

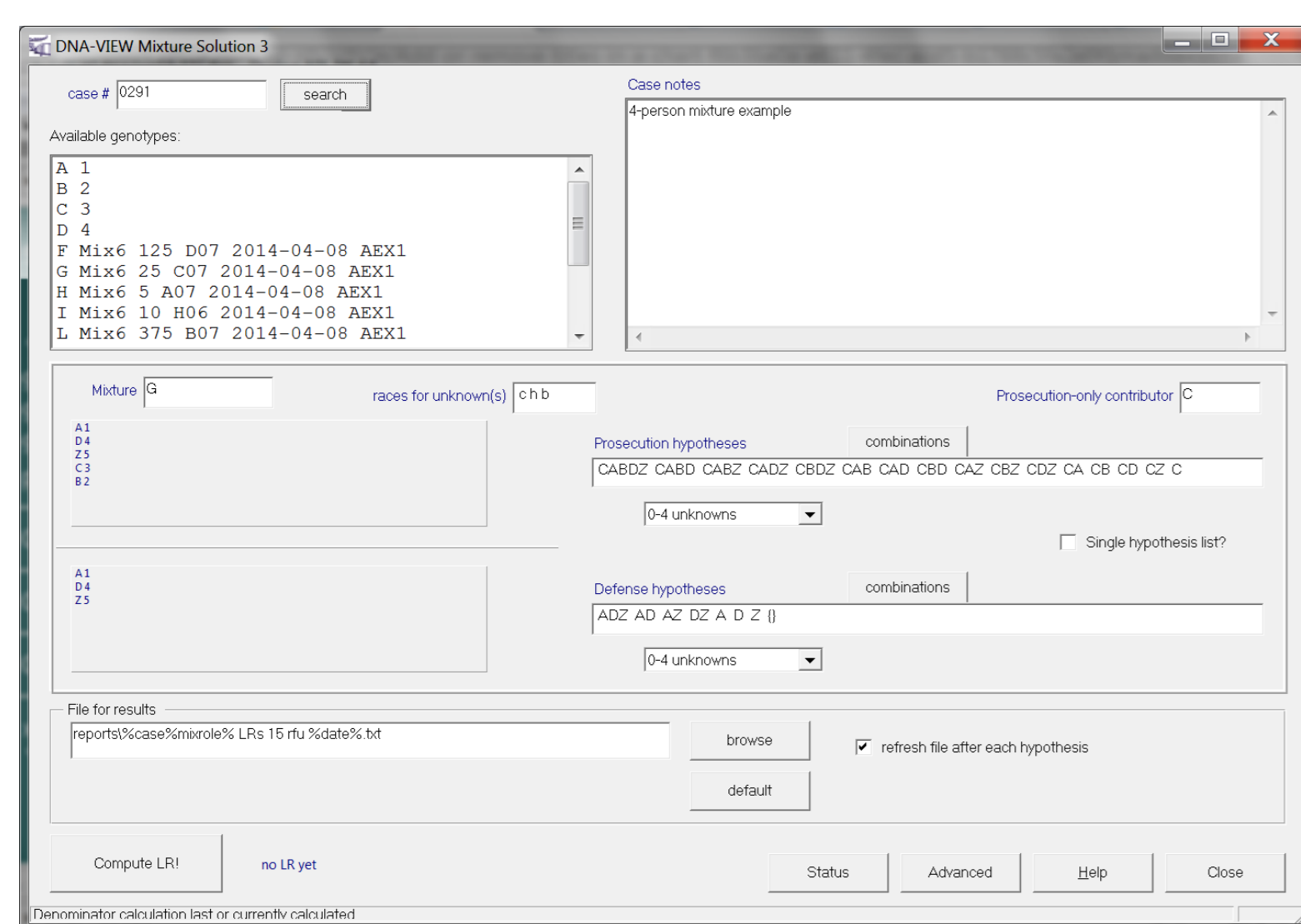
The DNA·VIEW® Mixture Solution

