Statistics Applied to Economics

Degree in Economics

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Content I

Poisson probability function

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How do we get last expression from the previous one?

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Using a Taylor series expansion $e^t = 1 + t + t^2/2! + t^3/3! + \ldots$

Historical notes

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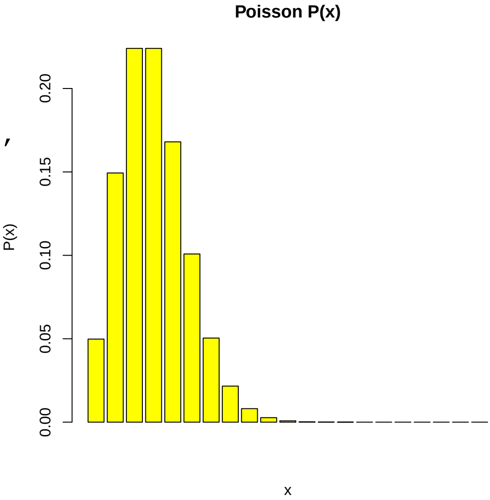
- See `http://en.wikipedia.org/wiki/Siméon_Denis_Poisson`.

What does it look like?

```
> x <- 0:1
> dpois(x,lambda=3)
[1] 0.04978707 0.14936121
> x <- 0:20
> barplot(dpois(x,lambda=3),
          col="yellow",
          xlab="x",
          ylab="P(x)",
          main="Poisson P(x)")
```



Moment generating function

$$\varphi_X(u) \overset{\text{def}}{=} E[e^{uX}] \quad = \quad \sum_{x=0}^{\infty} e^{ux} P_X(x) = \sum_{x=0}^{\infty} e^{ux} \frac{e^{-\lambda}\lambda^x}{x!} \tag{1}$$

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\end{aligned}
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&= \sum_{x=0}^{\infty} \frac{e^{-\lambda}(\lambda e^u)^x}{x!} \\
&= e^{-\lambda} \sum_{x=0}^{\infty} \frac{(\lambda e^u)^x}{x!} \qquad (1)
\end{aligned}
$$

$$(2)$$

Moment generating function

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&= \sum_{x=0}^{\infty} \frac{e^{-\lambda}(\lambda e^{u})^{x}}{x!} \nonumber \\
&= e^{-\lambda} \sum_{x=0}^{\infty} \frac{(\lambda e^{u})^{x}}{x!} \tag{1} \\
&= e^{-\lambda} e^{\lambda e^{u}} \tag{2} \\
& \tag{3}
\end{align}
$$

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&= e^{-\lambda} \sum_{x=0}^{\infty} \frac{(\lambda e^u)^x}{x!} && (1) \\
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How do we get (2) from (1) above?

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Yet another use of $e^t = 1 + t + t^2/2! + t^3/3! + \ldots$.

Mean and variance

- Remember:

$$\alpha_1 = \left[\frac{\partial \varphi_X(u)}{\partial u} \right]_{u=0} \qquad \alpha_2 = \left[\frac{\partial^2 \varphi_X(u)}{\partial u^2} \right]_{u=0}$$

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How to obtain the variance from $\alpha_1 = E[X]$ and $\alpha_2 = E[X^2]$?

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$m = \alpha_1 = \lambda$ and $\sigma^2 = \alpha_2 - (\alpha_1)^2 = \lambda$.

Sum of independent Poisson variables

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and we recognize in the last expression the mgf of a Poisson random variable with $\lambda = \lambda_1 + \ldots + \lambda_n$.

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Would *the average* of $X_1, \ldots, X_n$ be Poisson-distributed?

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No, $\varphi_{\overline{X}}(u) = e^{(\lambda_1+\ldots+\lambda_n)(e^{u/n}-1)}$ which is **not** the mgf of a Poisson.

Poisson as a limit of the binomial

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Remember what additional condition was required on $\varphi_Z(u)$?

