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

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

is of wide importance.

- $C^{321}_{21,21} = 2$: 
  \[
  \begin{array}{c|c|c|}
  1 & 2 & 1 \\
  \hline
  2 & 1 & \ \\
  \end{array}
  \]  
  and
  \[
  \begin{array}{c|c|c|}
  1 & 2 & \ \\
  \hline
  & 1 & \ \\
  \end{array}
  \]  
  but not
  \[
  \begin{array}{c|c|c|}
  2 & 1 & 1 \\
  \hline
  1 & & \ \\
  \end{array}
  \]  

- 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 $K^\nu_{\lambda,\mu}$.

**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”**: $(-1)^{|\lambda|+|\mu|-|\nu|} K^\nu_{\lambda,\mu} \geq 0$ (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:  
\[
T = \begin{array}{ccc}
1 & 1 & 2 \\
1 & 1 & 2 \\
2 & & \\
\end{array} : \text{content } (2,1) \text{ (three genes). One \textit{genotype} of this } T \text{ is } \begin{array}{ccc}
 & 1 & \\
1 & & \\
2 & & \\
\end{array}. \text{ This has word } 112 \text{ (ballot).}
\]

**Genomic tableau theorems:** standardization, jeu de taquin, Knuth equivalence, Bender-Knuth involution, a symmetric polynomial.
**Theorem:** (O. Pechenik-Y. '15) $K_{\lambda,\mu}^\nu = (-1)^{|\nu| - |\lambda| - |\mu|}$ times \# ballot genomic tableaux of shape $\nu/\lambda$ and content $\mu$.

- 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 $n \leq 8$).
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. Friedland ’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.
We give the first proved rule for $E_{\lambda,\mu}^\nu$
(D. Anderson-S. Griffeth-E. Miller positive):

**Theorem:** (O. Pechenik-Y. ’15)

$$E_{\lambda,\mu}^\nu = \sum_T (-1)^{d(T)} \times \text{boxwt}(T) \times \text{edgewt}(T)$$

where the sum is over edge-labeled genomic tableaux of content $\mu$
and shape $\nu/\lambda$.

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

$$T_1 = \begin{array}{cc}
1_1 & 1_2 \\
2_1
\end{array},
T_2 = \begin{array}{cc}
1_1 & 1_2 \\
2_1
\end{array},
T_3 = \begin{array}{cc}
1_1 & 1_2 \\
2_1
\end{array},
T_4 = \begin{array}{cc}
1_1 & 1_2 \\
2_1
\end{array},
T_5 = \begin{array}{cc}
1_1 & 1_2 \\
2_1
\end{array}$$

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

$$\left(1 - \frac{t_1}{t_2}\right) \frac{t_3}{t_4} + \left(1 - \frac{t_2}{t_3}\right) \frac{t_3}{t_4} - \left(1 - \frac{t_1}{t_2}\right) \left(1 - \frac{t_2}{t_3}\right) \frac{t_3}{t_4} + \ldots$$
- \(d(T) = \sum_G (|G| - 1)\) where the sum is over all genes \(G\) and \(|G|\) is the (multiset) cardinality of \(G\).

- \(\text{edgewt}(T) := \prod_\ell 1 - \frac{t_{\text{Man}(x)}}{t_{r-i+N_{ij}+1+\text{Man}(x)}}\), where \(\ell = ij \in \mathbf{x}\) and \(\mathbf{x}\) is in row \(r\).

- A nonempty box \(ij \in \mathbf{x}\) in row \(r\) is \textbf{productive} if \(i_{j+1} \notin \mathbf{x} \rightarrow\).

- \(\text{boxwt}(T) := \prod_{ij \in \mathbf{x} \text{ productive}} t_{\text{Man}(x)+1}^{t_{\text{Man}(x)+1}} t_{r-i+N_{ij}+1+\text{Man}(x)}\).
Idea of proof

The proof concerns establishing the “Chevalley recurrence”:

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

$$
+ \sum_{\delta \in \nu^-} (-1)^{|\nu/\delta|+1} K^\delta_{\lambda,\mu} \text{wt}(\delta/\lambda)
$$

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”.

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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.