2021 组合与计算生物研讨会

5月28日（地点：报告厅415）		
主持人：王军		
8:30-9:00	开幕式、合影	
9:00-9:30	报告人	向青
	题目	CAMERON-LIEBLER LINE CLASSES IN PG(3, q)
9:30-10:00	报告人	吴耀坤
	题目	格子点阵树状程度
10:00-10:20	茶歇	
主持人：张之正		
10:20-10:50	报告人	马欣荣
	题目	From the (f,g) to (α,β): an inversion formula conjectured by L.C.Hsu
10:50-11:20	报告人	魏传安
	题目	Some q-supercongruences modulo the fourth power of a cyclotomic polynomial
11:20-11:50	报告人	王晓霞
	题目	The Research fo Ramanujan--type Supercongruences
主持人：李春		
14:30-15:00	报告人	贺平安
	题目	Understanding the unimodal distributions of cancer occurrence rates, it takes two factors for a cancer to occur
15:00-15:30	报告人	杨家亮
	题目	几个医疗数据库及其应用
15:30-15:50	茶歇	
主持人：贺平安		
15:50-16:20	报告人	郑小琪
	题目	The DNA methylation Haplotype (mHap) format and mHapTools
16:20-16:50	报告人	张伟伟
	题目	Complete deconvolution of DNA methylation signals from complex tissues: a geometric approach
16:50-17:20	自由讨论	

报告摘要

From the (f,g) to (α,β): an inversion formula conjectured by L.C.Hsu

马欣荣（苏州大学）

Abstract: My talk is mainly concerned with a fifteen-year-old conjecture posed by Hsu and Ma (J. Math. Res. & Exposition25(4) (2005), 624-624), which is called the (α,β)-inversion formula and analogous to the (f,g)--inversion formula. In this talk, I will present a full proof for this conjecture.

Our argument is based on the well-known fact that the nth divided difference of any polynomial of degree m must be zero while m<n.

In addition, some concrete inverse formulas are presented. These applications display that the (α,β)-inversion formula is indeed a useful tool to deal with reciprocal relations of sequences such as elliptic divisible sequences and other sequences given by the elliptic hypergeometric series and the partial theta functions.

My talk is based on joint work with Dr. Jin Wang and particularly dedicated to the memory of our mentor L. C. Hsu.

Some q-supercongruences modulo the fourth power of a cyclotomic polynomial

魏传安（海南医学院）

Abstract: With the help of the creative microscoping method recently introduced by Guo and Zudilin and the Chinese remaindertheorem for coprime polynomials, we establish a q-supercongruence with two parameters modulo $[n]\Phi_n(q)^3$. Here $[n] = (1-q^n)/(1-q)$ and $\Phi_n(q)$ is the n-th cyclotomic polynomial in q. In particular, we confifirm a recent conjecture of Guo and give a complete q-analogue of Long's supercongruence. The latter is also

a generalization of a recent q-supercongruence obtained by Guo and Schlosser.

格子点阵树状程度

吴耀坤（上海交通大学）

Abstract:演讲人将简要汇报其与学生钱程阳、熊彦禛最近对格子点阵树状程度的一个定义以及相关工作。

CAMERON-LIEBLER LINE CLASSES IN PG(3*; q*)

向青（南方科技大学）

Abstract: Cameron-Liebler line classes are sets of lines in PG(3, q) having many interesting combinatorial properties. These line classes were first introduced by Cameron and Liebler in theirstudy of collineation groups of PG(3, q) having the same number of orbits on points and linesof PG(3, q). During the last decade, Cameron-Liebler line classes have received considerableattention from researchers in both finite geometry and algebraic combinatorics. In the originalpaper by Cameron and Liebler, the authors gave several equivalent conditions for a set of linesof PG(3, q) to be a Cameron-Liebler line class; later Penttila gave a few more of such characterizations. We will use one of these characterizations as the definition of Cameron-Liebler lineclass. Let $\mathbf{L}$ be a set of lines of PG(3, q) with $|\mathbf{L}| = x(q^2+q+1)$, x is a nonnegative integer.We say that $\mathbf{L}$ is a *Cameron-Liebler line class with parameter* x if every spread of PG(3, q)contains x lines of $\mathbf{L}$. It turned out that Cameron-Liebler line classes are closely related tocertain subsets of points (tight sets) of the Klein quadric.

