How to deploy the Sample Submission Shiny App

Prerequisites

Required R version

R version 3.5.1

Required packages:

Following packages are required to run the application:

readr, pdftools, png, rmarkdown, seqinr, shiny, shinyjs, shinyBS, stringr, yaml, V8

Required Files

The app needs some files in the App directory to run cleanly

Config.yaml

Cofing.yaml contains all important parameters to control the App. The typical config file looks like:

```
orders_directory: ./outputs
maximum_upload_megabytes: 40.0
user_inputs_file_name: user_inputs.yaml
available_groups:
   IMB_EW: Eva Wolf
   IMB_BU: Falk Butter
   EXT_CF: External
db_summary_file: Available_species_DBs.csv
available_proteases:
   undefined
   AspN
   GluC
   LysC
   Chymotrypsin
```

Fields description:

orders_directory: specify the output directory for all orders

user_inputs_file_name: specify the name of file, which contains all form inputs and additional information from the filled form

db_summary_file: a file containing a summary of all selectable Fasta-Databases. Such a file can be created with the function createSummaryFileOfFastaFiles().

Available species DBs.csv

This file contains a summary of all selectable Fasta-Databases. Such a file can be created with the function createSummaryFileOfFastaFiles(). The fasta file paths must be reachable from the shiny app. See the function documentation for more details.