

# COMP 204

For loops, nested loops: Putting it all together

Mathieu Blanchette

## Clinical trial example

A clinical trial is something pharmaceutical companies perform to test the efficacy and safety of drugs they develop. In the simplest type of clinical trial, participants receive a treatment and we observe the effect.

Suppose you are doing a clinical trial for a drug that reduces hypertension (high blood pressure). In each patient, you measured the blood pressure *before* they started taking the drug, and one month *after* starting the drug. In addition, for each patient, we observe the genotype of the P450 gene: "AA", "Aa", or "aa". The data is stored in a list of tuples.

See `clinicalTrial1.py`

# Clinical trial example

**Part 1:** Calculate the average change in blood pressure following treatment.

See `clinicalTrial1.py`

**Part 2:** Some patients died before the end of the study. Their blood pressure is recorded as 0. Take this into consideration to only report average reduction in blood pressure among patients who are still alive(!).

See `clinicalTrial2.py`

## Clinical trial example

**Part 3:** The death rate among patients is alarmingly high. You suspect that patients with different P450 genotypes may react differently to the drug. Calculate the rate of survival among patients of AA, Aa, and aa genotypes.

See `clinicalTrial3.py`

**Part 4:** You've realized that patients of the aa genotype should stop taking the drug (if they are still alive!). You need to call them. You have a `phoneDirectory` with your patients' phone numbers, stored as a list of tuples. Write a program to produce the list of phone numbers to call.

See `clinicalTrial4.py`

# Mutagenic radiations

Radiations induce mutations (changes) in DNA sequences. Radiotherapy is a particular type of cancer treatment where the region of the body where the tumor is located is irradiated, causing mutations in the tumor cells' genome, and eventually killing them. But it also caused mutations in normal cells, which is bad for the patient.

You have sequenced the DNA of cancer patients before and after radiotherapy. You have also done the same thing in patients who did not receive radiotherapy treatment.

# Mutagenic radiations

Question: Determine whether radiotherapy really increases the number of mutations in normal cells. To do this, build a histogram of the number of mutations sustained by treated patients, and a histogram of the number of mutations sustained by untreated patients.

See: `mutagenicRadiation.py`

Reminder: A histogram reports the number of patients with 0 mutations, the number with 1 mutation, the number with 2 mutations, etc.

Example:

