



Jose Iglesias

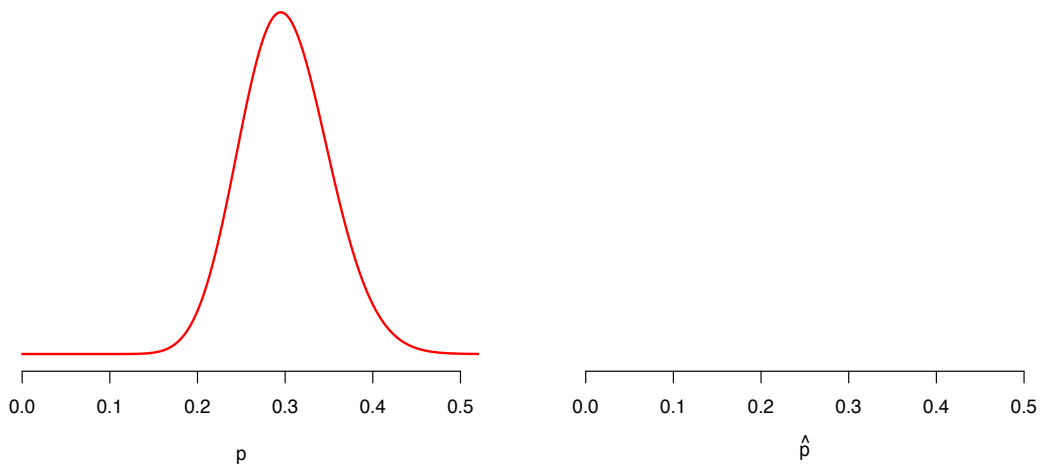
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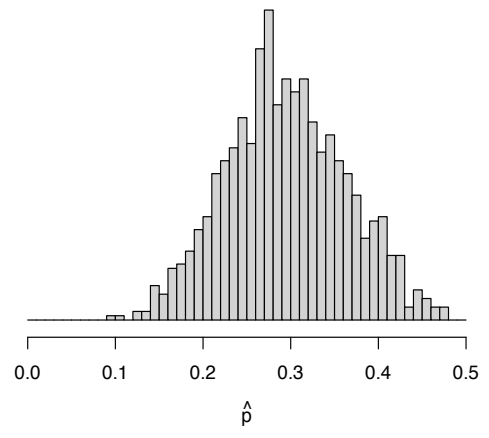
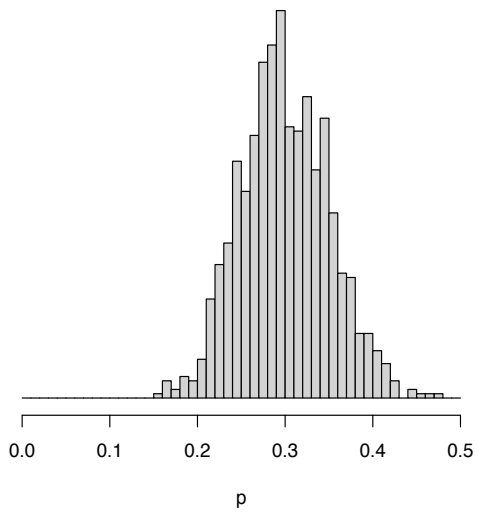
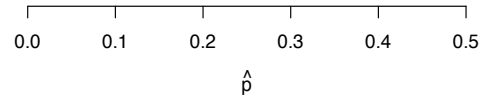
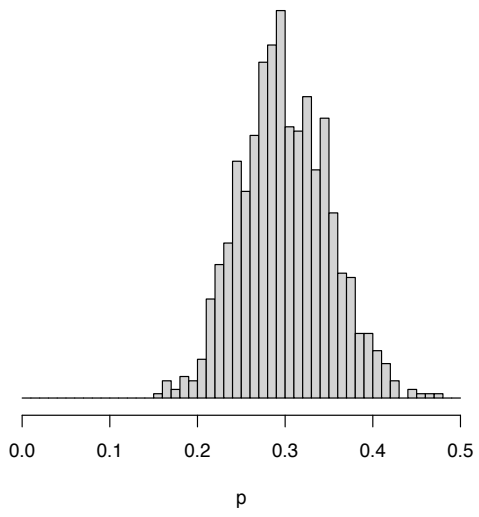
#1 SS | Bats: R, Throws: R | Detroit Tigers

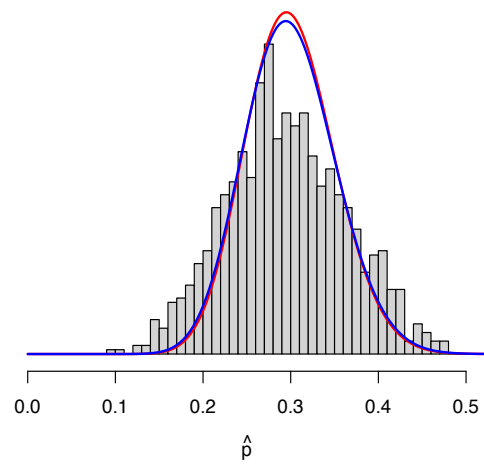
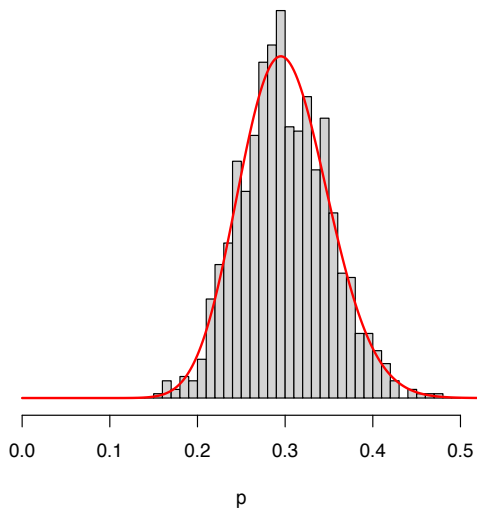
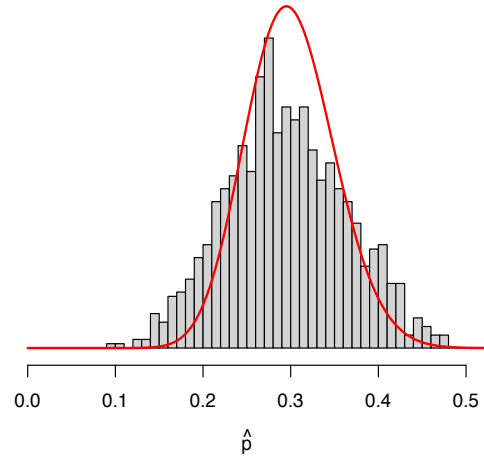
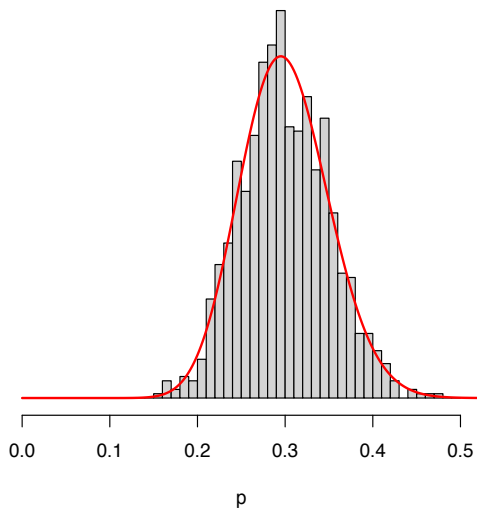
Birth Date: January 5, 1990 (Age: 24)
 Birthplace: Havana, Cuba
 Experience: 3 years
 College: None
 Ht/Wt: 5-11, 185 lbs.