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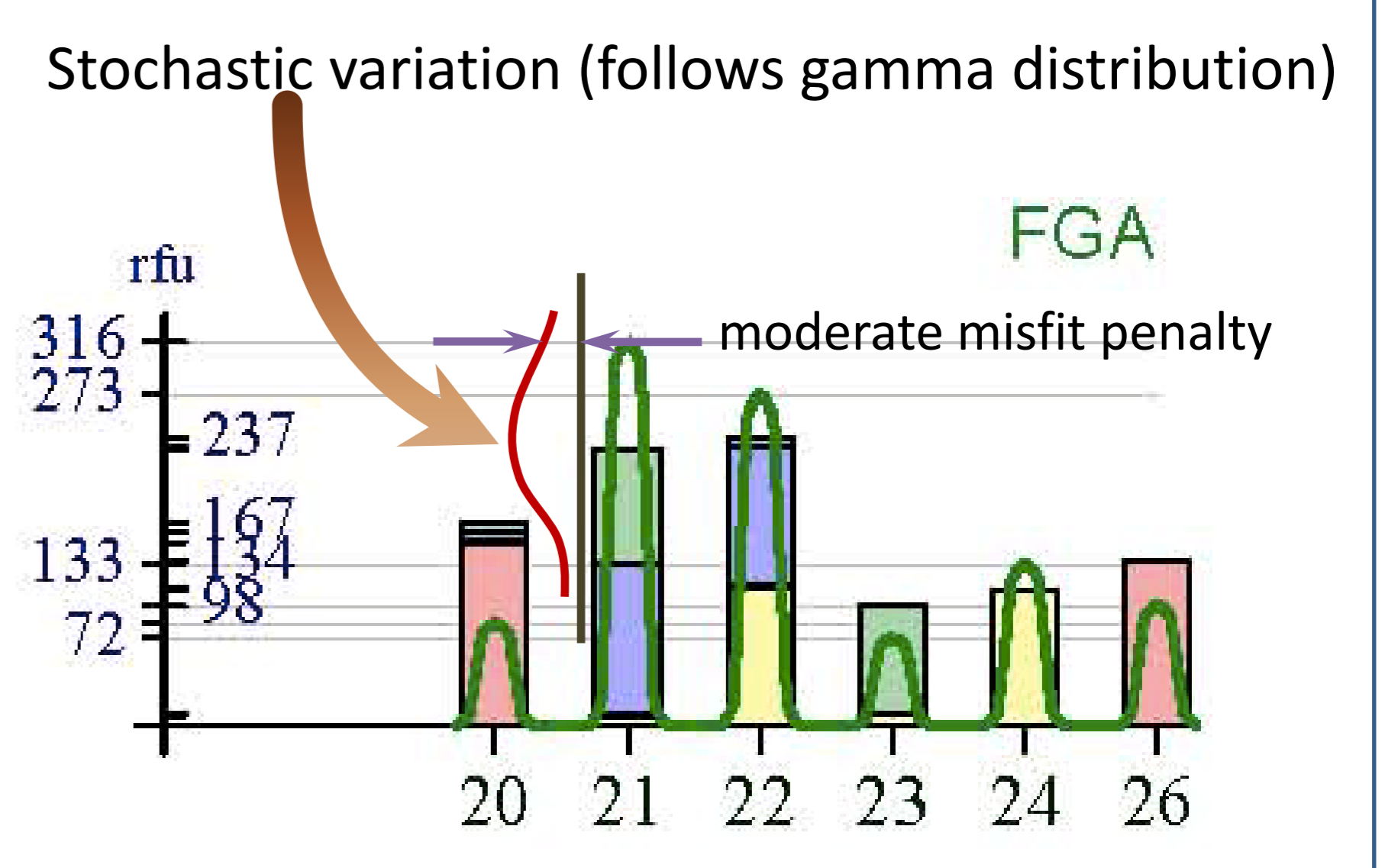
