

P5.2 Statistics for Medicine

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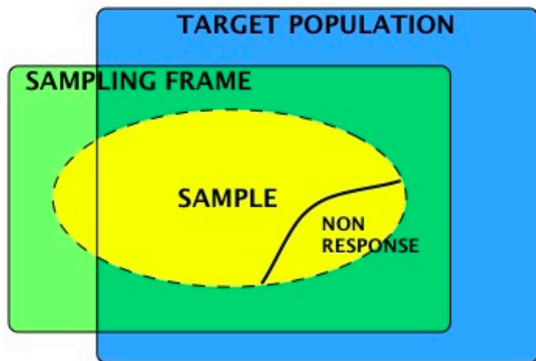


1 Inference



<https://ictpmmp.weebly.com/lecture-notes.html>

what about inference



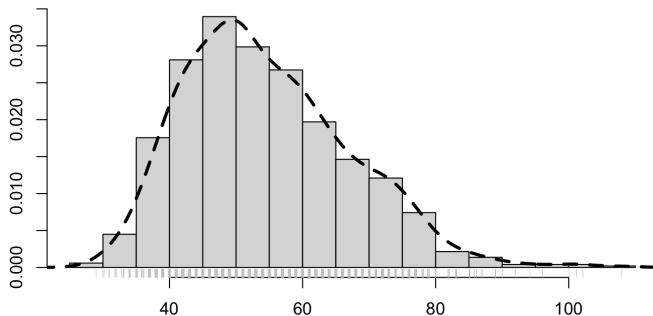
<https://ictpmmp.weebly.com/lecture-notes.html>

Mismatching variability with reliability

Dispersion

- | | |
|---------------------------------------------------|---------------------------------------------------|
| <input checked="" type="checkbox"/> S.E.mean | <input checked="" type="checkbox"/> Std.deviation |
| <input type="checkbox"/> Coefficient of Variation | <input type="checkbox"/> MAD |
| <input type="checkbox"/> MAD Robust | <input type="checkbox"/> IQR |
| <input type="checkbox"/> Variance | <input type="checkbox"/> Range |
| <input type="checkbox"/> Minimum | <input type="checkbox"/> Maximum |

Mismatching variability with reliability



<https://ictpmmp.weebly.com/lecture-notes.html>

Mismatching variability with reliability

```

Cleared...
> sample(data$HDLchol, 49)
[1] 43 53 46 59 54 48 65 42 45 70 72 51 70 37 38 54 41 57 57 44 76 45 50 46 53
[26] 55 55 68 53 67 48 54 63 39 64 60 63 61 43 70 72 50 42 38 33 49 46 41 63

> memory = numeric(1000); for(i in 1:1000) { memory[i] =
  mean(sample(data$HDLchol, 49)) }

> mean(memory)
[1] 54.64218

> sd(memory)
[1] 1.713793

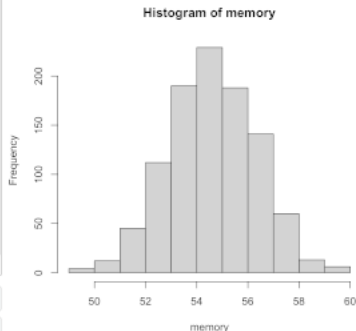
> sd(data$HDLchol)/7
[1] 1.778389

```

```
hist(memory)
```

Run Code

Clear Output



<https://ictpmmp.weebly.com/lecture-notes.html>

Mismatching variability with reliability

$$\frac{\sigma}{\sqrt{n}}$$

	HDLchol
Valid	1025
Mean	54.685
Std. Error of Mean	0.387
Std. Deviation	12.392

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Mismatching variability with reliability



Yu-Kang Tu and Mark Gilthorpe.

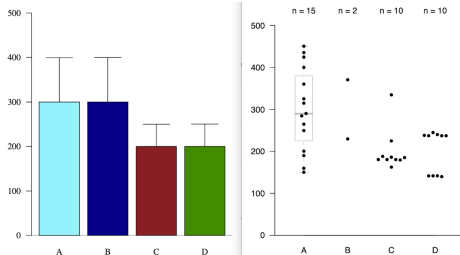
The most dangerous hospital or the most dangerous equation?

<https://bmchealthservres.biomedcentral.com/articles/10.1186/1472-6963-7-185>

<https://ictpmmp.weebly.com/lecture-notes.html>

Mismatching variability with reliability

transfected endothelial cells. **C** shows migration assay for control *igcz* and *robo4* siRNA transfected cells to Serum or AP-Slit2N in either upper (U), lower (L) or both chambers as indicated. Error bars in **A** ($n = 3$), and **B** ($n = 3$) represent SD while in **C** represent SEM ($n = 4$). **D** shows pull-down analysis of Cdc42-GTP levels in AP and AP-Slit2N (25 ng/ml) transfected endothelial cell lysates for 5 and 15 minutes respectively. \pm indicates



Tatsuki Koyama.

Beware of Dynamite

<https://biostat.app.vumc.org/wiki/pub/Main/TatsukiRcode/Poster3.pdf>