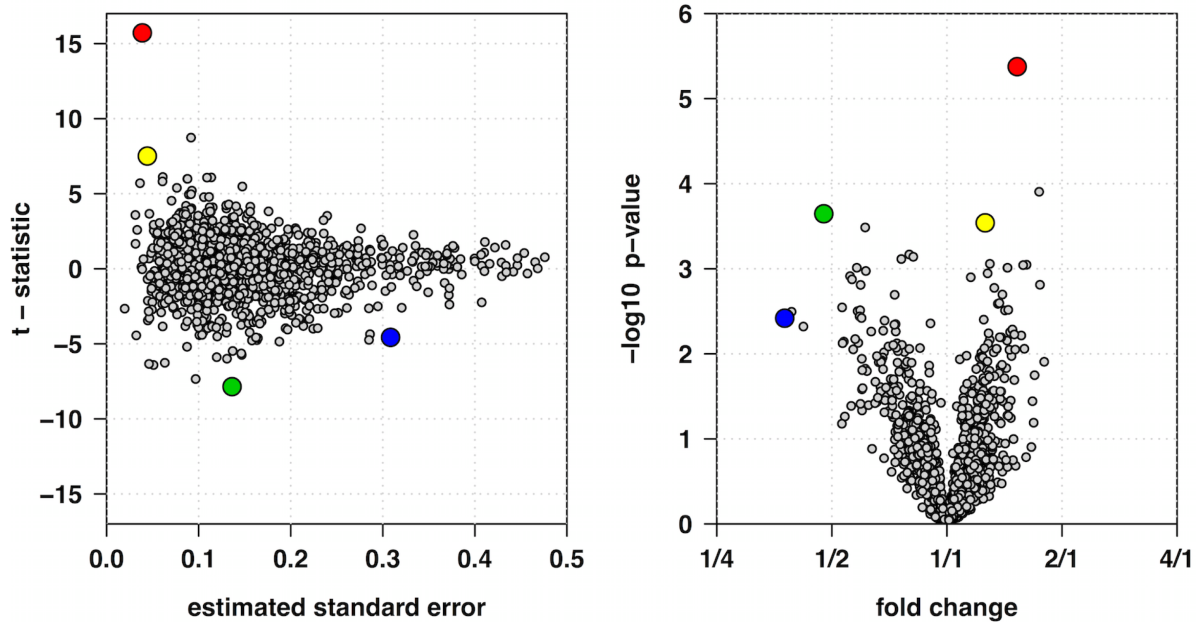
DATE	OPP	RESULT	AB	R	H	2B	3B	HR	RBI	BB	SO	SB	CS	OBP	SLG	OPS	AVG
Apr 1	@ NYY	W 8-2	5	1	3	0	0	0	1	0	1	0	0	.600	.600	1.200	.600
Apr 3	@ NYY	W 7-4	4	1	2	1	0	0	0	0	1	0	0	.556	.667	1.223	.556
Apr 4	@ NYY	L 4-2	3	0	2	0	0	0	0	0	0	0	0	.583	.667	1.250	.583
Apr 5	@ TOR	W 6-4	0	0	0	0	0	0	0	0	0	0	0	.615	.667	1.282	.583
Apr 6	@ TOR	L 5-0	Did not play														
Apr 7	@ TOR	W 13-0	5	1	2	1	0	0	0	0	1	0	0	.556	.647	1.203	.529
Apr 8	vs BAL	W 3-1	3	0	0	0	0	0	0	0	0	0	0	.476	.550	1.026	.450
Monthly Totals			20	3	9	2	0	0	1	0	3	0	0	.476	.550	1.026	.450

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- Assume that the **true** (unobservable) protein variances follow a scaled inverse χ^2 distribution:

$$\frac{1}{\sigma_p^2} \sim \frac{1}{d_0 \times s_0^2} \times \chi_{d_0}^2.$$

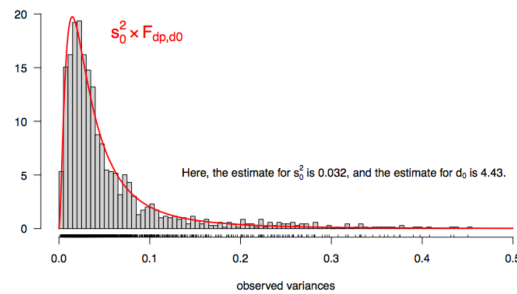
We estimate the parameters d_0 and s_0^2 later from the observed data.

