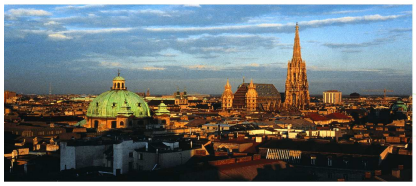
www.bioinf.boku.ac.at



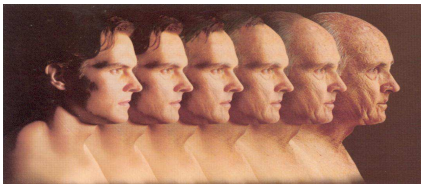
The Kreil group has labs in **Vienna, Austria**, and at the University of **Warwick**, one of the top ranked universities in the **UK** with a particularly strong tradition of **interdisciplinary collaboration**, located just an hour's drive from London.
Our work is **methods oriented** yet close to **experimental data**, with methods developments focused by **biological questions**.

Research Interests

Molecular determinants of ageing – quantitative response to adult-specific RNAi

We have identified candidate genes that reliably **increase longevity** *and* **fitness** in response to adult specific RNAi knock down in *Drosophila*. This is remarkable because for genes increasing longevity there normally is a *trade-off* between fitness and longevity. We are now analysing **time course data** collected over adult lifespan, comparing the genome scale molecular phenotype in response to RNAi knock down versus matched controls.

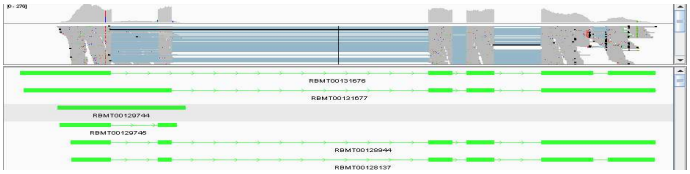
- There are now opportunities, for:
  1) **causality detection or network inference** and
  2) **improved interpretation of profiling outcomes** by systematic **integration of knowledge** from databases and literature.



Alternative transcript specific profiling by RNA-Seq or high-density microarrays

As part of a large **FDA benchmarking study**, we have demonstrated that models for alternative transcript specific profiling by **RNA-Seq** can be applied to the latest generation of **microarrays**. Interestingly, RNA-Seq suffers considerable noise as only a few reads fall on sequence regions that can **discriminate alternative transcripts**, whereas microarrays can be designed to probe these regions systematically and thus demonstrably yield more information about subtle biological differences.

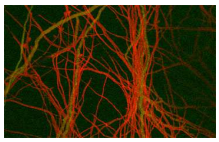
- There are two opportunities, for:
  1) application of **high-sensitivity alternative transcript specific profiling** to an appropriate biological question from your lab and
  2) building on our **prototype model to integrate probe properties across chips** (cross-chip correlations for the Gaussian Process model affinities).

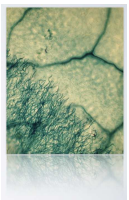


Joint transcriptome / proteome analysis of host-parasite interactions (bio-control)

Collaborators have studied the **interaction between a crop and a fungal pest**, and between the **pest and its biocontrol agent**, with both **transcript** and **protein expression profiles** available. Also, **phospho-proteomics** data are being collected.

- There is now an opportunity:
  1) to develop and apply methods for the **integrated analyses of multi-track differential expression data** (transcripts, proteins, phospho-modifications).

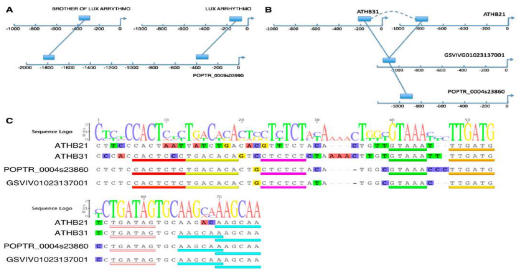




Was barley adapted to drought in ancient Nubia? - Evolution of archeological barley DNA

Collaborators have captured 250 million bases of **genomic barley sequence from multiple archeological samples**. They are working on inferring alleles from SNP data, and there is an opportunity to be involved in algorithm development.

- There are now opportunities to be involved with:
  1) further **development of the allele prediction algorithm** and
  2) the **high throughput analysis of the gene roster through time** - looking for evidence of phylogenetic change through time as well as SNPs associated with gene function.



We are looking for collaborators and exceptional young scientists to visit or join our team.

David P. Kreil

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