P5.2 Statistics for Medicine

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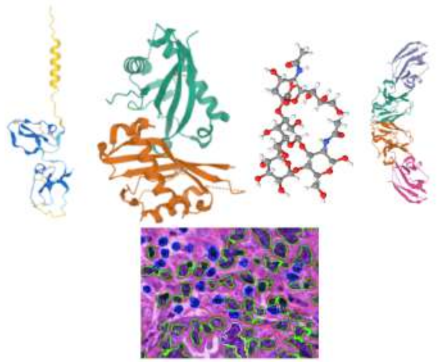
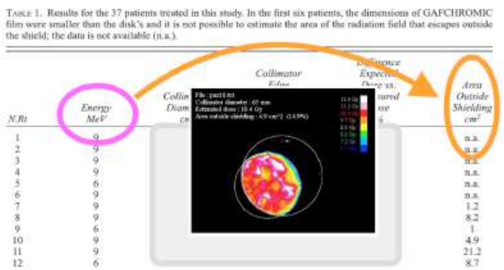
Recap /1

Recap /2

Our goal /1



Our goal /2



In vivo dosimetry and shielding disk alignment verification by EBT3 GAFCHROMIC film in breast IOERT treatment

Mara Severgnini,[1a] Mario de Denaro,[1] Marina Bortul,[2] Cristiana Vidali,[3]

TABLE 1. Results for the 37 patients treated in this study. In the first six patients, the dimensions of GAFCHROMIC film were smaller than the disk's and it is not possible to estimate the area of the radiation field that escapes outside the shield; the data is not available (n.a.).

N.Pt	Energy MeV	Area Outside Shielding cm^2
1	9	n.a.
2	9	n.a.
3	9	n.a.
4	9	n.a.
5	6	n.a.
6	9	n.a.
7	9	1.2
8	9	8.2
9	6	1
10	9	4.9
11	9	21.2
12	6	8.7

Today

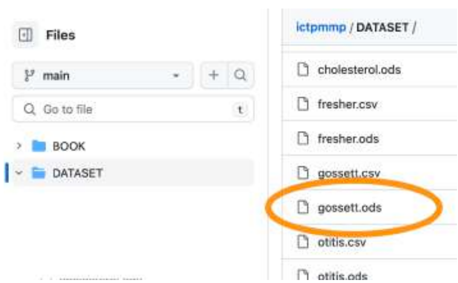
the **univariate** inferential analysis

classical - frequentist

bayesian

Monte Carlo - permutation

Today



1 the T test: the basics

Figure: William Sealy Gossett

Not Kiln-Dried	Kiln-Dried	Difference
1903	2009	+106
1935	1915	-20
1910	2011	+101
2496	2463	-33
2108	2180	+72
1961	1925	-36
2060	2122	+62
1444	1482	+38
1612	1542	-70
1316	1443	+127
1511	1535	+24

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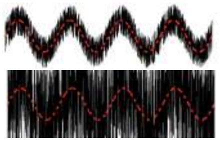
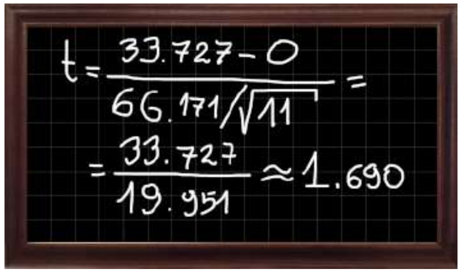


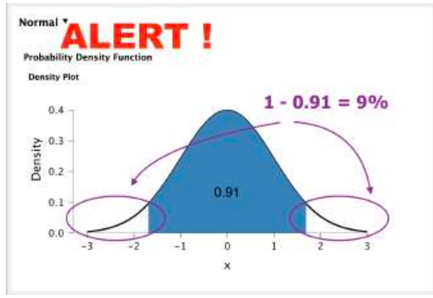
	difference
Valid	11
Mean	33.727
Std. Deviation	66.171
Std. Error of Mean	19.951

- Detecting a signal from noise

$$t = \frac{m - \mu}{s/\sqrt{n}}$$



Gosset discoveries /1



normal distribution does not work!

