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Introduction to examination project



Examination project

- Project 2 was designed as exercise for the examination project
- R Examination project
 - 4 credits





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Files (on SP)

	Namn
	Huvudmapp
<input type="checkbox"/>	PK_data PK files for examination project
<input type="checkbox"/>	SNP_data SNP files for examination project
<input type="checkbox"/>	final_project_key.pdf File containing project assignment no.
<input type="checkbox"/>	Instructions for examination project.pdf
<input type="checkbox"/>	Introduction to examination project.pdf
<input type="checkbox"/>	project_examination_template.Rmd R-markdown template for examination project

Files (on SP)

- Document "final_project_key.pdf"
 - You have been given a number
 - Find the two files (on SP) with your number:
 - stuxx.csv
 - Big_pharma_BPI1889_data_200mg_xx.csv

Name	Data
Chowdhury, Sidratul Jannat	21
Christina Autoshi, Baidya	26
Cobar, Flordelyn	5
Janani, Marjaneh	15

Data in

1. `stuxx.csv` is the expected output from your Python examination projects, i.e. wide format of SNP information
 2. `Big_pharma_BPI1889_data_200mg_xx.csv` is long format with drug concentrations of study assessed in project 2
- Use both files to assess impact of genetic variation on PK using R

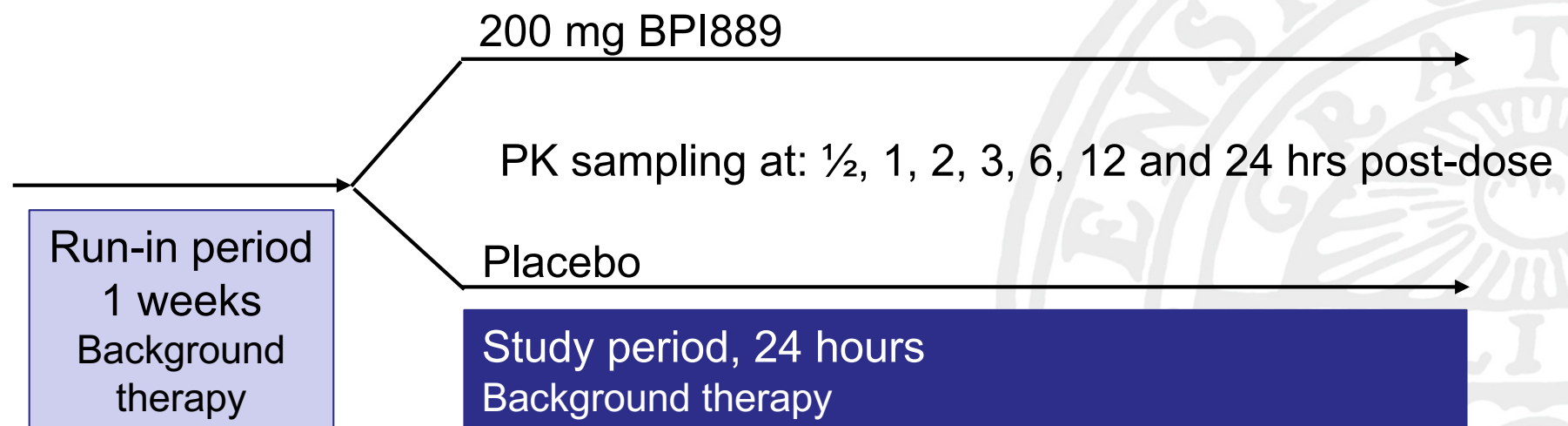
Time lines

- **Thursd 29th – Tuesday 4th**
 - Work on the project – minimal tutoring
- **Tuesday 4th at 17:00**
 - Deadline
- **Friday 7th**
 - Feedback on project
- **Friday 14th at 17:00**
 - Deadline for revision



The story

- Modelling scientist at Big Pharma Inc.
- Received clinical trial data from phase 1
- PK and genetic information collected



Tasks

1. Identify which individuals have functional SNP's and classify individuals as wildtype, heterozygote variant or homozygote variant.
2. Arrange genetic info in suitable format to merge with PK data

Using Python

Tasks

3. Perform graphical exploration
 - PK of BPI1889
 - Demographics (covariates)
4. Assess relationship between genetic variation and **elimination** and investigate **clinical impact**
 - Classify relationship between genetic variation and elimination as additive, recessive or dominant
5. Create report
 - Include all calculations and graphics to support your conclusion

Using R

Tips from pharmacokineticist

- **Elimination:**

$$CL = \text{Dose} / AUC$$

requires calculation of AUC (trapeziodal rule – google)

- **Clinical impact:**

average concentration of 200 mg, 400 mg and 800 mg

$$C_{av} = \text{Dose} * F / (CL * \tau)$$

where $F = 0.9$ and $\tau = 24 \text{ h}$