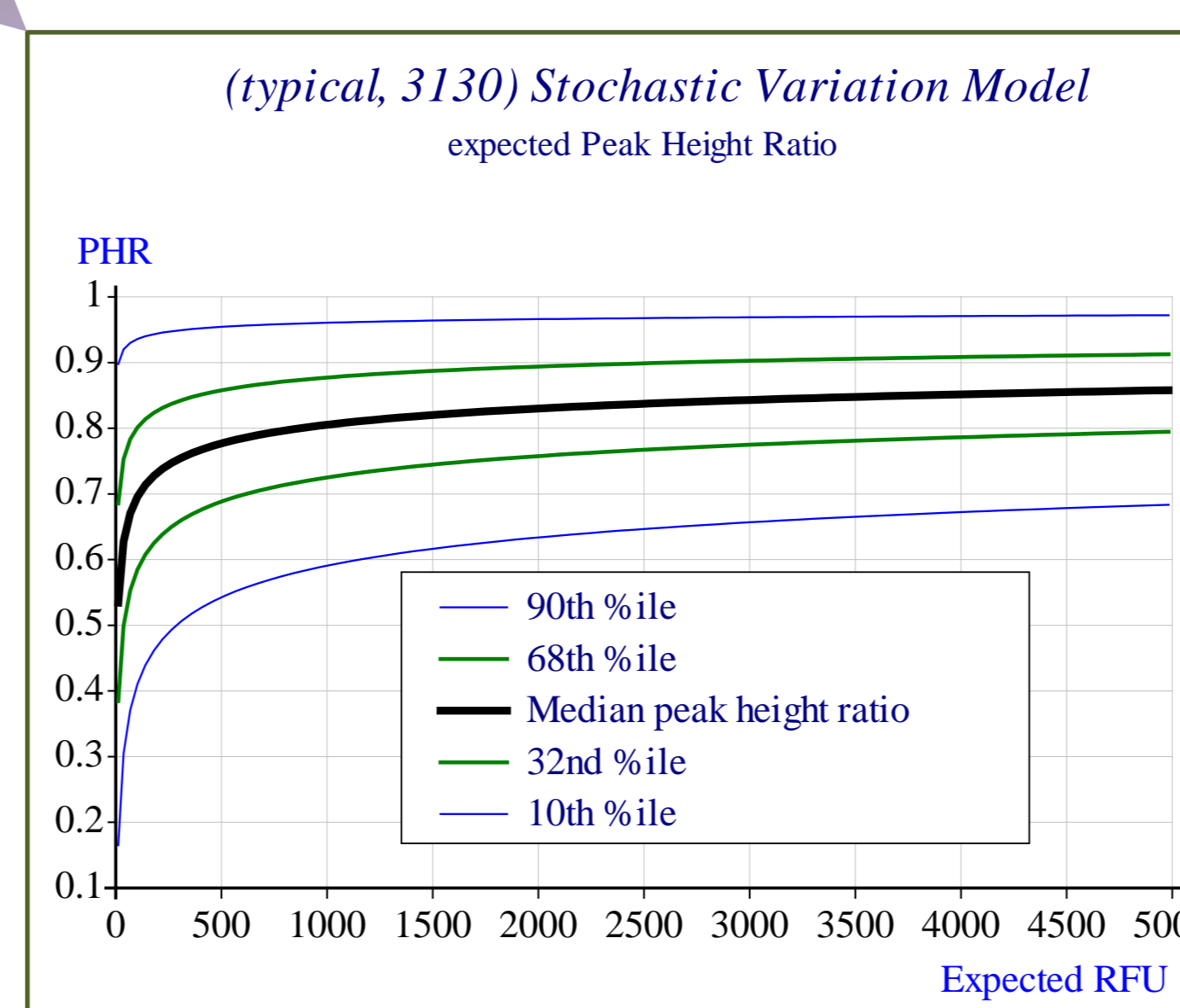
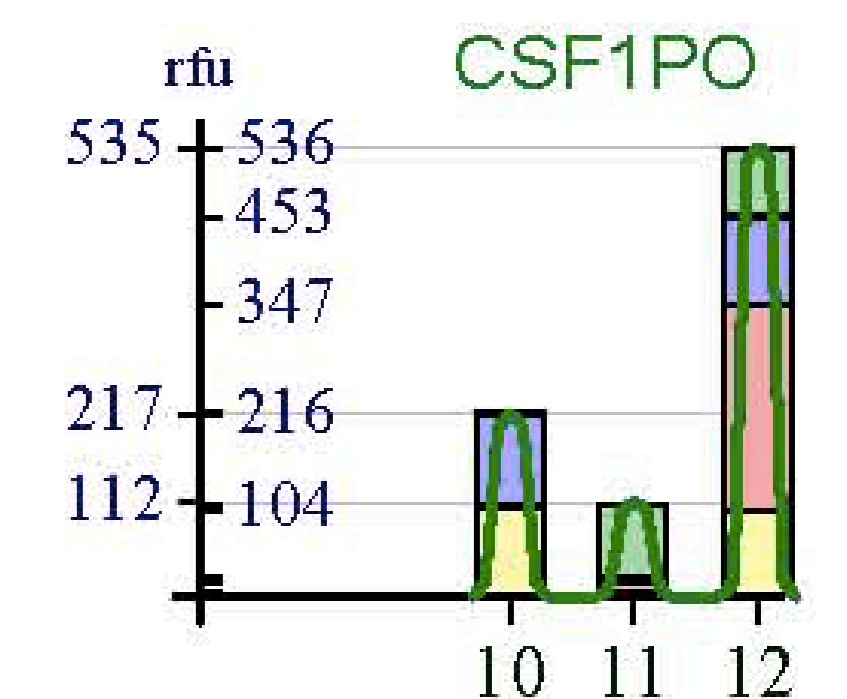