Gosset discoveries /2

$$t = \frac{m - \mu}{s/\sqrt{n}}$$

- (**independency**) in a random sample from a gaussian distribution $N(\mu, \sigma)$, estimating the sample mean m do not convey any information in estimating the sample standard deviation s, and vice versa.
- (**a novel random variable**) the random variable $t = \frac{m-\mu}{s/\sqrt{n}}$ possesses an explicit density function, which is not a gaussian, but can be numerically computed.

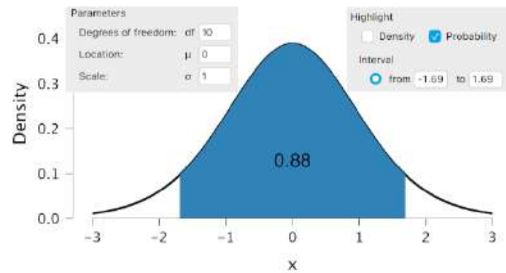
VOLUME VI MARCH, 1908 No. 1

BIOMETRIKA.

THE PROBABLE ERROR OF A MEAN.

BY STUDENT.

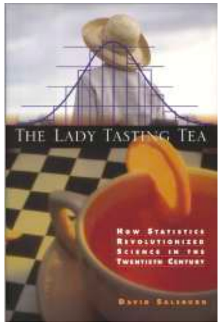
JASP: **Scaled Shifted Student's t**



JASP: **Classical** One Sample T-Test

Table: One Sample T-Test

	t	df	p
difference	1.690	10	0.122



JASP: **Classical** One Sample T-Test

Table: One Sample T-Test

	t	df	p
difference	1.690	10	0.122

Ronald Fisher's idea on significance level

1. The conventional significance level of 5%
2. The freedom to choose the significance level
3. significance level and sample size impact on the test power
4. statistical or clinical significance?
5. Absence of evidence, or evidence of absence?

JASP: **Classical** One Sample T-Test

Table: One Sample T-Test

	t	df	p
difference	1.690	10	0.122

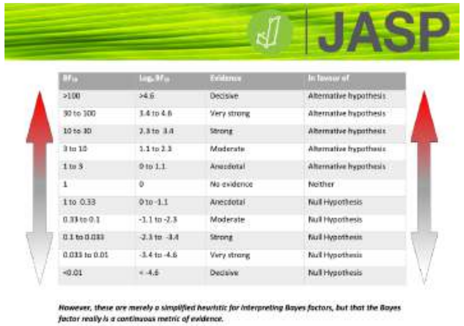
Table: Bayesian One Sample T-Test

	BF_{10}	error %
difference	0.885	0.004

Table: One Sample T-Test

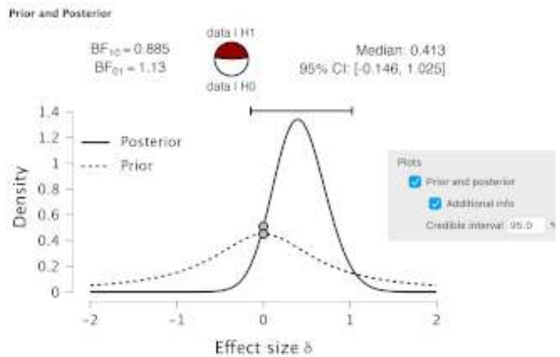
	t	df	p
difference	1.690	10	0.122

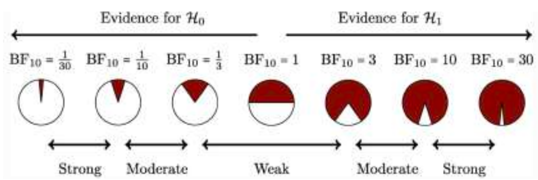
$$BF_{10} = \frac{P(D|M_1)}{P(D|M_0)} = 0.885$$



