# BSC 4934: Projects List

1. **Epigenetics and its consequences**: Epigenetics refers to changes in phenotype (appearance) or gene expression caused by mechanisms other than changes in the underlying DNA sequence. One of these mechanisms is DNA methylation. The Human Epigenome Project (HEP) aims to study DNA methykation in a comprehensive manner. See http://www.epigenome.org/ and the associated publications at http://www.epigenome.org/index.php?page=publications.
2. **Horizontal Gene Transfer (HGT)**: A significant fraction of genes in prokaryotic genomes have been subject to horizontal transfer. These transfer events confer a selective advantage on the recipients, typically for adaptation to its environmental niche. Issues include how to identify the occurrence of HGT, the source of HGTs, and the kind of advantage it confers. Start with a review (Koonin *et al.* 2001).
3. **DNA Barcoding and Signature Discovery:** DNA barcoding is a technique in which species identification is performed by using DNA sequences from a small fragment of the genome, with the aim of contributing to a wide range of ecological and conservation studies in which traditional taxonomic identification is not practical (Lahaye *et al.* 2008). Also look at (Phillippy *et al.* 2007) and the work on ViroChip (Wang *et al.* 2002; Wang *et al.* 2003).
4. **MicroRNA**: These are short RNAs that regulate cellular processes by complementary base pairing at target sites. Start with the reviews (Bartel 2004; Storz *et al.* 2005). You may focus on finding targets of miRNA (Ragan *et al.* 2009), OR on finding small RNAs in bacteria (Vogel and Sharma 2005; Washietl *et al.* 2005), OR on RNA structure prediction (Shapiro *et al.* 2007), OR on Riboswitches (Barrick and Breaker 2007).
5. **Copy Number Variants (CNV)**: CNVs account for a substantial amount of genetic variation in humans. CNVs are associated with specific chromosomal rearrangements and genomic disorders. CNVs result in differential levels of gene expression and account for a significant proportion of normal phenotypic variations. Start with a review (Freeman *et al.* 2006).
6. **Applications of Next Generation Sequencing (NGS) Technologies**: RNA-Seq is an important application of NGS that provides accurate profiling of the entire transcriptome. Start with a review of next generation sequencing techniques (Shendure and Ji 2008) and a review of RNA-Seq (Wang *et al.* 2009). Alternatively, you may focus on ChIP-Seq,which is yet another application of NGS to do a genome-wide profile of transcription factor binding (Mardis 2007).

## References


Barrick, J. E. and R. R. Breaker (2007). "The Power of Riboswitches." Scientific American(January): 50.

Bartel, D. P. (2004). "MicroRNAs: genomics, biogenesis, mechanism, and function." Cell **116**(2): 281-97.

Freeman, J. L., G. H. Perry, L. Feuk, R. Redon, S. A. McCarroll, D. M. Altshuler, H. Aburatani, K. W. Jones, C. Tyler-Smith, M. E. Hurles, N. P. Carter, S. W. Scherer and C. Lee (2006). "Copy number variation: new insights in genome diversity." Genome Res **16**(8): 949-61.

Koonin, E. V., K. S. Makarova and L. Aravind (2001). "Horizontal gene transfer in prokaryotes: quantification and classification." Annu Rev Microbiol **55**: 709-42.

Lahaye, R., M. van der Bank, D. Bogarin, J. Warner, F. Pupulin, G. Gigot, O. Maurin, S. Duthoit, T. G. Barraclough and V. Savolainen (2008). "DNA barcoding the floras of biodiversity hotspots." Proc Natl Acad Sci U S A **105**(8): 2923-8.

Mardis, E. R. (2007). "ChIP-seq: welcome to the new frontier." Nat Methods **4**(8): 613-4.

Phillippy, A. M., J. A. Mason, K. Ayanbule, D. D. Sommer, E. Taviani, A. Huq, R. R. Colwell, I. T. Knight and S. L. Salzberg (2007). "Comprehensive DNA signature discovery and validation." PLoS Comput Biol **3**(5): e98.

Ragan, C., N. Cloonan, S. M. Grimmond, M. Zuker and M. A. Ragan (2009). "Transcriptome-wide prediction of miRNA targets in human and mouse using FASTH." PLoS One **4**(5): e5745.

Shapiro, B. A., Y. G. Yingling, W. Kasprzak and E. Bindewald (2007). "Bridging the gap in RNA structure prediction." Curr Opin Struct Biol **17**(2): 157-65.

Shendure, J. and H. Ji (2008). "Next-generation DNA sequencing." Nat Biotechnol **26**(10): 1135-45.

Storz, G., S. Altuvia and K. M. Wassarman (2005). "An abundance of RNA regulators." Annu Rev Biochem **74**: 199-217.

Vogel, J. and C. M. Sharma (2005). "How to find small non-coding RNAs in bacteria." Biol Chem **386**(12): 1219-38.

Wang, D., L. Coscoy, M. Zylberberg, P. C. Avila, H. A. Boushey, D. Ganem and J. L. DeRisi (2002). "Microarray-based detection and genotyping of viral pathogens." Proc Natl Acad Sci U S A **99**(24): 15687-92.

Wang, D., A. Urisman, Y. T. Liu, M. Springer, T. G. Ksiazek, D. D. Erdman, E. R. Mardis, M. Hickenbotham, V. Magrini, J. Eldred, J. P. Latreille, R. K. Wilson, D. Ganem and J. L. DeRisi (2003). "Viral discovery and sequence recovery using DNA microarrays." PLoS Biol **1**(2): E2.

Wang, Z., M. Gerstein and M. Snyder (2009). "RNA-Seq: a revolutionary tool for transcriptomics." Nat Rev Genet **10**(1): 57-63.

Washietl, S., I. L. Hofacker and P. F. Stadler (2005). "Fast and reliable prediction of noncoding RNAs." Proc Natl Acad Sci U S A **102**(7): 2454-9.