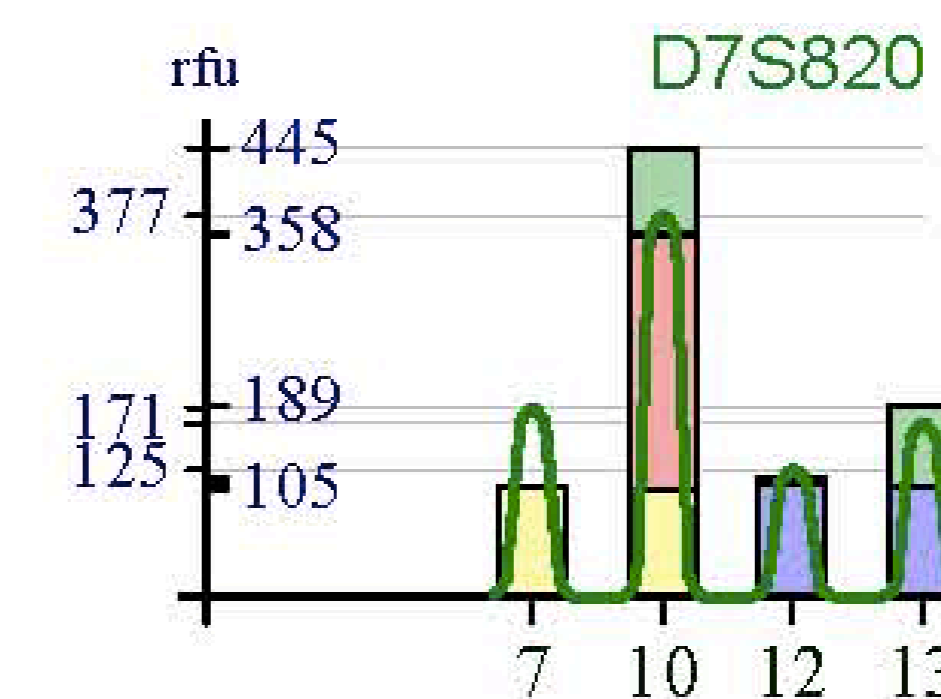
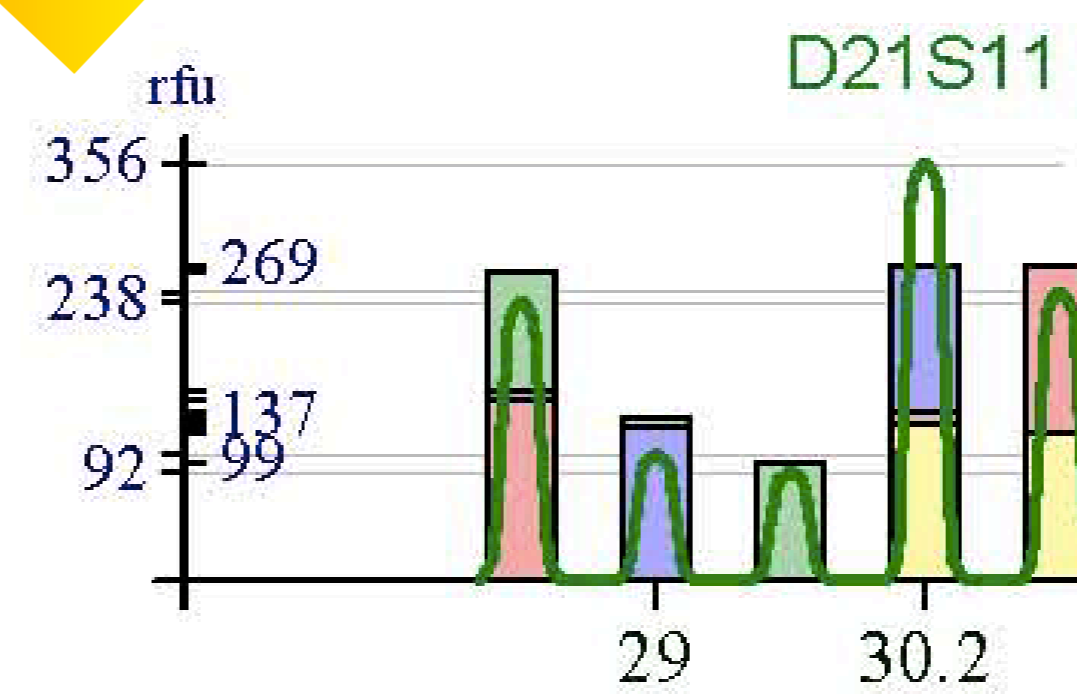
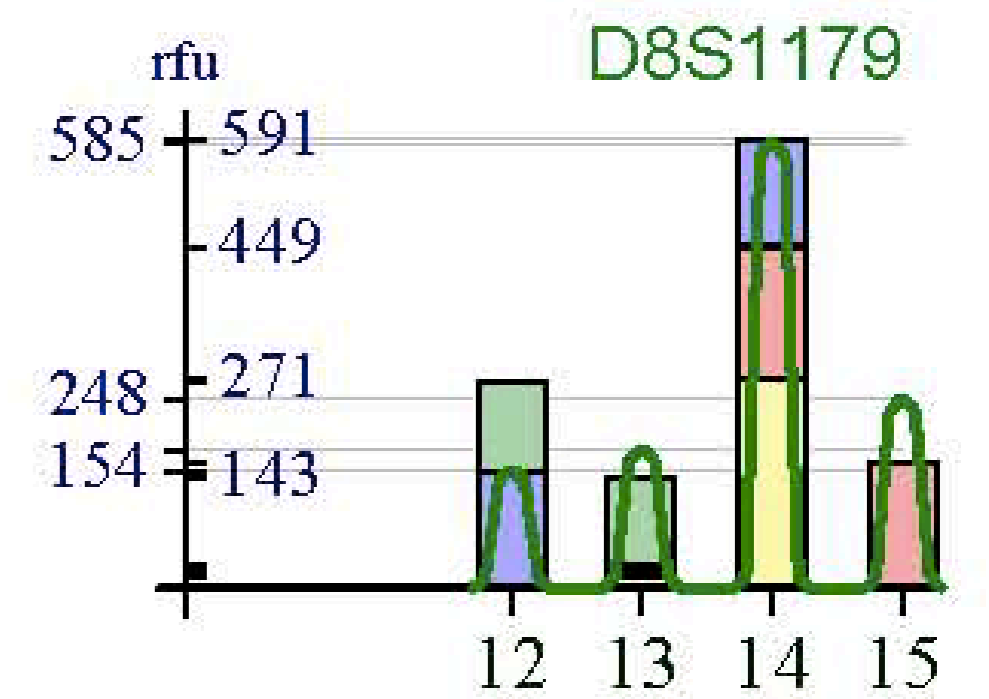
