

Schedule of the Workshop on Molecular Evolution (Shanghai, 2017)

The lab of Molecular Systematics & Ecology

	Jan 7 (Sat.)	Jan 8 (Sun.)	Jan 9 (Mon.)	Jan 10 (Tue.)	Jan 11 (Wend.)	Jan 12 (Thur.)
8:30 – 11:30	<p>Chenhong Li</p> <ul style="list-style-type: none"> • Introduction • Null hypotheses in molecular evolution • Idealized population 	<p>Hongjie Li & Guoxing Yin,</p> <ul style="list-style-type: none"> • Time calibration • Biogeography 	<p>Qian Wang</p> <ul style="list-style-type: none"> • Systematic errors in phylogenetic analysis • GC-bias paper, method, our solution and implementation 	<p>Fangyuan Cheng & Weicai Wang</p> <ul style="list-style-type: none"> • ABC • dadi 	<p>Junning Liu, & Qiaoyun Ai</p> <ul style="list-style-type: none"> • Drawing with R, DNA barcoding methods • Simulation, fastsimcoal • IMA2 • Simulated data for quantifying eDNA 	<p>Jiamei Jiang</p> <ul style="list-style-type: none"> • Genome analysis • Sex-determination in fishes & sharks • Genome-assisted selection
13:30 – 16:30	<p>Hongjie Li & Guoxing Yin</p> <ul style="list-style-type: none"> • Concatenated gene tree • Species tree SVDquartets 	<p>Anirban Sarker</p> <ul style="list-style-type: none"> • Paleogeography of Indian subcontinent <p>Shuli Song</p> <ul style="list-style-type: none"> • Paleogeography of East Asia 	<p>Fangyuan Cheng & Weicai Wang</p> <ul style="list-style-type: none"> • Population genomics • Summary statistics 	<p>Shuli Song</p> <ul style="list-style-type: none"> • Adaptive evolution • HYPHY, PAML & EP 	<p>Hao Yuan</p> <ul style="list-style-type: none"> • Genome alignment, lastz, mauve • Bioperl 	<p>Junman Huang & Ying Wang</p> <ul style="list-style-type: none"> • eDNA analyses