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It has to be continuous $u = 0$.

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What problems would you anticipate calculating $P_X(x)$?

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Large factorials might be the only problem ($69! = 1.711225 \times 10^{98}$).

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  so each probability can be obtained from the previous multiplying by $\frac{\lambda}{x}$. (First one, $P_X(0;\lambda) = e^{-\lambda}$.)

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- Avoids large factorials.

Practical use of the limiting distribution (III)

```
> dbinom(x=2,size=50,prob=0.1)          # Exact binomial
[1] 0.0779429
> dpois(x=2,lambda=50*0.1)              # Poisson approxi
[1] 0.08422434
> pnorm((2.5-5)/sqrt(50*0.1*.9)) - pnorm((1.5-5)/sqrt(
[1] 0.06981634
> dbinom(x=2,size=500,prob=0.01)        # Exact binomial
[1] 0.08363103
> dpois(x=2,lambda=500*0.01)            # Poisson approxi
[1] 0.08422434
> pnorm((2.5-5)/sqrt(500*0.01*.99)) - pnorm((1.5-5)/sq
[1] 0.07273327
```

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- Many units, n, with small probability p of failure, and $np < 18$ give a Poisson-distributed number of units failing.

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  - Many soldiers, small probability of dying by horse kick $\Rightarrow$ number of soldiers dead approximately Poisson-distributed.
  - Many phone lines, small probability of one of them being in use $\Rightarrow$ simultaneaous calls placed at any one moment Poisson-distributed.
  - Many houses insured against fire, small probability of any of them catching fire in the insurance period $\Rightarrow$ total number of claims in that period Poisson-distributed.

The “rare events” model

- Many units, n, with small probability p of failure, and $np < 18$ give a Poisson-distributed number of units failing.
- Examples:
  - Many soldiers, small probability of dying by horse kick $\Rightarrow$ number of soldiers dead approximately Poisson-distributed.
  - Many phone lines, small probability of one of them being in use $\Rightarrow$ simultaneaous calls placed at any one moment Poisson-distributed.
  - Many houses insured against fire, small probability of any of them catching fire in the insurance period $\Rightarrow$ total number of claims in that period Poisson-distributed.
  - Arrival intervals i.i.d. exponentially distributed, $f_X(x) = \theta e^{-\theta x} \Rightarrow$ total number of arrivals in $(T, T+t)$ Poisson-distributed with $(T, T+t)$ Poisson-distributed with $\lambda = \theta t$.

Example 1 (I)

Consider a company with 120 workers. On average, they spend 10% of their time calling to the outside. They place calls independently of each other.

- What is the mean value of the number of people simultaneously calling outside?

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- What are your conclusions? Is it better to provide a centralized service or not?

Example 1 (II)

- What is the mean value of the number of people simultaneously calling outside?
- If there are 16 outgoing phone lines, what is the probability of being able to service all calls?
- Two divisions, respectively 80 and 40 people and 10 and 6 lines. Probability of being able to service all calls?

```
> 120 * 0.1
[1] 12
> #
> ppois(16,lambda=12)
[1] 0.898709
> #
> ppois(10,80*0.1) *
   ppois(6,40*0.1)
[1] 0.7255885
```

Example 2

Your are auditing a company. They claim high quality of their records, with a proportion of 0.1% at most containing errors. You screen 4000 records, uncovering 6 mistakes (i.e., a proportion of 0.15%, or 50% larger than their alleged error rate). What would you conclude about the veracity of their claims?

- Assuming their claims are right, total number of errors in 4000 records Poisson distributed, with $\lambda = 4000 \times 0.001 = 4$ in the worst case.
- If $\lambda = 4$, the probability of over 5 errors is

  ```
  > 1 - ppois(5,lambda=4)
  [1] 0.2148696
  ```

  which is by no means small.
- There is no conclusive evidence to challenge their claim: with $\lambda = 4$, 6 errors out of 4000 records is by no means abnormal.

