Scientific Project

Master GENIOMHE

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Further development on FTAG Finder, a pipeline to identify Tandemly Arrayed Genes

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Abstract: *D uplicate genes is an important component of genomes. They have a particular role in genome evolution, allowing species to explore new gene functionality offering a pool of usable genes to build on. TODO:*

keywords: duplicate genes, tandemly arrayed genes, pipeline

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Acronyms

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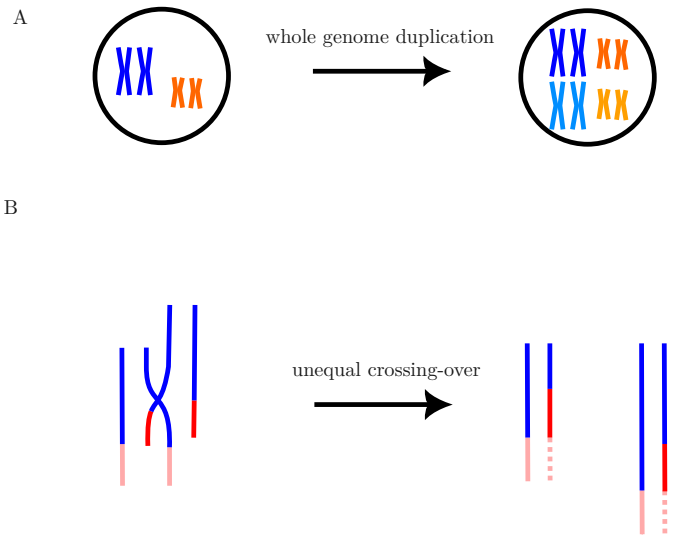
1 Context

1.1 Duplication mechanisms



Multiple mechanisms may lead to gene duplication. We review them in this section.

1.1.1 Segment duplication

1.1.2 Retroduplication

Retrotransposons, or RNA transposons is one type of transposable element. Retrotransposons share a similar structure and mechanism with retroviruses. They may replicate in the genome through a mechanism known as "copy-and-paste". These transposons are typically composed of a reverse transcriptase gene. This enzyme gene may proceed in the reverse transcription of an mRNA transcript into DNA sequence which can then be inserted elsewhere in the genome.

1.1.3 Transduplication

DNA transposons are another type of transposable element whose transposition mechanism can also lead to gene duplication. This type of transposable element moves in the genome through a mechanisms known as "cut-and-paste". A typical DNA transposon contains a transposase gene. This enzyme recognize two sites surrounding the donnor transposon sequence in the chromosome resulting in a DNA cleavage and excision of the transposon. The transposase can then insert the transposon in a new place of the genome. Similarly to retrotransposon, if a gene was present between the two cleavage sites of the donnor transposon, it may move with the transposed sequence.

1.1.4 Tandem Duplication

1.1.5 Polyploidisation

Alloployploidisation

Autopolyploidisation

Polyploidisation mechanisms

Polyspermy

Non-reduced gametes

1.1.6 Unequal crossing-over

A crossing-over may occur during cell division. A fragment of chromosome is exchanged between two chromatids of a pair of chromosome. If the cleavage of the two chromatids occured

at different positions on both chromosomes, the shared fragments may have different lengths. When the repair of missing fragment is performed, the resulting chromosome will incorporate a duplicate region of the chromosome, leading to a potential duplication for genes present in this region, as represented in figure 1.1. This mechanism leads to the duplication of the whole set of genes present in the inserted fragment. These genes are duplicated one after the other in second array of genes placed after the original one and are thus called Tandemly Arrayed Genes.

1.2 Role of duplicate genes in genome evolution

In his book *Evolution by Gene Duplication*, Susumu Ohno proposed that gene duplication plays a major role in species evolution (Ohno, 1970).

1.3 Methods to identify duplicate genes

Lallemand et al. review the different methods used to detect duplicate genes. These methods are dependant on the type of duplicate genes they target (Lallemand et al., 2020).

1.3.1 FTAG Finder

Developped in the LaMME laboratory, this pipeline targets the detection of gene family and tandemly arrayed genes from a given species' proteome (Bouillon et al., n.d.).

Estimation of homology links between genes

This steps consists in establishing a relation between each genes in a genome. In this step, the typical tool involved is `BLAST` (Basic Local Alignment Search Tool) (Altschul et al., 1990) run on the whole proteome.

Several `BLAST` metrics can be used as an homology measure, such as bitscore, identity percentage, E-value or modifications of thoses. The choice of the metrics used may have an impact on the results of graph clustering step (Gibbons et al., 2015).

Identification of gene families

Based on the homology links between each pair of genes, we construct a weighted undirected graph whose vertices corresponds to genes and edges to homology links. Then, a graph clustering algorithm is applied on this graph in order to infer the gene families.

The team choosed to propose three clustering algorithms: Single linkage, Markov Clustering or Walktrap.

2 Objectives

2.1 Extend the existing Galaxy pipeline

Galaxy is a web-based platform for performing accessible data analysis pipeline, mostly used for genomic data analysis (Goecks et al., 2010).

Last year, Séanna Charles, worked on the Galaxy's version of the FTAG Finder pipeline (Charles, 2023) during her M1 intenship. I will continue this work.

2.2 Port FTAG Finder pipeline on a workflow manager

Another objective of my internship will be to port FTAG Finder on a workflow manager better suited to larger and more reproducible analysis.

We will have to make a choice for the tool we will use. The two main options are Snakemake and Nextflow. Snakemake is a python powered workflow manager based on rules *à la* GNU Make (Köster and Rahmann, 2012). Nextflow, is a groovy powered workflow manager, which rely on data flows (Di Tommaso et al., 2017). Both are widely used in the bioinformatics community, and their use have been on the rise since they came out in 2012 and 2016 respectively (Djaffardjy et al., 2023).

These tools ease the deployment of large scale data analysis workflow with reproducible output.

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Summary