Selective Sweeps and Positive Selection

Objective: To give a presentation of about 40-90 minutes duration at the end of the week covering the key aspects of the selective sweeps and positive selection.
Characterizing and understanding the genome is very important. The last decade has been faced with a challenge in relationship to this. Protein coding genes constitute 1.5%, RNA coding genes probably less than this. The amount of DNA under puryifying (negative) selection is at least 5%, but how many position have experience the opposite?

The Big Questions:

If comparing two species, for instance human and chimpanzee how many selective sweeps can be unambiguously identified?
Which percentage is under positive selection at a give time point?
Which techniques models are used to identify positive selections?
What kind of interpretation do selective sweeps have?
Do they come uniformly or in lumps?
Do different species have different regimes of positive selective sweeps.

References

Nielsen, R et al. (2006)
Myers, S. et al. ()
Eanes
McDonald and Kreitman

McVean G. (2007) The structure of linkage disequilibrium around a selective sweep. Genetics. 175(3):1395-406.