Example 3

Five hundred school children enjoy recreation. The probability that any of them injures himself and comes to the infirmary of the school to have a wound bandaged is $p = 0.01$. How many bandages must the infirmary stock at the beginning of the day so that the probability of running out is less than 0.001?

- The number of children injured is distributed as $\mathcal{P}(\lambda = 5)$.
- Bandages required are less than or equal

  ```
  > qpois(0.999,lambda=5)
  [1] 13
  ```

  with probability 0.999, so enough to stock 13.
- Let's check:

  ```
  > 1 - ppois(12:13,lambda=5)
  [1] 0.002018852 0.000697990
  ```

  We see indeed that 12 would not be enough and 13 is.

Example 4

The probability of a type of cancer in children of school age is 0.001 per children-year (=1 out of 1000 children on the average). You are suspicious of the mobile phone antennas erected in the vicinity of your district public shool, and find out that out of 400 children, 3 have contracted the disease. Is that an abnormal incidence rate?

- The number of cancer cases is distributed as $\mathcal{P}(\lambda = 0.4)$.
- The probability of less than or equal to 0, 1, 2, 3, 4 cases is:

  ```
  > ppois(0:4,lambda=0.4)
  [1] 0.6703200 0.9384481 0.9920737 0.9992237 0.
  ```

  so 3 cases is fairly rare, happening by pure chance less than 1% of the time.

Example 4 (continued)

Setup like of the previous example. You collect data on all 1300 schools with 400 children each within 200m of mobile phone antennas. Have 540 cases of cancer in all, worst one alone had 4 cases. What would you say?

- Total number of cases is $\mathcal{P}(\lambda = 0.4 \times 1300)$. Then,

  ```
  > 1 - ppois(539,lambda=1300*0.4)
  [1] 0.1956853
  ```

  doesn't look abnormal; expected about 19% of the time.
- The school with 4 cases does look abnormal *in isolation:*

  ```
  > 1 - ppois(3,lambda=0.4)
  [1] 0.0007762514
  ```

- As the worst case among the 1300 schools examined, it can no longer be considered abnormal:

  ```
  > 1 - ( ppois(3,lambda=0.4) )^1300
  [1] 0.6356057
  ```

Reminder of some useful relationships

- $b(p,n) \xrightarrow{d} \mathcal{P}(\lambda = np)$ as $n \to \infty$ with $np < 18$.

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- $\mathcal{P}(\lambda) \xrightarrow{d} N(\lambda, \lambda)$ as $\lambda \to \infty$.
- If $Z_n \sim b(p, n)$, then $Z_n/n \xrightarrow{p} p$ as $n \to \infty$.

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- . . .or the rudiments of music before you can play piano.
- *The roots of knowledge are bitter, but the fruit is very sweet* (Rabindranath Tagore)

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How do you think $\Gamma(r)$ changes with r?

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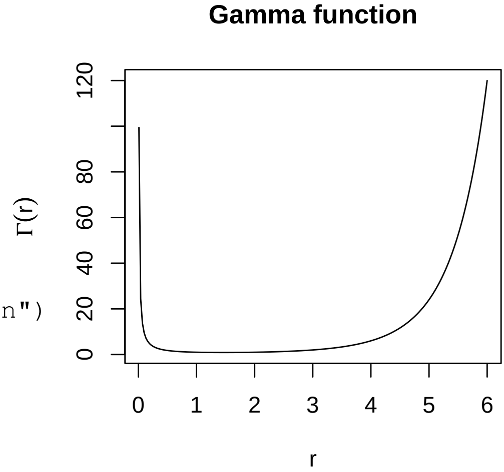
Clearly, $\Gamma(r) \to \infty$ as $r \to \infty$, but also as $r \to 0$.