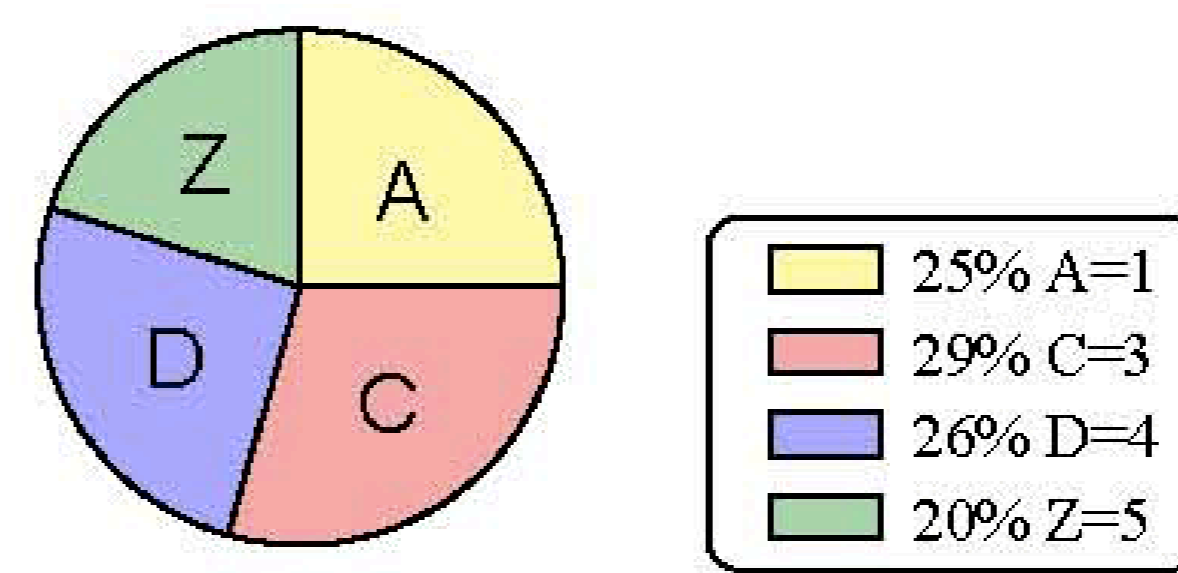
Continuous-model mixture analysis