We will talk about a recent construction of a new infinite family of Cameron-Liebler lineclasses with parameter $x=\frac{(q+1)^2}{3}$ for $q \equiv 2 \pmod 3$. When q is an odd power of 2, thisfamily of Cameron-Liebler line classes represents the first infinite family of Cameron-Lieblerline classes ever constructed in PG(3, q), q even. This talk is based on joint work with TaoFeng, Koji Momihara, Morgan Rodgers and Hanlin Zou.

The Research fo Ramanujan--type Supercongruences

王晓霞（上海大学）

Abstract: According to Ramanujan's summation formulas for $1/\pi$, Van Hamme conjectured 13 supercongruences which are marked by (A.2)--(M.2), and all of them have been proved and refined. The methods and techniques of studying congruences including: WZ method, p-adic analysis and application of hypergeometric series transformation formula, etc. Applying the ``creative microscoping'' method which is first proposed by Guo and Zudilin and combing the Chinese remainder theorem for coprime polynomials, we establish many q-supercongruences with the help of some basic hypergeometric summations and transformations. Some of them are the q-analogues of Van Hamme's supercongruences.

Understanding the unimodal distributions of cancer occurrence rates
it takes two factors for a cancer to occur

贺平安（浙江理工大学）

Abstract: Data from the SEER reports reveal that the occurrence rate of a cancer type generally follows a unimodal distribution over age, peaking at an age that is cancer-type specific and ranges from 30+ through 70+. Previous studies attribute such bell-shaped distributions to the reduced proliferative potential in senior years but fail to explain why some cancers have their occurrence peak at 30+ or 40+.We present a computational model to offer a new explanation to such distributions. The model uses two factors to explain the observed age-dependent cancer occurrence rates: cancer risk of an organ and the availability level of the growth signals in circulation needed by a cancer type, with the former increasing and the latter decreasing with age. Regression analyses were conducted of known occurrence rates against such factors for triple negative breast cancer, testicular cancer and cervical cancer; and all achieved highly tight fitting results, which were also consistent with clinical, gene-expression and cancer-drug data. These reveal a fundamentally important relationship: while cancer is driven by endogenous stressors, it requires sufficient levels of exogenous growth signals to happen, hence suggesting the realistic possibility for treating cancer via cleaning out the growth signals in circulation needed by a cancer.

几个医疗数据库及其应用

杨家亮（北京元码基因）

Abstract:

本报告主要介绍几个医疗数据库的搭建，并应用机器学习算法挖掘数据库为一些医学问题提供初步解决方案，如肿瘤突变负荷预测等。

Complete deconvolution of DNA methylation signals from complex tissues: a geometric approach

张伟伟（东华理工大学）

Abstract: It is a common practice in epigenetics research to profile DNA methylation on tissue samples, which is usually a mixture of different cell types. To properly account for the mixture, estimating cell compositions has been recognized as an important first step. Many methods were developed for quantifying cell compositions from DNA methylation data, but they mostly have limited applications due to lack of reference or prior information. We develop Tsisal, a novel complete deconvolution method which accurately estimate cell compositions from DNA methylation data without any prior knowledge of cell types or their proportions. Tsisal is a full pipeline to estimate number of cell types, cell compositions, and identify cell-type-specific CpG sites. It can also assign cell type labels when (full or part of) reference panel is available. Extensive simulation studies and analyses of seven real data sets demonstrate the favorable performance of our proposed method compared with existing deconvolution methods serving similar purpose.

The DNA methylation Haplotype (mHap) format and mHapTools

郑小琪（上海师范大学）

Abstract: Bisulfite sequencing (BS-seq) is currently the gold standard for measuring genome-wide DNA methylation profiles at single nucleotide resolution. Most analyses focus on mean CpG methylation and ignore methylation states on the same DNA fragments (DNA methylation haplotypes). Here, we propose mHap, a simple DNA methylation haplotype format for storing DNA BS-seq data. This format reduces the size of a BAM file by 40 to 140-fold while retaining complete read-level CpG methylation information. It is also compatible with the Tabix tool for fast and random access. We implemented a command-line tool, mHapTools, for converting BAM/SAM files from existing platforms to mHap files as well as post-processing DNA methylation data in mHap format. With this tool, we processed all publicly available human reduced representation bisulfite sequencing (RRBS) data and provided these data as a comprehensive mHap database.