$\Gamma(r)$ in R

```
> gamma(5)
[1] 24
> factorial(4)
[1] 24
> curve(gamma,from=0.01,
       to=6,n=200,
       ylab=expression(
             Gamma(r)
            ),
       xlab="r",
       main="Gamma function")
```



The gamma distribution $\gamma(a, r)$ (I).

- It is clear that

$$F_X(x) = \frac{1}{\Gamma(r)} \int_0^x t^{r-1} e^{-t} dt$$

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- Density function therefore is:

$$f_X(x) = \frac{a^r}{\Gamma(r)} t^{r-1} e^{-at}$$

The gamma distribution $\gamma(a, r)$ (II).

- Alternative parameterizations:

$$\begin{aligned} f_X(x) &= \frac{a^r}{\Gamma(r)} t^{r-1} e^{-at} \\ f_X(x) &= \frac{1}{\Gamma(r) s^r} t^{r-1} e^{-t/s} \end{aligned}$$

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- …although you will rarely use the $\gamma(a, r)$ directly.

The gamma distribution $\gamma(a, r)$ in R

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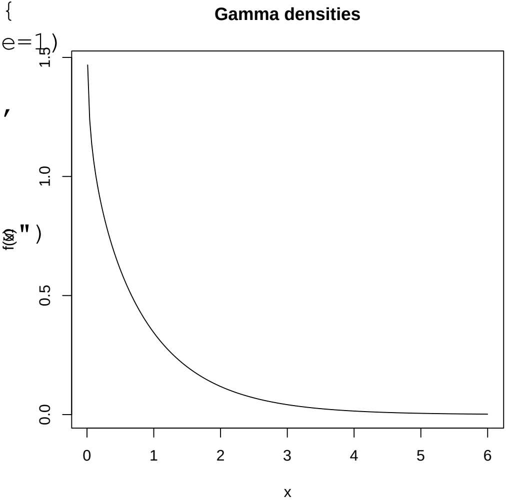
- In either case, r is the “shape” parameter and a the “rate” (or s is the “scale”) parameter.
- Only one of rate or scale needs to be specified.

What does the $\gamma(a, r)$ look like? (I)

```
> gammar0.9 <- function(x) {
   dgamma(x,shape=0.9,scale=1)
   }
> curve(gammar0.9,from=0.01,
      to=6,n=200,
      ylab="f(x)",
      xlab="x",
      main="Gamma densities")
```



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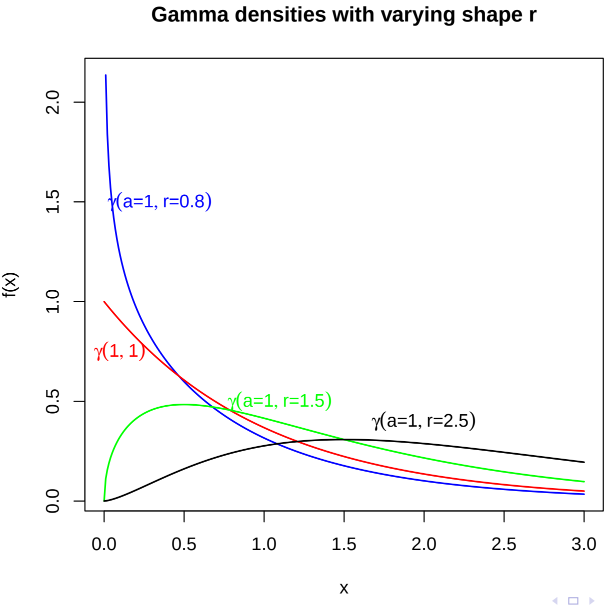