- If the data for a particular protein are normally distributed with variance σ_p^2 , it follows for the observed sample variance that

$$s_p^2 | \sigma_p^2 \sim \frac{\sigma_p^2}{d_p} \times \chi_{d_p}^2,$$

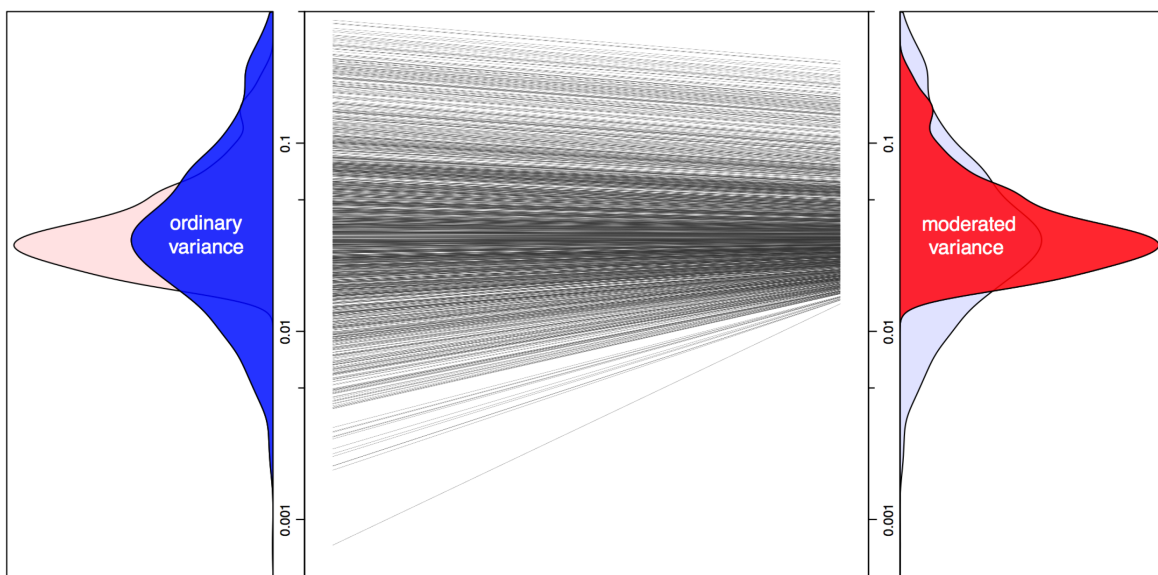
where d_p are the degrees of freedom associated with the experiment.

- This implies that the observed sample variances s^2 follow a scaled F distribution: $s^2 \sim s_0^2 \times F_{d_p, d_0}$.



- For the test statistics the observed variances are shrunk towards the prior values with the degree of shrinkage depending on the relative sizes of the observed and prior degrees of freedom:

$$s_p^2 \text{ [moderated] } = \frac{d_0 \times s_0^2 + d_p \times s_p^2}{d_0 + d_p}.$$

