

## 课程大纲 COURSE SYLLABUS

1.	<b>课程代码/名称 Course Code/Title</b>	肿瘤系统生物学
2.	<b>课程性质 Compulsory/Elective</b>	选修
3.	<b>开课单位 Offering Dept.</b>	医学院人体细胞生物学及遗传系
4.	<b>课程学分/学时 Course Credit/Hours</b>	3
5.	<b>授课语言 Teaching Language</b>	英文
6.	<b>授课教师 Instructor(s)</b>	徐鹰
7.	<b>开课学期 Semester</b>	秋季
8.	<b>是否面向本科生开放 Open to undergraduates or not</b>	是
9.	<b>先修要求 Pre-requisites</b>	(如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.)  分子与细胞生物学
10.	<b>教学目标 Course Objectives</b>	(如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.)  通过本课程, 学生将学会如何通过肿瘤组织组学数据分析、建模, 解析肿瘤发生、发展、转移及转移后肿瘤生物学的驱动力及分子机理。学生的成绩将取决于他们的项目成绩。项目将要求有创新性。
11.	<b>教学方法 Teaching Methods</b>	(如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.)  线下课程。 =
12.	<b>教学内容 Course Contents</b>	(如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.)
	<b>Week 1</b>	<b>An introduction to cancer and cancer research</b>
		- A historic perspective of cancer research (0.5 week) - Cancer hallmarks (0.5 week)
	<b>Week 2</b>	<b>Cancer omic data and analysis techniques</b>
		- Cancer omic data (0.5 week) - Functional databases of genes/proteins (0.5 week)

<b>Week 3</b>	<b>Cancer omic data and analysis techniques II</b>
	<ul style="list-style-type: none"> <li>- KEGG and GO pathway databases (0.5 week)</li> <li>- Differential expression analyses and pathway enrichment analyses (0.5 week)</li> <li>- Statistical methods for information derivation from gene-expression data (0.5 week)</li> </ul>
<b>Week 4</b>	<b>Tissue repair, chronic inflammation, and oxidative stress</b>
	<ul style="list-style-type: none"> <li>- Tissue structure and repair as informed by transcriptomic data analysis (0.5 week)</li> <li>- Chronic inflammation, causes and consequence: statistical inference of transcriptomic data (0.5 week)</li> </ul>
<b>Week 5</b>	<b>Tissue repair, chronic inflammation, and oxidative stress II</b>
	<ul style="list-style-type: none"> <li>- Bioinformatic analyses of relationships among chronic inflammation, hypoxia, and oxidative stress (0.5 week)</li> <li>- Cancer prone vs. cancer independent chronic inflammation as informed by transcriptomic data analyses (0.5 week)</li> </ul>
<b>Week 6</b>	<b>Tissue repair, chronic inflammation, and oxidative stress III</b>
	<ul style="list-style-type: none"> <li>- What do immune cells do throughout cancer evolution? (1 week)</li> </ul>
<b>Week 7</b>	<b>Survival pressure and metabolic reprogramming: a bioinformatics perspective</b>
	<ul style="list-style-type: none"> <li>- Animals that develop cancer vs. those that do not develop cancer: what do the comparative transcriptomic data analyses inform us (1 week)</li> </ul>
<b>Week 8</b>	<b>Survival pressure and metabolic reprogramming: a bioinformatics perspective II</b>
	<ul style="list-style-type: none"> <li>- Tissues rich in hyaluronic acids: a soil for cancer to develop as informed by transcriptomic data analysis (0.5 week)</li> <li>- When inflammation meets with iron, the nature of the issue changes: intracellular alkalosis and extracellular acidosis: chemical homeostasis and issues caused when the homeostasis is disrupted (0.5 week)</li> </ul>
<b>Week 9</b>	<b>Survival pressure and metabolic reprogramming: a bioinformatics perspective III</b>
	<ul style="list-style-type: none"> <li>- Systematic metabolic reprogramming in cancer: the drivers, commonalities and uniqueness across different cancer types as informed by transcriptomic data analyses (1 week)</li> </ul>
<b>Week 10</b>	<b>Survival pressure and metabolic reprogramming: a bioinformatics perspective IV</b>
	<ul style="list-style-type: none"> <li>- De novo biosynthesis of nucleotides vs cancerous cell proliferation: a bioinformatics perspective (0.5 week)</li> <li>- Sialic acid biosynthesis and deployment vs. cancer cell migration: a bioinformatics perspective (0.5 week)</li> </ul>

<b>Week 11</b>	<b>Survival mechanisms: epigenomic alteration and genomic mutations</b>
	<ul style="list-style-type: none"> <li>- Red queen hypothesis, a modern version of Darwin's Evolutionary Principle: a general framework (0.5 week)</li> <li>- Cell polarity: the infrastructure for cellular localization and transportation and associated analyses of transcriptomic data (1 week)</li> </ul>
<b>Week 12</b>	<b>Survival mechanisms: epigenomic alteration and genomic mutations II</b>
	<ul style="list-style-type: none"> <li>- Mutations in tumor suppressor genes: what do they actually do in cancer development based on transcriptomic data analyses? (0.5 week)</li> <li>- Mutations in proto-oncogenes: what did they do in the ancient time based on phylogenetic and transcriptomic data analyses? (0.5 week)</li> </ul>
<b>Week 13</b>	<b>Cancer evolution: a bioinformatics perspective</b>
	<ul style="list-style-type: none"> <li>- A model for cancerous cell proliferation and migration: derived based on computational biology and chemistry modeling (1 week)</li> </ul>
<b>Week 14</b>	<b>Cancer evolution: a bioinformatics perspective II</b>
	<ul style="list-style-type: none"> <li>- A model for cancer metastasis: the drivers and mechanisms based on transcriptomic data analyses (1 week)</li> </ul>
<b>Week 15</b>	<b>Cancer evolution: a bioinformatics perspective III</b>
	<ul style="list-style-type: none"> <li>- A model for post-metastatic cancer biology: derived based on computational biology and chemistry modeling (1 week)</li> </ul>
<b>Week 16</b>	<b>Cancer diagnosis and treatment</b>
	<ul style="list-style-type: none"> <li>- Biomarker prediction (0.5 week)</li> <li>- Current treatment paradigms (0.5 week)</li> </ul>
<b>13. 课程考核</b>	
<b>Course Assessment</b>	
<p>(① 考核形式 Form of examination; ②. 分数构成 grading policy; ③ 如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.)</p> <p><b>考查 等级制</b>  <b>研究生: 项目报告: 50%; 项目 presentation: 25%; 文章述评: 25%</b>  <b>本科生: 项目报告: 50%; 项目 presentation: 40%; 出勤: 10%</b></p>	
<b>14. 教材及其它参考资料</b>	
<b>Textbook and Supplementary Readings</b>	
Cancer Bioinformatics, Ying Xu, Juan Cui, Dave Puett, Springer, 2014 (中译本, 科学出版社, 2016)。	