SILS Seminar

Thursday 11 May 16:00 - 17:00 C1.110

“The body calendar: Chronological age determination using DNA methylation markers and massive parallel sequencing”

Jana Naue

Over the last few years it became clear that additional information is hidden within epigenetic modifications, and that especially DNA methylation (DNAm) could provide useful evidence to the criminal justice system. Within this project, specific changes in DNAm levels upon age progression at selected loci were used to develop an objective scientific tool to determine the chronological age of an (unknown) individual. This information can be used to narrow down the list of suspects during criminal investigations or to determine the age of a person in other legal contexts such as human trafficking. Promising age-dependent markers were first selected using a random forest regression model and public available DNAm 450K microarray data. Afterwards an amplicon based massive parallel sequencing (MPS) approach was developed and 312 whole blood samples analyzed. 104 samples of these were used to test the model that was built on the other 208 samples. Within the seminar, a short introduction into the field of forensic genetics and the development as well as results of the age-determination tool will be presented.

“Activity related conformational changes of penicillin binding proteins”

Nils Meiresonne

One of the mechanisms of beta-lactam antibiotic resistance requires the activity of D,D-carboxypeptidases (D,D-CPases) involved in peptidoglycan (PG) synthesis, making them putative targets for new antibiotic development. Activity of PG synthesizing enzymes is often correlated with their association with other proteins. The PG layer is maintained in the periplasm in between the two membranes of the Gram-negative cell envelope. Because no methods existed to detect *in vivo* interactions in this compartment we have developed and validated a Förster Resonance Energy Transfer (FRET) assay. Using the donor-acceptor pair mNeonGreen-mCherry, periplasmic protein interactions were detected in fixed and in living bacteria, in single samples or in plate reader 96-wells format. We show that the D,D-CPases PBP5, PBP6a and PBP6b change dimer conformation between resting and active states. Complementation studies and changes in localization suggest that active and inactive forms of D,D-CPases have different functions and that their balance ensures robust PG synthesis.

Followed by drinks in the common room