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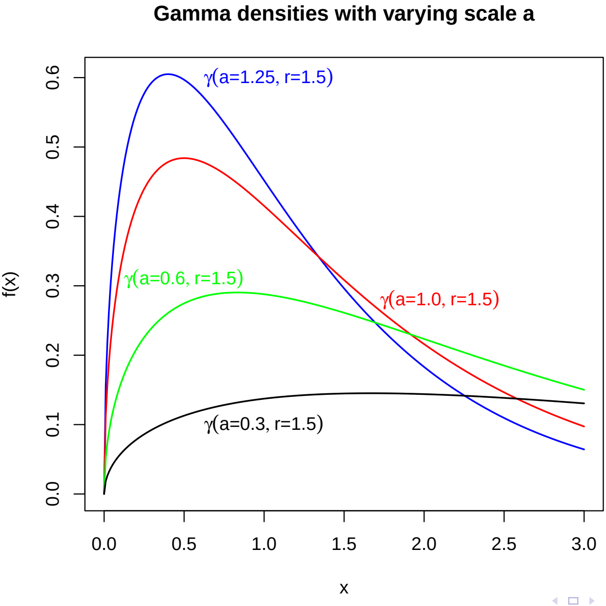

Moment generating function of the $\gamma(a, r)$ (I).

$$\varphi_X(u) \quad = \quad E[e^{uX}] = \int_o^\infty \frac{a^r}{\Gamma(r)} x^{r-1} e^{-ax} e^{ux} dx$$

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&= \frac{a^r}{\Gamma(r)} \left[\frac{(a-u)^r}{\Gamma(r)} \right]^{-1}
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&= \left(1 - \frac{u}{a} \right)^{-r}
\end{aligned}$$

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See how the integral went away?

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It is equal to content within brackets in next-to-last expression.

Moment generating function of the $\gamma(a, r)$ (II).

- Let $X = X_1 + \ldots + X_n$ independent gamma random variables with equal scale parameter and respectively $r_1, \ldots, r_n$ as shape parameter. Then:

  $$\begin{aligned} \varphi_X(u) &= \left(1 - \frac{u}{a}\right)^{-r_1} \cdots \left(1 - \frac{u}{a}\right)^{-r_n} \\ &= \left(1 - \frac{u}{a}\right)^{-(r_1 + \ldots + r_n)} \end{aligned}$$

  so X is $\gamma(a, r_1 + \ldots + r_n)$ distributed.

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- The same does not hold if the scale parameters are not equal.

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- Let $Y = cX$ with $X \sim \gamma(a, r)$. Then $Y \sim \gamma(a/c, r)$.

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Moment generating function of the $\gamma(a, r)$ (III).

- Let $Y = cX$ with $X \sim \gamma(a, r)$. Then $Y \sim \gamma(a/c, r)$.
- Simple rescaling of a gamma gives again a gamma with arbitrary first parameter.
- Proof is trivial:

$$\begin{aligned}\varphi_{cX}(u) &= E[e^{ucX}] = \varphi_X(cu) \\ &= \left(1 - \frac{cu}{a}\right)^{-r} \\ &= \left(1 - \frac{u}{a/c}\right)^{-r}\end{aligned}$$

so cX is $\gamma(a/c, r)$ distributed.

Mean and variance of $\gamma(a, r)$.

- Mean and variance are now easy to compute:

$$\begin{aligned}
\left[\varphi'_X(u)\right]_{u=0} &= \left[-r\left(1-\frac{u}{a}\right)^{-r-1}\left(-\frac{1}{a}\right)\right]_{u=0} \\
&= \frac{r}{a} \\
\left[\varphi''_X(u)\right]_{u=0} &= \left[r(r+1)\left(1-\frac{u}{a}\right)^{-r-2}\left(-\frac{1}{a}\right)^2\right]_{u=0} \\
&= \frac{r^2}{a^2}+\frac{r}{a^2}
\end{aligned}$$

Hence, $m = r/a$ and $\sigma^2 = \alpha_2 - (\alpha_1)^2 = r/a^2$.

