**附件一：培训安排**

* **主讲教师**

Professor Shizhong Xu （<http://statgen.ucr.edu/people/shizhongxu.html>）

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华中农业大学章元明教授，将应邀于6月29号下午讲授其领衔的团队在《Briefings in Bioinformatics》和《PLoS Computational Biology》等杂志最新发表的统计基因组学新方法、软件。（<http://cpst.hzau.edu.cn/Article/showdetail.asp?userid=4233>）。

上海交通大学王起山教授（<http://www.agri.sjtu.edu.cn/Data/View/2342>）、马裴裴讲师将协助徐士忠教授开展上机培训。

* **培训时间**

理论讲授时间: 6月26 ~30日上午9:00-12:00

上机培训时间: 6月26 ~30日下午14:00-16:30

* **参考书**

Electronic copy of course material will be delivered prior to the start of the class. The majority of the course material was extracted from Xu’s (2012) textbook entitled Principles of Statistical Genomics, Spinger Publisher, New York.

* **计算机程序**

1. SAS programs (Student Version is free for Students)
2. R programs (freely downloadable from public website)

* **培训大纲**

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| **Chapter** | **Topic** |
| 1 | Mating Designs for Genetic Analysis |
| 2 | Recombination Fraction and Linkage Map Construction |
| 3 | QTL Mapping in Experimental Populations |
| 4 | QTL Mapping in Random Populations |
| 5 | QTL Mapping for Discrete Traits |
| 6 | Linear Mixed Model and BLUP |
| 7 | Genome-wide Association Studies |
| 8 | Meta-Analysis of Multiple GWAS Data |
| 9 | Genotype by Environment Interaction |
| 10 | Statistical Prediction and Cross Validation |
| 11 | Bayesian Approach to Genomic Selection |
| 12 | Genomic Best Linear Unbiased Prediction |
| 13 | Genomic Selection using Partial Least Squares |
| 14 | Genomic Prediction via Support Vector Machine |
| 15 | Detection of Genome-wide Selection Signatures |
| 16 | Microarray Differential Expression Analysis |
| 17 | Model Based Cluster Analysis of Microarray Data |
| 18 | Quantitative Trait Associated Microarray Data Analysis |