

## **A computational pipeline for whole genome sequencing analysis of *Mycobacterium tuberculosis* complex isolates**

---

# TBseq

Version 1.2.0 (2017-03-13)

### **TBseq release**

TBseq/

LICENCE.pdf	(v1.2.0)
README.pdf	(v1.2.0)
VERSION.pdf	(v1.2.0)
TBseq.pl	(v1.2.0)

TBseq/lib/

TBreads	(v1.2.0)
TBbwa	(v1.2.0)
TBmerge	(v1.2.0)
TBrefine	(v1.2.0)
TBpile	(v1.2.0)
TBtable	(v1.2.0)
TBvariants	(v1.2.0)
TBjoin	(v1.2.0)
TBamend	(v1.2.0)
TBstrains	(v1.2.0)
TBgroups	(v1.2.0)

---

---

TBseq/opt/

samtools	(v1.3.1)
sambamba	(v0.6.5)
IGV-tools	(v2.3.88)
picard-tools	(v2.7.1)
BWA	(v0.7.15)
GATK	(v3.6)

TBseq/var/

cat/

MTB_Gene_Categories.txt	(v1.0)
-------------------------	--------

ref/

M._abscessus_CIP-104536T_2014-02-03.fasta
M._abscessus_CIP-104536T_2014-02-03_genes.txt
M._chimaera_DSM44623_2016-01-28.fasta
M._chimaera_DSM44623_2016-01-28_genes.txt
M._fortuitum_CT6_2016-01-08.fasta
M._fortuitum_CT6_2016-01-08_genes.txt
M._tuberculosis_H37Rv_2015-11-13.fasta
M._tuberculosis_H37Rv_2015-11-13_genes.txt

res/

Base_Calibration_List.vcf	(v1.0.0)
Base_Calibration_List.vcf.idx	(v1.0.0)
MTB_Extended_Resistance_Mediating.txt	(v1.0.0)
MTB_Resistance_Mediating.txt	(v1.0.0)