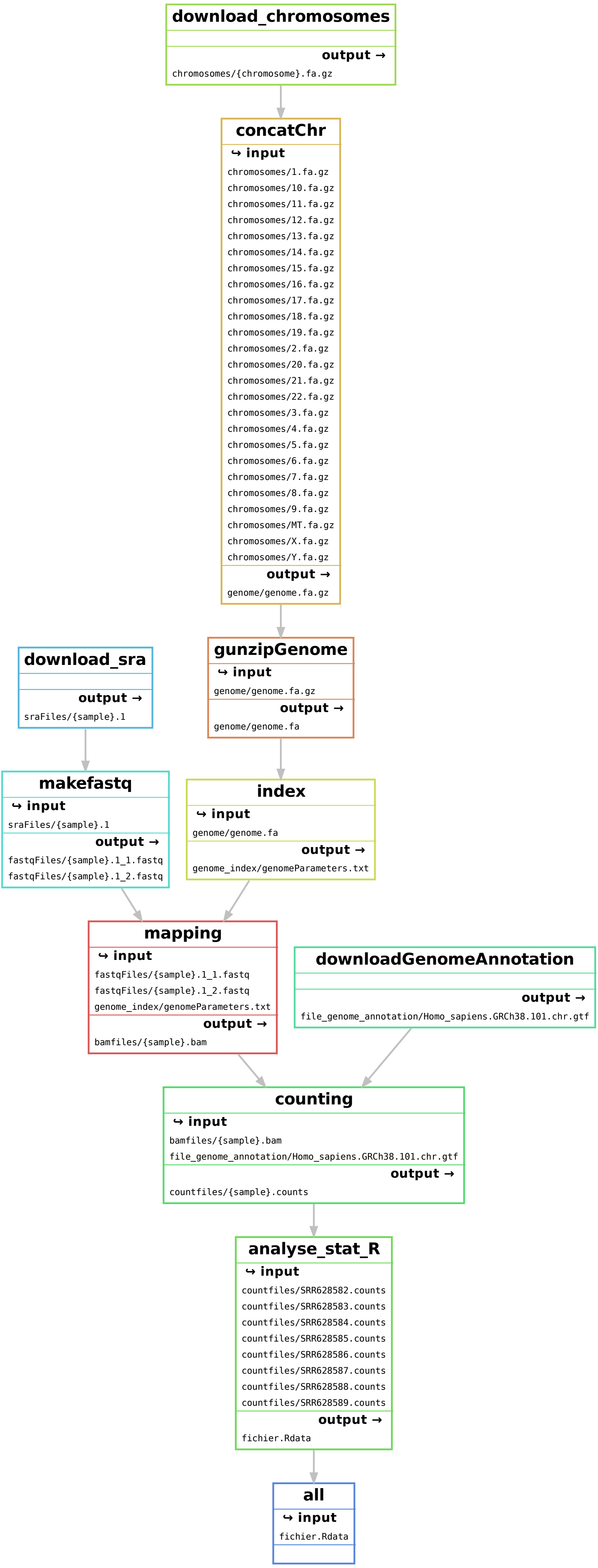
download_chromosomes
output →
chromosomes/{chromosome}.fa.gz
concatChr
↪ input
chromosomes/1.fa.gz
chromosomes/10.fa.gz
chromosomes/11.fa.gz
chromosomes/12.fa.gz
chromosomes/13.fa.gz
chromosomes/14.fa.gz
chromosomes/15.fa.gz
chromosomes/16.fa.gz
chromosomes/17.fa.gz
chromosomes/18.fa.gz
chromosomes/19.fa.gz
chromosomes/2.fa.gz
chromosomes/20.fa.gz
chromosomes/21.fa.gz
chromosomes/22.fa.gz
chromosomes/3.fa.gz
chromosomes/4.fa.gz
chromosomes/5.fa.gz
chromosomes/6.fa.gz
chromosomes/7.fa.gz
chromosomes/8.fa.gz
chromosomes/9.fa.gz
chromosomes/MT.fa.gz
chromosomes/X.fa.gz
chromosomes/Y.fa.gz
output →
genome/genome.fa.gz
download_sra
output →
sraFiles/{sample}.1
gunzipGenome
↪ input
genome/genome.fa.gz
output →
genome/genome.fa
makefastq
↪ input
sraFiles/{sample}.1
output →
fastqFiles/{sample}.1_1.fastq
fastqFiles/{sample}.1_2.fastq
index
↪ input
genome/genome.fa
output →
genome_index/genomeParameters.txt
mapping
↪ input
fastqFiles/{sample}.1_1.fastq
fastqFiles/{sample}.1_2.fastq
genome_index/genomeParameters.txt
output →
bamfiles/{sample}.bam
downloadGenomeAnnotation
output →
file_genome_annotation/Homo_sapiens.GRCh38.101.chr.gtf
counting
↪ input
bamfiles/{sample}.bam
file_genome_annotation/Homo_sapiens.GRCh38.101.chr.gtf
output →
countfiles/{sample}.counts
analyse_stat_R
↪ input
countfiles/SRR628582.counts
countfiles/SRR628583.counts
countfiles/SRR628584.counts
countfiles/SRR628585.counts
countfiles/SRR628586.counts
countfiles/SRR628587.counts
countfiles/SRR628588.counts
countfiles/SRR628589.counts
output →
fichier.Rdata
all
↪ input
fichier.Rdata