BF_{10}	$\log_e BF_{10}$	Evidence	In favour of
>100	>4.6	Decisive	Alternative hypothesis
30 to 100	3.4 to 4.6	Very strong	Alternative hypothesis
10 to 30	2.3 to 3.4	Strong	Alternative hypothesis
3 to 10	1.1 to 2.3	Moderate	Alternative hypothesis
1 to 3	0 to 1.1	Anecdotal	Alternative hypothesis
1	0	No evidence	Neither
1 to 0.33	0 to -1.1	Anecdotal	Null Hypothesis
0.33 to 0.1	-1.1 to -2.3	Moderate	Null Hypothesis
0.1 to 0.033	-2.3 to -3.4	Strong	Null Hypothesis
0.033 to 0.01	-3.4 to -4.6	Very strong	Null Hypothesis
<0.01	< -4.6	Decisive	Null Hypothesis

However, these are merely a simplified heuristic for interpreting Bayes factors, but that the Bayes factor really is a continuous metric of evidence.





In conclusion

A 2-sided Bayesian one-sample t-test comparing the sample population difference (m = 33.7) to the null mean ($\mu = 0$) returns a p-value = .122, not significant according an α level of 0.10. The BF_{01} of 0.885 suggests anecdotal evidence in favour of the alternative hypothesis: therefore the observed data are 1.13 times more likely to have occurred under the null than under the alternative hypothesis.

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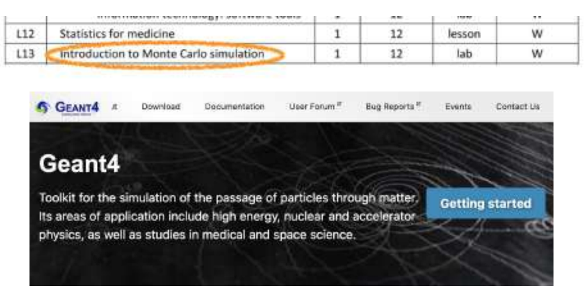
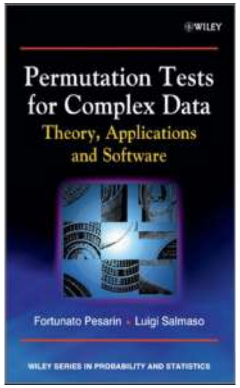
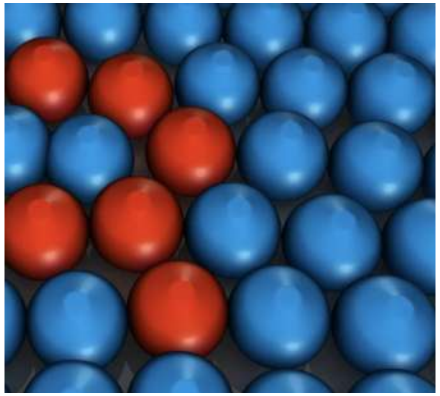
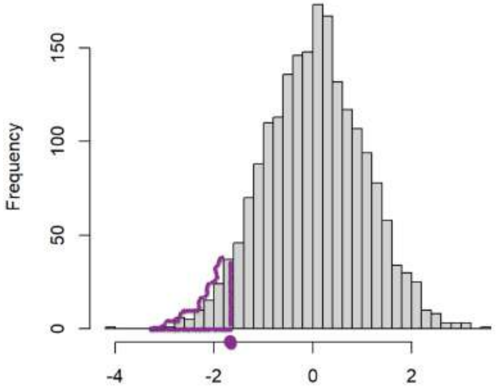






repetition	red mean	blue mean	test statistic
1	4.3	4.8	...
2	5.1	4.4	...
3	3.6	5.1	...
4	4.7	4.9	...
5	5.1	4.3	...
...		...	
1000000	4.4	4.8	...



Differences between two groups

the `roma` dataset

Variable	Level	Counts	Total	Proportion
Histology	benign	171	210	0.814
	malignant	39	210	0.186

- can we exploit `logHE4` to predict `Histology`?
- can we exploit `logCA125` to predict `Histology`?
- can we exploit `logCA19-9` to predict `Histology`?
- can we exploit `logCEA` to predict `Histology`?

Differences between two groups