

# Homework 1

## Introduction

Many software tools exist to perform analyses relevant to genetic epidemiology. In this homework assignment the focus is on software for genetic association analysis / population genetics (select 1).

## Specific questions

- What is population genetics?
- Why is population genetics important in the context of genetic epidemiology in general or genetic association studies in particular?
- Does a classification of software tools exist for genetic association analysis / population genetics? If so, what are the criteria used to classify these software tools?
- What should be the minimal properties of software tools to perform a genetic association study or to carry out population genetics?
- Consider for instance R GenABEL, R SNPassoc and PLINK and describe / compare the general features of these software tools in the context of genetic association analyses / population genetics:
  - IT requirements
  - Data input/output formats
  - Possibilities to perform Quality Control (QC) checks
  - Type of questions that can be addressed using these tools
  - What types of study designs are supported

[Different groups may select different pairs of software tool. However, note that in subsequent assignments we will use R GenABEL, R SNPassoc and/or PLINK.]

Write a small report (see general guidelines to homework assignments/project)

**Final due date:** 30 April 2013