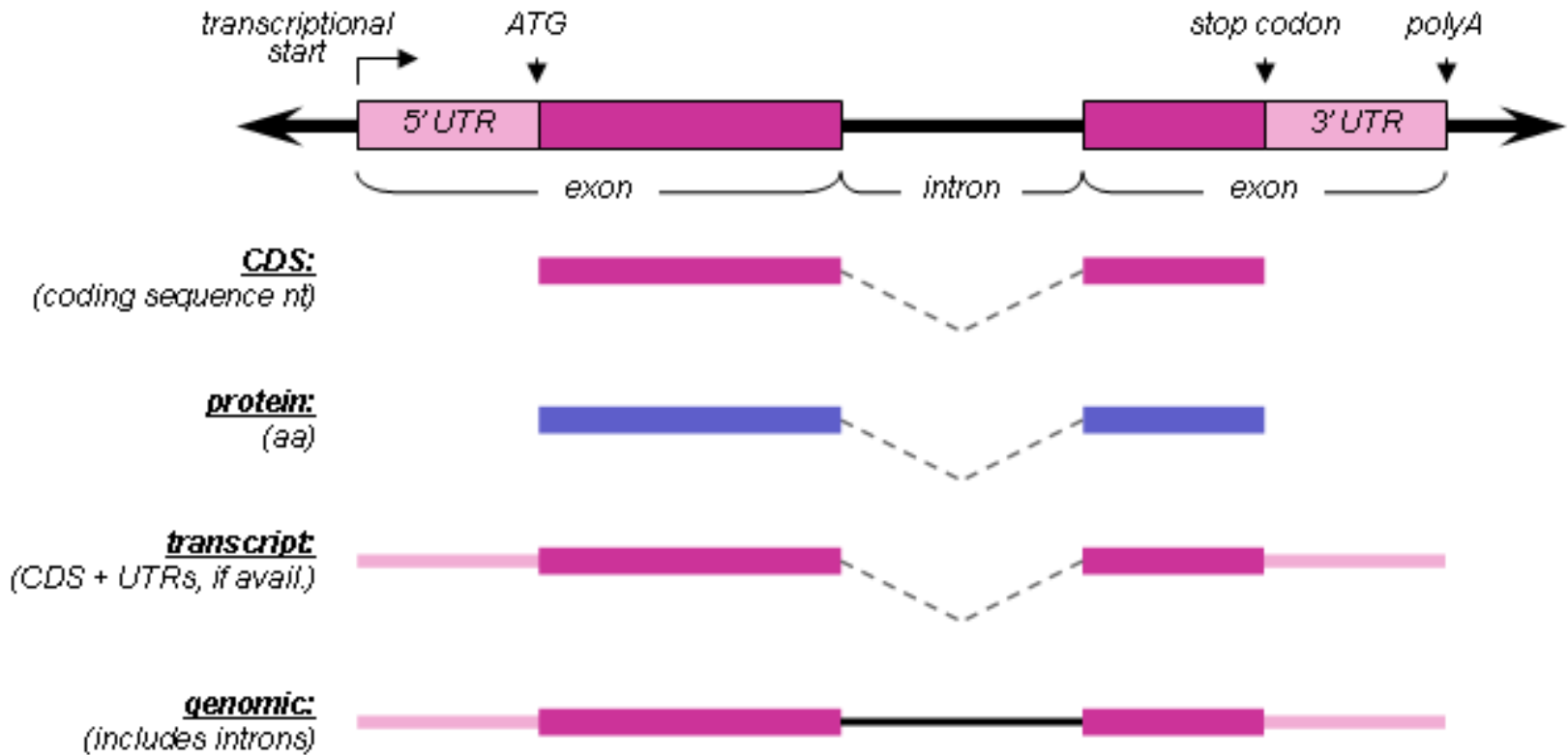
Análise: comparação de genomas

# Comparação de genomas:





# Anotação manual de proteínas completas



# Anotação manual de proteínas completas

Artemis Feature Edit: Gene\_01

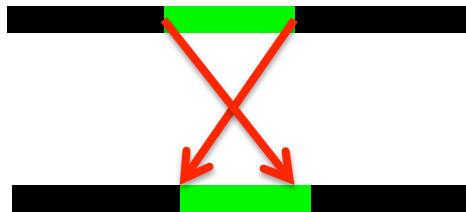
Key:

Location:

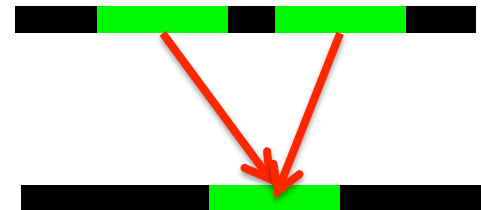
```
/locus_tag="Gene_01"  
/product="putative lypoyltransferase"  
/curation="Tiago Mendes"  
/similarity="Similar to Leishmania braziliensis; lypoyltransferase; 734 aa; 100% id in 705  
aa"
```

# Comparação de genomas

**Inversão**



**Duplicação/deleção**



**Alteração da sintenia**

