Metarhizium\_chromosome\_transfer

This is the repository of the shell sripts that were used to determine the horizontal transfer of an accessory chromosome within Metarhizium robertsii and between M. robertsii and M. guizhouense.

The following software tools are required:

Dependencies

* [all2vcf](https://github.com/MatteoSchiavinato/all2vcf)
* [bcftools](https://samtools.github.io/bcftools/bcftools.html) (version: 1.14)
* [bedtools](https://github.com/arq5x/bedtools2) (version: 2.25.0)
* [BioKIT](https://jlsteenwyk.com/BioKIT/) (version: 0.1.3)
* [bowtie2](https://github.com/BenLangmead/bowtie2) (version: 2.4.4)
* [braker2](https://github.com/Gaius-Augustus/BRAKER) (version: 2.1.6)
* [busco](https://busco.ezlab.org/) (version: 5.5.0)
* [bwa-mem2](https://github.com/bwa-mem2/bwa-mem2) (version: 2.2.1)
* [Canu](https://canu.readthedocs.io/en/latest/) (version: 2.1.1)
* [fastqc](https://github.com/s-andrews/FastQC) (version: 0.12.1)
* [Flye](https://github.com/fenderglass/Flye) (version: 2.8.3)
* [FMLRC2](https://github.com/HudsonAlpha/fmlrc2) (version: 0.1.4)
* [gffread](https://github.com/gpertea/gffread) (version: 0.12.7)
* [medaka](https://github.com/nanoporetech/medaka) (version: 1.4.3)
* [minimap2](https://github.com/lh3/minimap2) (version: 2.24-r1122)
* [mummer](https://github.com/mummer4/mummer) (version: 4.0.0rc1)
* [nanofilt](https://github.com/wdecoster/nanofilt) (version: 2.3.0)
* [picard](https://github.com/broadinstitute/picard) (version: 2.24.0)
* [pilon](https://github.com/broadinstitute/pilon/wiki) (version: 1.24)
* [racon](https://github.com/isovic/racon) (version: 1.4.20)
* [REPET3](https://urgi.versailles.inra.fr/Tools/REPET) (version: 3.0)
* [rust](https://www.rust-lang.org/learn) (version: 1.74.1)
* [samtools](https://www.htslib.org/) (version: 1.3.1)
* [tapestry](https://github.com/johnomics/tapestry) (version: 1.0.0)
* [trimmomatic](http://www.usadellab.org/cms/?page=trimmomatic) (version: 0.39)
* [whatshap](https://github.com/whatshap/whatshap) (version: 1.6)

Data:

Sequencing reads have been deposited in the Sequence Read Archive and are available under the BioProject PRJNA1017668. The Nanopore-based assemblies and Gene annotations were deposited at NCBI under the BioProjects PRJNA1015426, PRJNA1015429, PRJNA1015431. The links to the previously published sequencing reads and assemblies are given below:

