Genomic tableaux and equivariant K-theory of Grassmannians

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Overview

Goal: I will give a prequel of how we arrived at the solution to the A. Knutson-R. Vakil conjecture in terms of **genomic tableaux** – with emphasis on their other applications.

- The Schubert basis $\{\sigma_\lambda\}$ of $H^*(X)$; $X = Gr_k(\mathbb{C}^n)$
- The *tableau theory behind* the Littlewood-Richardson coefficients

$$\sigma_\lambda \cdot \sigma_\mu = \sum_\nu C_{\lambda,\mu}^{\nu} \sigma_\nu$$

  is of wide importance.
- $C_{21,21}^{321} = 2$:

		1
	1	
2		

and

		1
	2	
1		

but not

		2
	1	
1		

- We extend **this rule and its accompanying theory** to (equivariant) K-theory and then resolve the A. Knutson-R. Vakil conjecture by a bijection.

$[\mathcal{O}_{X_\lambda}]$ =Schubert structure sheaves form a basis of the Grothendieck ring $K^0(X)$. Define structure constants $K_{\lambda,\mu}^{\nu}$.

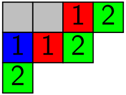
Example: $[\mathcal{O}_{X_{(1)}}] \cdot [\mathcal{O}_{X_{(1)}}] = [\mathcal{O}_{X_{(2)}}] + [\mathcal{O}_{X_{(1,1)}}] - [\mathcal{O}_{X_{(2,1)}}]$

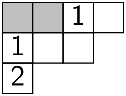
"Positivity": $(-1)^{|\lambda|+|\mu|-|\nu|} K_{\lambda,\mu}^{\nu} \geq 0$ (A. Buch '02, M. Brion '02).

Sample K-analogues of classical theory: (Pieri) C. Lenart '00; (LR rule) A. Buch '02; (Hopf algebras) T. Lam-P. Pylyavskyy '07; (insertion) A. Buch-A. Kresch-M. Shimozono-H. Tamvakis-Y '08 and R. Patrias-P. Pylyavskyy '14; (jeu de taquin) H. Thomas-Y. '09; (Knuth equivalence) A. Buch-M. Samuel '13; (longest increasing subsequences) H. Thomas-Y. '11 (Cyclic sieving) O. Pechenik '14, T. Pressey-A. Stokke-T. Visentin '14 and B. Rhoades '15; (Demazure atoms) C. Monical '15+,...

We develop an analogue of *semistandard tableaux*.

Definition of genomic objects (by example): Genomic tableau:

$T =$  : content $(2,1)$ (three genes). One **genotype** of

this T is . This has word 112 (ballot).

Genomic tableau theorems: standardization, jeu de taquin, Knuth equivalence, Bender-Knuth involution, a symmetric polynomial.

Genomic tableaux II

Theorem: (O. Pechenik-Y. '15) $K_{\lambda,\mu}^{\nu} = (-1)^{|\nu|-|\lambda|-|\mu|}$ times # ballot genomic tableaux of shape ν/λ and content μ.

- For $Y = OG(n, 2n+1)$ we have an analogous rule in terms of shifted genomic tableaux.
- Want a rule for $Z = LG(n, 2n)$.

Conjecture: (O. Pechenik-Y. '15) $|K_{\lambda,\mu}^{\nu}(Y)| \leq |K_{\lambda,\mu}^{\nu}(Z)|$ (true for $n \leq 8$).

Equivariant cohomology/K-theory of X

In earlier work H. Thomas-Y. '12 we found a lift to $H_T(X)$ of the classical LR rule (after A. Knutson-T. Tao '03).

(This work found application (D. Anderson-E. Richmond-Y., '14) to prove *equivariant saturation* and *equivariant Horn* in connection to the S. Frieldland '00 problem on the eigenvalues of matrices $A + B \geq C$. This extends the work on the Horn problem: A. Knutson-T. Tao '99, A. Knutson-T. Tao-C. Woodward '04 and others.)

