Identifying
Rare SNV's and Clonal Structure
from mRNA-seq data

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Literature Review

Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing

Peter J. Campbell*, Erin D. Pleasance*, Philip J. Stephens*, Ed Dicks*, Richard Rance*, Ian Goodhead*, George A. Follows†, Anthony R. Green†, P. Andy Futreal*‡, and Michael R. Stratton*‡§

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- Our Goal: a genome-wide approach using SOLiD RNA-seq data

Big Ideas

- Deeply sequenced 2 matched CLL samples

- Quality filter like mad

- Test statistic $X \sim \max\{ \text{Mult}(x_1, x_2, x_3, x_4) \}$
  - Distribution from a Poissonization argument

- Never mind, just use Binomial!

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Conclusion

- Identified 3 rare subclones in CLL2 mRNA

- These do not appear in the DNA (??!)

- Currently verifying by Sanger sequencing.

- Thanks!

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