READ ME

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Contents

1 First Data

- Contains Data and R Code that was used to solve the fist Steps (see R Notebook "Step–by–step.Rmd" for more Information on the Steps)

- Original Files
    - alltogether_modified.prt
    - alltogether_modified.gen.fasta.gen
    - alltogether_modified.lst.txt
    - FixedMutations_OverTime.txt
    - FixedMutations_over_time.pdf
    - FixedMutation_over_time_Mado.pdf
    - allSNPs_w_gene_position.tsv

- Files manipulated in Visual Studio Code
    - allSNPs_w_gene_position_spaced.tsv
    - alltogether_modified.gen.fasta – not nicely.gen
    - alltogether_modified.gen.fasta.AGTU.gen

- Outputs from R Notebook
    - Result_sorted.csv

- Other Files
    - By Hand.xlsx: Counted the nucleotides by hand to find the SNP reference from the gen.fasta data. This is where I found the Error
    - Confusion.xlsx: Excel table of not nicely search for the reference nucleotide from the gen.fasta data for the SNPs.

- Code: Step-by-step.Rmd

2 Infos

- Contains documents that have an informational purpose.

- Introduction paper: the first paper Mado gave me, that explains a lot about my data and why I do this project.

- Meetings: Notes from meetings with Mado

- Presentation in Labmeeting 23.09. (Mado): PPP from Mado about her talk in the Labmeeting

3 Papers

- Contains papers that could be useful.

- N.Surname – Year – Title