Mixture Solution™ is a computer program for solving mixture problems by a “continuous” approach – that is, the calculation takes into account the significance of peak height including varying contribution amounts along with random peak height variation.

- Visual aids – answer “black box” concern.
- Coherent simple model for likelihood computations
 - based mainly on stochastic variation, incorporates dropout, drop-in, stutter and allelic stacking naturally and without additional “moving parts.”
 - Robust: not sensitive to exact parameter values



Mixture L as ABCZ+0 unknowns
Maximum likelihood proportions:



“Casework model” (of Mixture Solution)

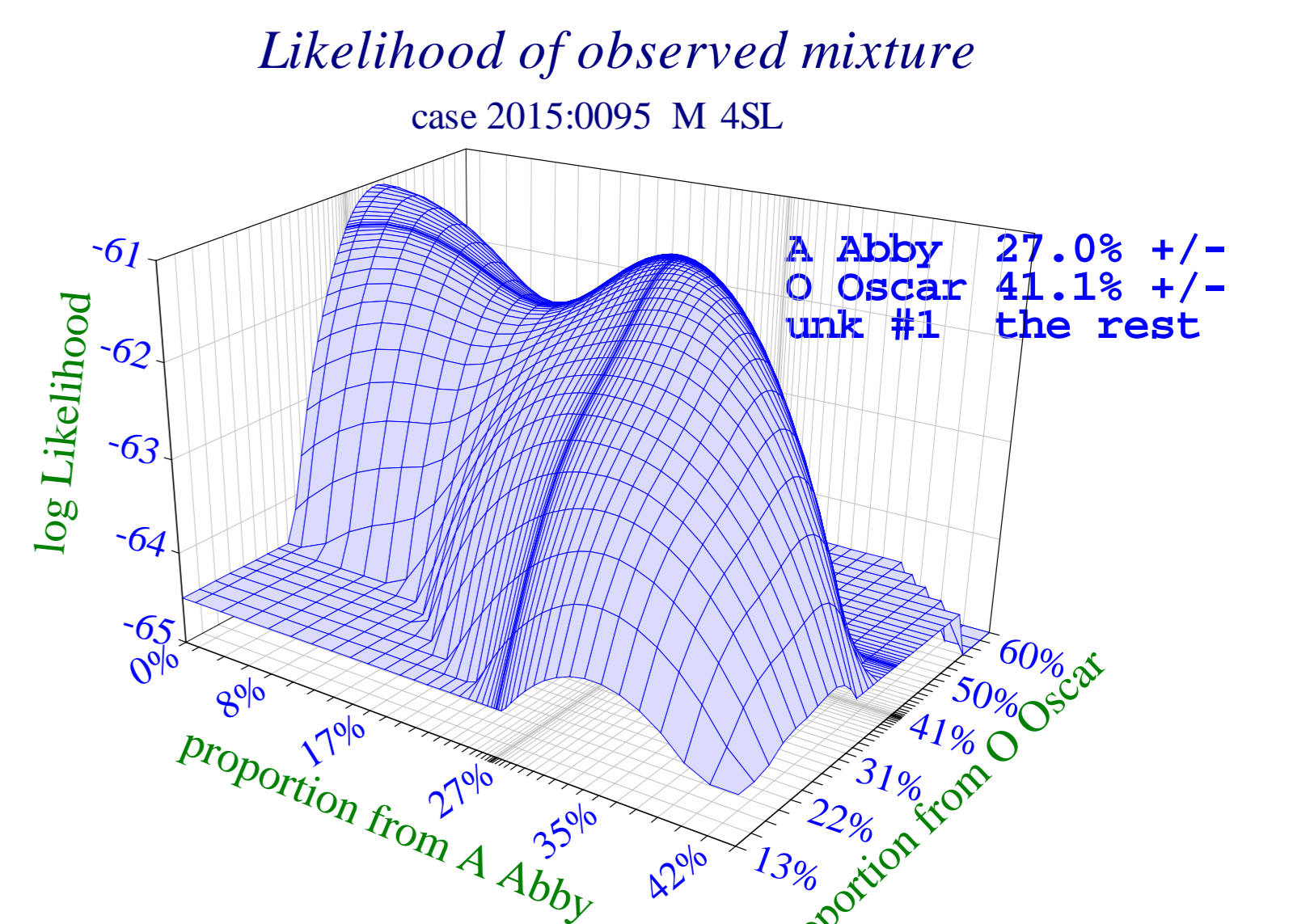
- Multiple potential contributors S, T, U, ...
- May be 2-person, may be 3-person ... mixture
- Explore automatically all (Hp-Hd) combinations

