

At home need to install everything from

```
conda list
```

```
conda activate /home/sunam226/.conda/envs/reademption  
  
reademption create --project_path READemption_analysis --species  
salmonella="Salmonella Typhimurium"
```

For us its methanosarcenia mazei

Grab data from web: put it in FTP_Source variable

```
FTP_SOURCE=ftp://ftp.ncbi.nih.gov/genomes/archive/old_refseq/Bacteria/Salmonella_e  
nterica_serovar_Typhimurium_SL1344_uid86645/
```

```
wget -O READemption_analysis/input/salmonella_reference_sequences/NC_016810.fa  
$FTP_SOURCE/NC_016810.fna  
wget -O READemption_analysis/input/salmonella_reference_sequences/NC_017718.fa  
$FTP_SOURCE/NC_017718.fna  
wget -O READemption_analysis/input/salmonella_reference_sequences/NC_017719.fa  
$FTP_SOURCE/NC_017719.fna  
wget -O READemption_analysis/input/salmonella_reference_sequences/NC_017720.fa  
$FTP_SOURCE/NC_017720.fna
```

remove everything in front of the NZ-number in sublime text editor, than save or replace header with (annotation file + reference file need to look the same)

```
sed -i "s/>/>NC_016810.1 /"  
READemption_analysis/input/salmonella_reference_sequences/NC_016810.fa  
sed -i "s/>/>NC_017718.1 /"  
READemption_analysis/input/salmonella_reference_sequences/NC_017718.fa  
sed -i "s/>/>NC_017719.1 /"  
READemption_analysis/input/salmonella_reference_sequences/NC_017719.fa  
sed -i "s/>/>NC_017720.1 /"  
READemption_analysis/input/salmonella_reference_sequences/NC_017720.fa
```

Download annotation file

```
wget -P READemption_analysis/input/salmonella_annotations
https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/210/855/GCF_000210855.2_ASM21085v
2/GCF_000210855.2_ASM21085v2_genomic.gff.gz
```

Download the raw reads:

```
wget -P READemption_analysis/input/reads http://reademptiondata.imib-
zinf.net/InSPI2_R1.fa.bz2
wget -P READemption_analysis/input/reads http://reademptiondata.imib-
zinf.net/InSPI2_R2.fa.bz2
wget -P READemption_analysis/input/reads http://reademptiondata.imib-
zinf.net/LSP_R1.fa.bz2
wget -P READemption_analysis/input/reads http://reademptiondata.imib-
zinf.net/LSP_R2.fa.bz2
```

Run the pipeline

create script: script_reademption.sh

```
#!/bin/bash
#SBATCH --job-name=reademption
#SBATCH --output=reademption.out
#SBATCH --error=reademption.err
#SBATCH --nodes=1
#SBATCH --tasks-per-node=1
#SBATCH --cpus-per-task=4
#SBATCH --mem=32G
#SBATCH --qos=long
#SBATCH --time=0-50:00:00
#SBATCH --partition=all
#SBATCH --export=NONE
#SBATCH --reservation=biol217

source ~/.bashrc

#activating conda
module load miniconda3/4.7.12.1
conda activate /home/sunam226/.conda/envs/reademption
reademption align -p 4 --poly_a_clipping --project_path READemption_analysis
reademption coverage -p 4 --project_path READemption_analysis
reademption gene_quanti -p 4 --features CDS,trRNA,rRNA --project_path
READemption_analysis
reademption deseq -l InSPI2_R1.fa.bz2,InSPI2_R2.fa.bz2,LSP_R1.fa.bz2,LSP_R2.fa.bz2
-c InSPI2,InSPI2,LSP,LSP -r 1,2,1,2 --libs_by_species
salmonella=InSPI2_R1,InSPI2_R2,LSP_R1,LSP_R2 --project_path READemption_analysis
reademption viz_align --project_path READemption_analysis
```

```
reademption viz_gene_quanti --project_path READemption_analysis  
reademption viz_deseq --project_path READemption_analysis  
conda deactivate  
jobinfo
```

```
sbatch script_reademption.sh
```