Outline of the course:
Genomic analyses with emphasis on single-step
Misztal, Lourenco, Andonov
Ulls väg 26, Ultuna-Uppsala, Sweden, VHC building, Tanngrisner 2 (floor 5)

Time: 9:00 – 17:00, <u>**meeting at the entrance hall at 8:45 every morning**</u>
Coffee break: 10:30 & 15:00, coffee/refreshments - provided by organizer
Lunch break: 12:00 – 13:00, you can bring our own food or go to one of nearby restaurants
Social Diner: Thu. Sep 5, 19:00, provided by organizer (details will be given on the course).

Sep 2:
1. Introduction to BLUPF90 family of programs
    1. Animal model
    2. Multiple trait model
    3. Maternal models
    4. Genomic model
2. Exercise: use of programs for data sets with single and multiple traits.

Sep 3:
1. Introduction to genomic selection
    1. Basis of SNP data
    2. Simulation of genomic data
    3. Data manipulation and bash scripting in Linux
2. Exercise: Data simulation and manipulation

Sep 4:
1. Methods based on SNP estimation (SNP_BLUP, BayesX)
    1. Methods based on genomic relationships
    2. Creation and handling of genomic relationship matrices with preGSf90
    3. GBLUP, GREML and GGIBBBS using blupf90
2. Exercise: use of above programs with simulated data

Sep 5:
1. Theory of Single-step GBLUP
    1. Single-step for populations under selection: bias, inflation, accuracy
    2. Forming Single-step equations
    3. Quality control for G
        1. Calling rate
        2. Parental exclusions
        3. Distributions of diagonals of G
        4. Differences between matched G and A22
    4. Heritability of gene content
    5. Elimination of sex and "0" chromosomes
    6. Eigenvalues/eigenvectors – population stratification
2. Validation methods
    1. R^2 for dairy bulls

2. Predictability for animals with records
3. Cross-validation when few genotyped animals with records (e.g., mortality or disease resistance)
4. Selection bias for in realized accuracies
3. Exercises: Single-step with simulated data set

Sep 6:
1. Course evaluation (obligatory for all participants)
2. Estimating SNP effects for GBLUP-based methods
3. Weighted GBLUP and ssGBLUP
    1. Linear weights
    2. NonlinearA weights
4. Genome-wide association (GWA) and p-values with postGSf90
5. Experiences and future with ssGBLUP
6. Exercises: Application of weighted ssGBLUP and GWA