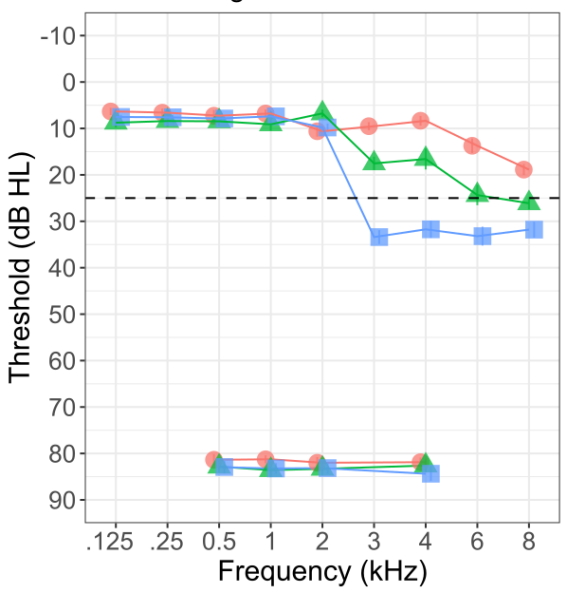
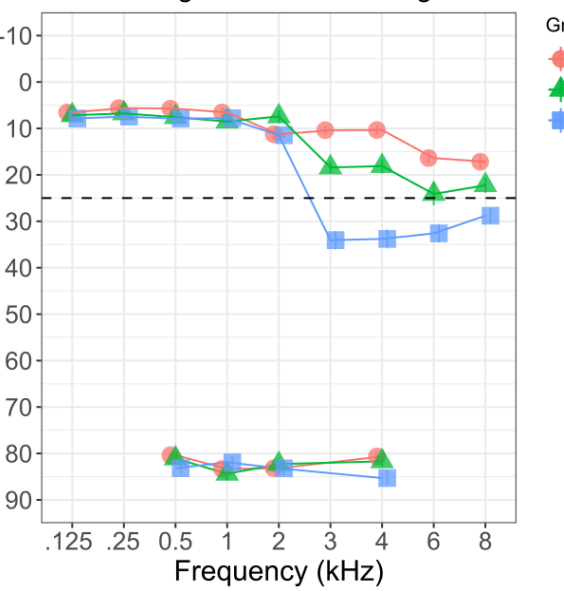


	A	B	C	D	E	F	G	H
1	ID	item.1	item.2	item.3	THI_1	THI_2	THI_3	THI_4
2	1	1	48	3	2	4	2	0
3	2	2	39	3	2	0	0	2
4	3	1	37	4	2	0	0	2
5	4	1	78	3	4	4	4	0
6	5	2	38	2	0	2	2	2
7	6	1	77	2	2	2	4	2
8	7	2	59	3	0	0	0	4
9	8	1	27	4	2	0	4	4
10	9	1	40	4	2	2	0	0
11	10	2	47	2	2	2	2	0
12	11	2	53	3	0	2	4	2
13	12	1	45	1	2	2	4	0
14	13	2	60	1	4	4	4	0
15	14	1	39	4	4	0	2	2
16	15	2	64	4	4	0	4	2
17	16	1	76	4	2	4	2	
18	17	2	40	4	4	2	4	
19	18	1	51	4	4	2	0	0
20	19	1	54	3	4	2	2	0

Audiogram with UCL - Left



Audiogram with UCL - Right



	M (N=25)	F (N=24)	Total (N=49)	p value
age				0.428
Mean (SD)	55.12 (16.48)	51.79 (12.29)	53.49 (14.53)	
Range	27.00 - 78.00	35.00 - 76.00	27.00 - 78.00	
hearing				0.352
No	3 (12.0%)	6 (25.0%)	9 (18.4%)	
Sometimes	9 (36.0%)	4 (16.7%)	13 (26.5%)	
Often	6 (24.0%)	8 (33.3%)	14 (28.6%)	
Always	7 (28.0%)	6 (25.0%)	13 (26.5%)	
THI score				0.179
Mean (SD)	52.40 (6.30)	49.67 (7.68)	51.06 (7.07)	
Range	42.00 - 66.00	34.00 - 60.00	34.00 - 66.00	

GitHub

https://github.com/NiklasEdvall/R_introduction

Varför ?

FAIR Principles

- **F**indability

Data och meta-data ska vara lätt att hitta och navigera för både människor och datorer.

- **A**ccessibility

Protokoll är tillgängliga, gratis och allmänt implementerbara.

- **I**nteroperability

Data kan användas och behandlas av program och system för analys, lagring och bearbetning.

- **R**euse

Data ska vara väl beskriven så den kan replikeras och/eller kombineras i olika miljöer/områden



Fördelar:

- + Alla har det
- + Lätt att mata in data

Nackdelar:

- Alla har det
- Ett minfält (sortera/filtrera/skiljetecken)
- Inget är spårbart
- Exempel: Gen-namn konverterade till datum


	Common name
BUB3	Mitotic checkpoint protein
CLOCK	clock circadian regulator
CSNK1E	casein kinase 1
EGF	epidermal growth factor
GH1	growth hormone 1
SST	somatostatin

04-Sep Septin 4

Autocorrect errors in Excel still creating genomics headache

Despite geneticists being warned about spreadsheet problems, 30% of published papers still contain mangled gene names in supplementary data.

Gene name errors are widespread in the scientific literature

Mark Ziemann, Yotam Eren & Assam El-Osta 

Genome Biology **17**, Article number: 177 (2016) | [Cite this article](#)


139k Accesses | **67** Citations | **3223** Altmetric | [Metrics](#)

Abstract

The spreadsheet software Microsoft Excel, when used with default settings, is known to convert gene names to dates and floating-point numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name conversions.

Excel: Why using Microsoft's tool caused Covid-19 results to be lost

By Leo Kelion
Technology desk editor

 5 October 2020



Graphpad Prism

- + Gör rimligt snygga figurer
- Dyrt



IBM SPSS

- + Ok script-språk (syntax)
- Rörig output
- Dyrt



SAS JMP

- + Ok script-språk
- Rörig output
- Dyrt



R



Rstudio



Python



Pandas

- + Gratis och lättillgängligt
- + Extremt flexibelt
- + Spårbarhet
- + Transparent
- + Reproducerbarhet
- + Lätt att dela
- + Datahantering + Statistik + Grafik
- Inlärningskurva

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