

Biostatistics BT2023

Lecture 5: Measure of central tendency

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Computer virus

How powerful computer and the program that runs these computers!

Just a few lines code can effect our lives in so many ways.

Examples

Story of Stuxnet

Power grid failure in Mumbai

Organization of the class

Biostatistics: The journal

Among the important scientific developments of the 20th century is the explosive growth in statistical reasoning and methods for application to studies of human health.

Examples include developments in likelihood methods for inference, epidemiologic statistics, clinical trials, survival analysis, and statistical genetics.

Substantive problems in public health and biomedical research have fueled the development of statistical methods, which in turn have improved our ability to draw valid inferences from data.

The objective of Biostatistics is to advance statistical science and its application to problems of human health and disease, with the ultimate goal of advancing the public's health.

Biostatistics is an online only journal publishing papers that develop innovative statistical methods with applications to the understanding of human health and disease, including basic biomedical sciences.

Papers should focus on methods and applications.

Introduction of original methodology should be grounded in substantive problems; there is the opportunity to present extensive analyses of data on the journal's website as supplementary material.

Authors are strongly encouraged to submit code supporting their publications. Authors should submit a link to a Github repository and to a specific example of the code on a code archiving service such as Figshare or Zenodo.

Reference: Oxford university press



Goal

Advancing health science research, education, and practice by turning data into knowledge and addressing the greatest public health issues of the 21st century.



Biostatistics department of Harvard university



Measure of central tendency

Example: the average height of the students in class

Arithmetical mean

$$\bar{x} = \sum_{i=1}^{n} x_i$$

Arithmetical mean of a grouped data

$$\bar{x} = \frac{\sum_{i=1}^{n} f_i x_i}{\sum_{i=1}^{n} f_i} = \frac{\sum_{i=1}^{n} f_i x_i}{N}$$



Arithmetical mean by transformation

X

$$y = ax$$
 ; $= a$

$$y = a + x$$
; $< y > = a + < x >$

$$y = a + cx$$
; $= a + c$

We can use above transformation to calculate mean by what is called "step deviation method"

	^	u
$\sum_{i=1}^{n} f_i d_i$	45	-25
$\bar{x} = a + \frac{\sum_{i=1}^{n} f_i d_i}{\sum_{i=1}^{n} f_i}$	5 0	-20
$ \angle i = 1 Ji $	60	-10
d = x - a	67	-3
a = provisional mean $\bar{x} = 70 + \frac{1}{8} = 70.125$	74	4
a = provisional mean $x = 70 + \frac{1}{8} = 70.125$		10
<pre>// I = common size of class interval</pre>	90	20



Mean for continuous data

Class	Interval
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-22

$\bar{x} = a + l \times \frac{\sum_{i=1}^{n} f_i d_i'}{\sum_{i=1}^{n} f_i}$	d _i ′f _i	$\mathbf{d_{i}'} = \frac{d_i}{l}$ $= \frac{d_i}{8}$	d _i = m _i - a = m _i - 28	Frequency (f _i)	Class Mark (m _i)	Class Intervals
$\angle i=1 Ji$	-30	-3	-24	10	4	0 - 8
$d_{i}^{'}=d_{i}/l$	-40	-2	-16	20	12	8 - 16
	-14	-1	-8	14	20	16 - 24
$28 + 8 \times \frac{-22}{100} = 26.24$	0	0	0	16	28	24 - 32
100	18	1	8	18	36	32 - 40
Its approximation since w	44	2	16	22	44	40 - 48
don't know the raw data	$\sum {d_i}' f_i =$			$\sum f_i = 100$		

nation since we v the raw data



Median

Arrange the data (n) in the ascending order

$$Median = rac{N^{\,th}}{2} term$$
 N= odd

$$Median = \frac{\frac{N}{2}^{th} + (\frac{N}{2} + 1)^{th}terms}{2} \qquad \text{N= even}$$

45. 50. 56 57 74 80 90 95



Mode

The highest frequency data point in the data set

Mark obtained

$$Mode = 4$$

Mode of Grouped Data = L + W[(Fm - F1)/((Fm-F1) + (Fm - F2))]

Range	Frequency
1-10	2
11-20	7
21-30	10
31-40	3
41-50	1

$$L = 21$$

$$W = 9$$

$$Mode = 24$$

$$F = 10$$

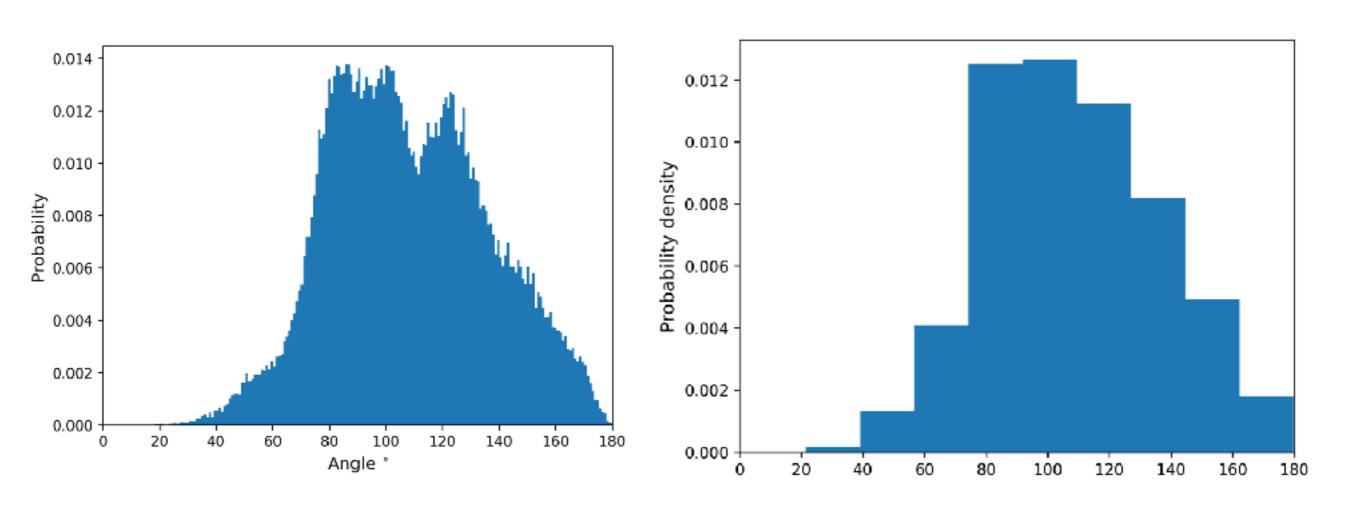
$$F1 = 7$$

$$F2 = 3$$



Histogram

Plot of the probability distribution



How to chose the bin



Useful commands in data analysis bioinformatics SED

sed -e 's/\(.*\)/\L\1/'

pr mts

pr -mts' ' coll.dat col2.dat >combine.dat

grep

grep -A1 'blah' logfile

Awk

column to row

row to column

awk '{for (i=1;i<=NF;i++) print \$i}' 2.dat >22.dat

Introduction to "github"

GitHub is a website for developers and programmers to collaboratively work on code



Next Class

2:30 PM Friday, 23 August 2022

Measure of dispersions