Tests of positive selection in the bird genome of great tit
Louise Dittmar

About myself

My name is Louise and I am 18 years old. I just graduated from the Heinrich-Hertz-Gymnasium in Berlin. Biology was always one of my favourite subjects and because a friend recommended it, I also took part in the biology olympiad. Thanks to the *Förderverein der Internationalen BiologieOlympiade e.V.*, I had the opportunity to do this internship. When I arrived at Sheffield I had just some programming experience and basic knowledge about evolution from school. It was the first time for me to live somewhere else with new people.

My working group

I interned with the Department for Animal and Plant Sciences (APS) in the working group of Dr Kai Zeng. The APS does a lot of research on different topics in the following categories: "ecology and environment", "evolution and behavior" and "plant and microbial biology". The group I joined is dealing with the analysis of genetical data with the purpose of learning about evolutionary processes, such as the interplay between selection and genetic drift.

My project

My project can be classified into the field of bioinformatics, as I processed genetical data at the computer to gain knowledge about evolutionary processes. We used great tit as a model species to identify genes which have been influenced by positive selection and draw conclusions on the evolution of this species. We ran tests on whole-genome-alignments from the recently sequenced great tit genome and also used data from ten resequenced birds from a population near Oxford.
We focused our analysis on protein coding parts of the genome and used statistical models based on the comparison of mutations that change the amino-acid, so called nonsynonymous mutations, and mutations that do not change the amino-acid, so called synonymous mutations. Because selection should mainly act on nonsynonymous mutations, an increased number of nonsynonymous substitutions (e.g. mutations that reached
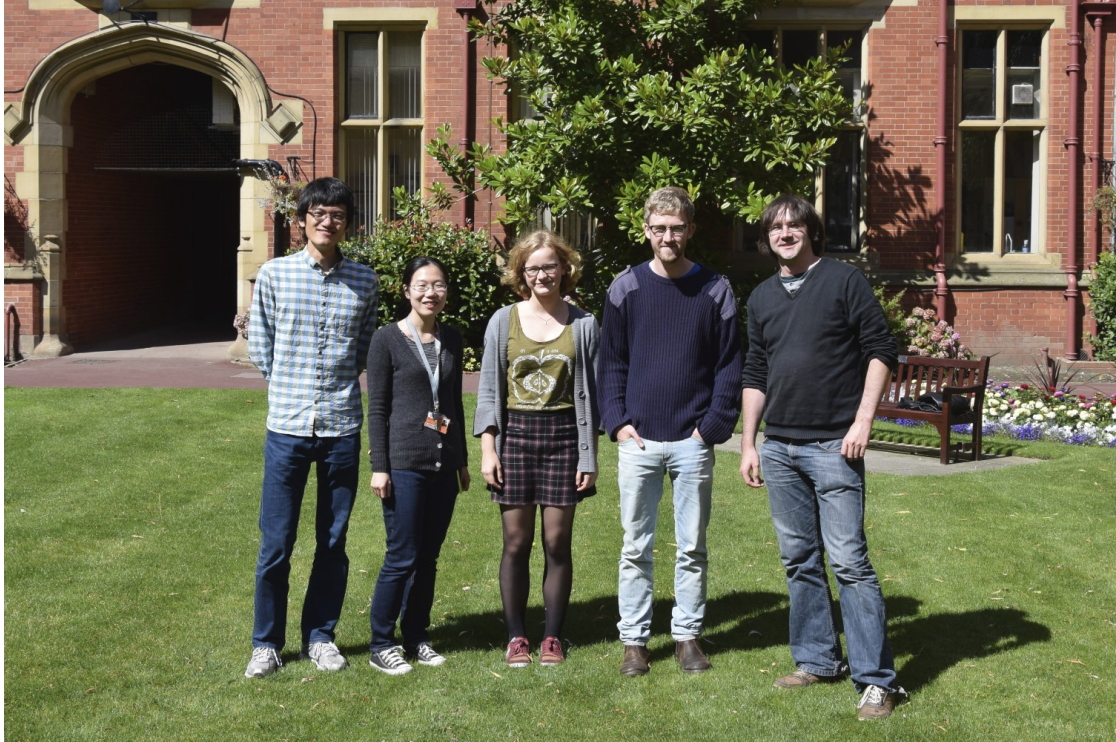
Figure 0.1: My working group: Dr Kai Zeng, Suo Qiu, me, Benjamin Jackson, Toni Ingolf Gossmann

fixation in a population) relative to synonymous substitutions can be used as an indicator for positive selection. For this test we compared great tit genes to genes with similar structure and function that have the same origin, so called orthologs, in other species.

We also performed a McDonald-Kreitman-test, which uses information about mutations which are currently segregating in a population relative to the number of observed substitutions. Substitutions are mutations which are fixed in a species but not in other related species. It therefore compares the number of synonymous and nonsynonymous mutations and substitutions. Similar to the test before only nonsynonymous mutations could have been under selection. Advantageous mutations should be favoured in a population and therefore become fixed more rapidly.

Finally, we investigated whether our findings can be explained by differences in recombination rate between different genomic regions.

Retrospect

I have never been sure about research being the right field of work for me, and I am not sure yet either. But meeting all these great people who showed me their work was amazing. I visited an underground greenhouse and stood in a swarm of butterflies. I also learned a lot about waiting and patience, because it seemed that few things in research are working the first time you try. My internship was extraordinary, because I learned Python, some R and Latex, but I was also able to improve my English a lot. It was really great to deal with a subject in such great depth, although a month seemed to be a really short time. In conclusion I will take a lot of things back home, which will definitely help me in future life.

Acknowledgements