Background. If you are interested in the effects of molecular mechanisms on genome evolution and adaptive processes in natural populations, this project might be perfect for you. DNA methylation can alter the activity of a region of the genome without affecting the actual DNA sequence. In mammals, DNA methylation is for example essential for correct development and also associated to key processes like aging, transposable element inhibition, the formation of barr bodies and imprinting. However, the prevalence of methylation in regulation of gene activity across taxonomic groups is largely unknown.

Here we propose to develop methylation profiles for two butterfly species, the wood white (*Leptidea sinapis*) and the painted lady (*Vanessa cardui*). The project aims will be to assess i) how/if the methylation level varies across the genome in butterflies, ii) if methylation level is associated with gene expression, and, iii) if methylation is associated with specific genomic features. To answer this, the student will use flash frozen tissues to extract DNA and RNA for each respective species. The RNA data will be used to quantify expression profiles and the DNA for bisulfite sequencing and methylation quantification. Please, contact Niclas Backström (see below) for further details.

**Specific aim of project:** Characterize the methylation landscape and investigate how methylation is associated with gene expression levels and genomic features in butterflies.

**Time:** Students can start any time of the year.  
**Contact:** Niclas Backström; niclas.backstrom@ebc.uu.se