***Understanding haplotypes and its current relevance – minding the missing info in genome***

Genomics has transformed all aspects of ecology and evolution. But how often do we use the full information contained in a continuous genome? Since establishment of classical genetics, we know that genes are carried on linear chromosomes. But until recently, owing to limitations in methods to sequence and subsequently analyse data, we have been mostly dealing with polymorphisms at single sites. But latest methods do have the potential to fuel the transformation from analysing single sites to continuous genomes. But is it worth making this step? Clearly, continuous genomes contain more raw information, but is that information worth to answer questions that could not previously be answered by site-based methods?

In this article,

First, we offer a perspective on the current shortcomings of population genetic analysis – problems that we can easily solve, and ones that are beyond our reach with site-based methods.

Second, we outline our opinion on how haplotypes can offer a step forward towards a truly genomic analysis.

Third, we justify why undertaking this issue is relevant in the current state of (population) genetics.

1. Current Limitations
2. What is a haplotype and how can we move forward?
   1. Define haplotypes
      1. Simplest way is haploid genotype
      2. Coalescence theory and ARG
   2. Evolutionary processes that shape haplotypes
   3. Haplotypes in practice (BOX - Examples from humans, non-model organisms, etc)
   4. Outstanding questions -
      1. Will haplo information increase power and accuracy of evol inference?
      2. How does intrinsic (Recombination rate, mutation, etc) and extrinsic factors (demography, etc) impact haplotypes?
      3. What features of haplotypes carry (e;g;, length, frequency, etc) the most information about evolutionary processes?
      4. ...
3. Current Relevance
   1. Methods to infer genealogies
   2. Sequencing methods