Background
Several different antimalarial drugs have been applied the last decade as treatment against uncomplicated malaria and prophylaxis of vulnerable groups. This has affected the genomes of the *P. falciparum* parasites in genes of relevance for drug tolerance/resistance, which can be observed by determining the temporal prevalence of these molecular markers in a given setting.

The assignment
Based on a limited literature study and as well, by the use of WWARN, molecular surveyor (http://www.wwarn.org/sp-molecular-surveyor), the assignment is to map the recent/current prevalence of markers of antimalarial drug resistance
The data should be entered into a geographical map setup in a PowerPoint slide.

How
Use search terms of the markers (e.g. “Pfcrt” or “chloroquine resistance transporter”) and *P. falciparum* and then Tanzania and/or Kenya

Limitations: Only for Tanzania and Kenya and only focus on the period from 2010-2018 (notice that publication date is not the same as sampling date! What we aim for is sampling date from 2010 to 2018).

All groups:
- Download a representative geographical map of the region (just Google Maps)
- Try to (relatively) pinpoint the exact location of where samples have been obtained using Google Maps. This can be tricky...
- Note the prevalence of mutants (see below for the various groups) in percentage and the sample size and the year(s) of sampling (as WWARN). Note the reference as: 1st author et al., year, journal, volume, issue
- Make a Power point slide with your findings and prepare for a brief presentation in plenum.

The groups:
- Grp1: Pf dhfr (Prevalence of triple 51-59-108 mutations)
- Grp2: Pf dhps (Prevalence of double 437-540 and triple 437-540-581 mutations)
- Grp3: Pfc rt (Prevalence of the 76T (and/or CVIET haplotype)
- Grp4: Pf mdr1 (Prevalence of the various Y86-F184-D1246 genotypes)