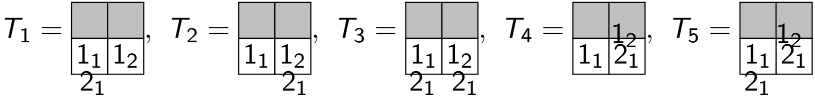
For $K_T(X)$, H. Thomas-Y. '12 conjectured a rule for the structure coefficients $K_{\lambda,\mu}^{\nu}$ in terms of edge-labeled increasing tableaux. This rule is positive in the sense of D. Anderson-S. Griffeth-E. Miller '11.

Edge labeled genomic tableaux I

We give the first proved rule for $E_{\lambda,\mu}^{\nu}$
(D. Anderson-S. Griffeth-E. Miller positive):

Theorem: (O. Pechenik-Y. '15)
$E_{\lambda,\mu}^{\nu} = \sum_T (-1)^{d(T)} \times \texttt{boxwt}(T) \times \texttt{edgewt}(T)$
where the sum is over edge-labeled genomic tableaux of content μ and shape ν/λ.

Example: To compute $K_{(2),(2,1)}^{(2,2)}$ for $\mathrm{Gr}_2(\mathbb{C}^4)$, the required tableaux are



Hence $K_{(2),(2,1)}^{(2,2)} =$

$$\left(1 - \frac{t_1}{t_2}\right)\frac{t_3}{t_4} + \left(1 - \frac{t_2}{t_3}\right)\frac{t_3}{t_4} - \left(1 - \frac{t_1}{t_2}\right)\left(1 - \frac{t_2}{t_3}\right)\frac{t_3}{t_4} + \dots .$$

Edge labeled genomic tableaux II

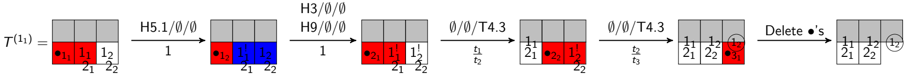
- $d(T) = \sum_{\mathcal{G}}(|\mathcal{G}| - 1)$ where the sum is over all genes $\mathcal{G}$ and $|\mathcal{G}|$ is the (multiset) cardinality of $\mathcal{G}$.
- $\texttt{edgewt}(T) := \prod_{\ell} 1 - \frac{t_{\mathrm{Man}}(\mathsf{x})}{t_{r-i+N_{i_j}+1+\mathrm{Man}(\mathsf{x})}}$, where $\ell = i_j \in \underline{\mathsf{x}}$ and x is in row r.
- A nonempty box $i_j \in \mathsf{x}$ in row r is **productive** if $i_{j+1} \notin \mathsf{x}^{\rightarrow}$.
- $\texttt{boxwt}(T) := \prod_{i_j \in \mathsf{x} \text{ productive}} \frac{t_{\mathrm{Man}(\mathsf{x})+1}}{t_{r-i+N_{i_j}+1+\mathrm{Man}(\mathsf{x})}}$.

Idea of proof

The proof concerns establishing the "Chevalley recurrence":

$$\sum_{\rho \in \lambda^+} (-1)^{|\rho/\lambda|+1} K^{\nu}_{\rho,\mu} = K^{\nu}_{\lambda,\mu}(1 - \mathtt{wt}(\nu/\lambda)) + \sum_{\delta \in \nu^-} (-1)^{|\nu/\delta|+1} K^{\delta}_{\lambda,\mu} \mathtt{wt}(\delta/\lambda)$$

Example of slides:



To do this, we develop a new jeu de taquin and good tableaux. In general, the slides are **not** weight-preserving on single tableaux! However, it **is** weight-preserving on the entirety of the LHS: we need some "sign-reversing involutions".

Conclusions and Summary

We originally developed genomic tableaux in order to give a first proof of an K_T rule. With this rule, we

1. solve the H. Thomas-A. Yong '12 conjecture
2. solve the A. Knutson-R. Vakil '05 conjecture
3. give generalized "squarefree positivity" (cf. A. Knutson '10)

This study forced us to introduce genomic tableaux in *ordinary* K-theory. These tableau are of independent interest and have a theory parallel to that of semistandard tableaux.