Continuous evaluation model

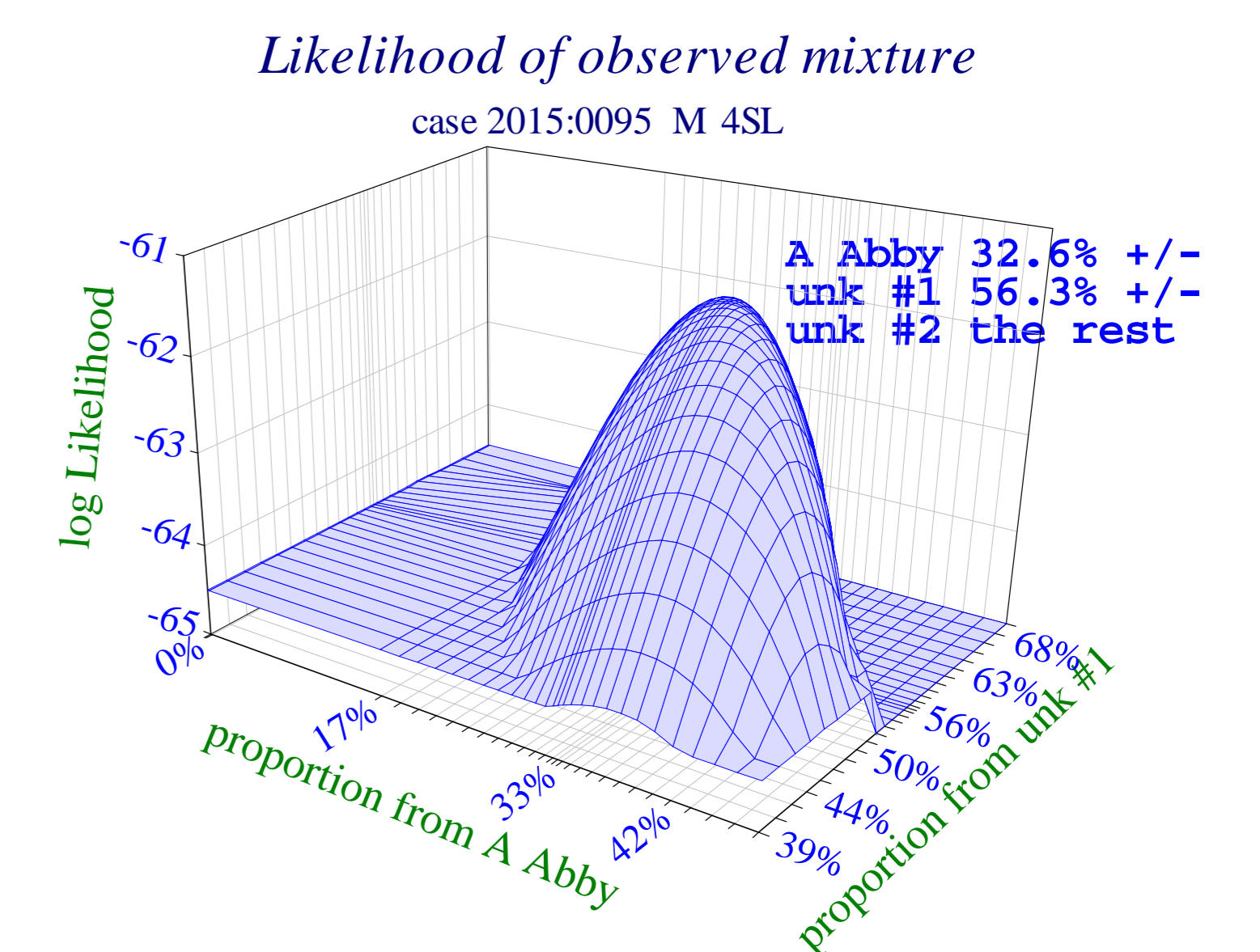
- LR for Hp vs Hd
- Stochastic behavior
- Dropout, dropin, stutter, ...