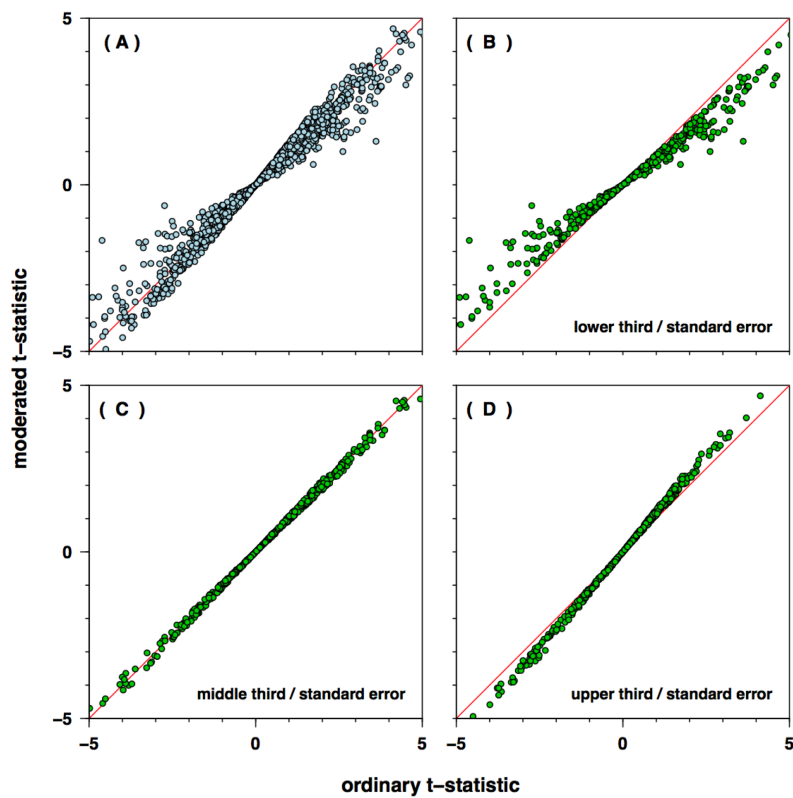


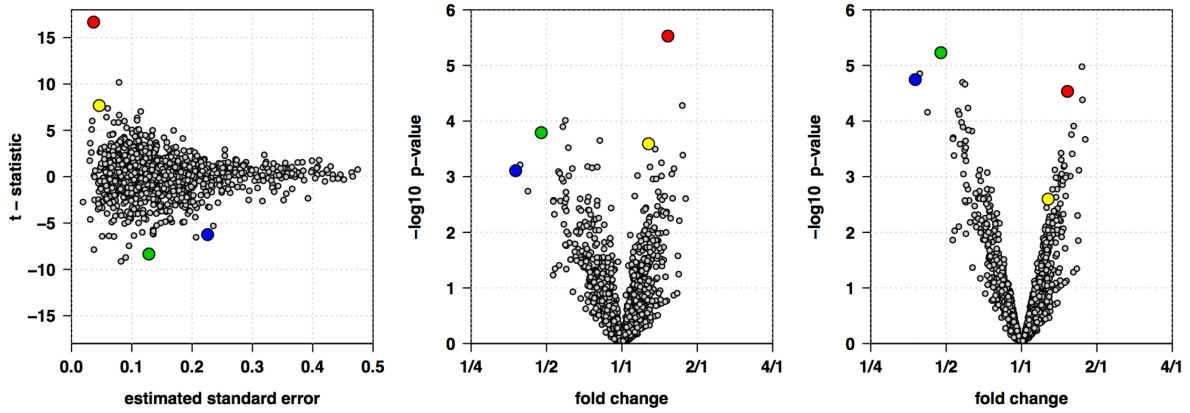
Ordinary t-statistic:

$$t_p = \frac{\text{estimated log fold change}}{\text{estimated standard error}} = \frac{\bar{X}_p - \bar{Y}_p}{s_p \sqrt{2/n}}$$

Moderated t-statistic:

$$t_{p[\text{moderated}]} = \frac{\text{estimated log fold change}}{\text{moderated standard error}} = \frac{\bar{X}_p - \bar{Y}_p}{s_{p[\text{moderated}]} \sqrt{2/n}}$$





At a false discovery rate control of 1% only 1 protein is declared differentially expressed when using ordinary t-statistics, compared to 23 proteins when moderated t-statistics are used.

FDR of 5%: 30 and 98 proteins, respectively; FDR of 10%: 120 and 184 proteins, respectively.