Hp=prosecution hypothesis
Hd=defense hypothesis
LR=evidence for Hp vs Hd

- Find best Hp & best Hd, & LR



LR=

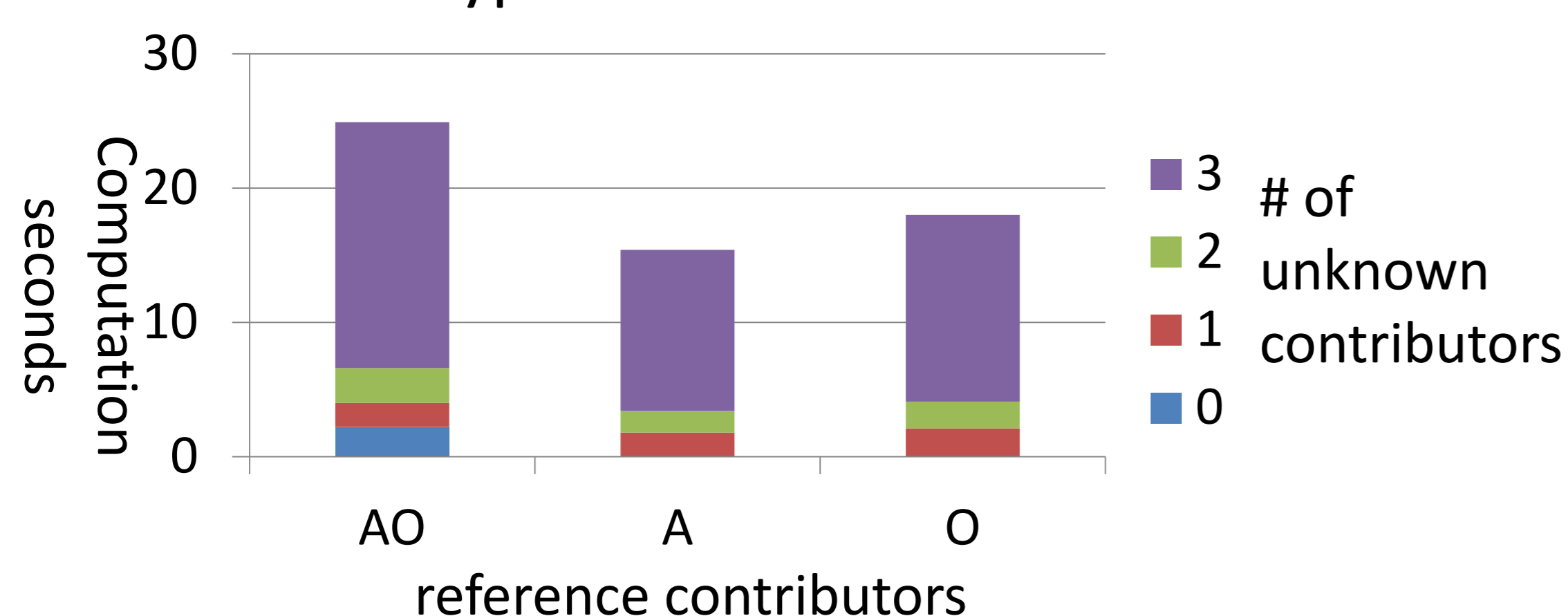


Explore & Solve

- Explores many hypotheses
- Decides appropriate # of unknown contributors
- Evaluates many different combinations of references as contributors
- Uses mathematics, not MCMC

quick!

65 seconds total time
10 hypotheses



Best hypotheses to:

- defend A
- defend O
- prosecute

		Defense hypotheses					
		A&2unk	A&3unk	O&2unk	O&3unk	O&1unk	A&1unk
Prosecution hypotheses	AO&2unk	LR=190 vs O	225	LR=660 vs A	1000	2E+13	8E+13
	AO&3unk	94	110	330	510	1E+13	4E+13
	AO&1unk	10	13	38	60	1E+12	4E+12
	AO&0unk	0	0	0	0	0	0

Strength of evidence (Likelihood Ratios)

References

Evaluating forensic DNA profiles using peak heights, allowing for multiple donors, allelic dropout and stutters, Roberto Puch-Solis, Lauren Rodgers, Anjali Mazumder, Susan Pope, Ian Evett, James Curran, David Balding, Forensic Science International: Genetics 7 (2013) 555–563
Computational aspects of DNA mixture analysis / Exact inference using auxiliary variables in a Bayesian network, Therese Graversen & Steffen Lauritzen, Stat Comput DOI 10.1007/s11222-014-9451-7