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  Hence, $m = r/a$ and $\sigma^2 = \alpha_2 - (\alpha_1)^2 = r/a^2$.
- It can also be checked that the mode is at $\frac{r-1}{a}$ (or zero, in case $r < 1$ and monotone decreasing density).

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How would you choose $\gamma(a, r)$ with mean 2 and variance 5?

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Matching moments.

Exponential distribution $\exp(\lambda)$ (I)

- A very important particular case occurs when $r = 1$. Then,

$$\gamma(a, r = 1) \quad = \quad \frac{a^r}{\Gamma(r)} x^{r-1} e^{-ax} = a e^{-ax}$$

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- Clearly, $F_X(x) = 1 - e^{-\lambda x}$.

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- The moment generating function comes straight from the $\gamma(a = \lambda, r = 1)$ general case:

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We get a variable distributed as $\gamma(\lambda, n)$.

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- Therefore $F_Y(y) = \Phi(\sqrt{y}) - \Phi(-\sqrt{y})$, and

$$\begin{aligned} f_Y(y) &= \phi(\sqrt{y}) \times \frac{1}{2\sqrt{y}} - \phi(-\sqrt{y}) \times \left(-\frac{1}{2\sqrt{y}}\right) \\ &= \phi(\sqrt{y})\frac{1}{\sqrt{y}} \\ &= \frac{1}{\sqrt{2\pi}} y^{-1/2} e^{-\frac{y}{2}} \qquad\qquad (y > 0) \end{aligned}$$

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What density is this a particular case of?

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It is clearly a $\gamma(a = \frac{1}{2}, r = \frac{1}{2})$.

Things you can easily check:

- If Y is square-normal, $E[Y] = 1$.
  (Try it both ways, using the "gamma ancestry" of Y and the direct approach: remember $Y = X^2$ and $X \sim N(0, 1)$).

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- If X is exponential(λ), $2\lambda X$ is $\gamma(\frac{1}{2}, 1)$.
- Mimic the method used to derive the square-normal density to find the log-normal density, i.e., the density of Y such that $\log_e(Y)$ is normal.

The χ_n^2 distribution

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- n usually called “degrees of freedom”.

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$$f_X(x) = \frac{\left(\frac{1}{2}\right)^{\frac{n}{2}}}{\Gamma\left(\frac{n}{2}\right)} x^{\frac{n}{2}-1} e^{-x/2}$$

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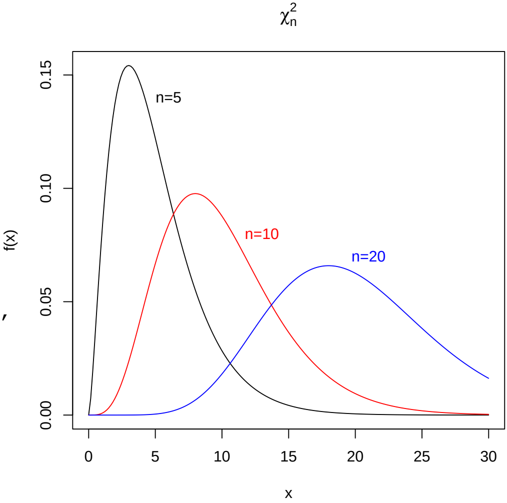
$\chi^2_n \xrightarrow{\mathrm{d}} N(n, 2n)$ by the CLT.

What does it look like? (II)

```
> chisqn <- function(x) {
     dchisq(x,df=n)
   }
> n <- 5
> curve(chisqn,
   from=0.0,to=30,n=200,
   ylab="f(x)",xlab="x",
   main=expression(chi[n]^2))
> n <- 10
> curve(chisqn,from=0.0,col="red",
       to=30,n=200,add=TRUE)
> n <- 20
> curve(chisqn,from=0.0,col="blue",
       to=30,n=200,add=TRUE)
> text(6,0.14,"n=5")
> text(13,0.08,"n=10",col="red")
> text(21,0.07,"n=20",col="blue")
```



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- $\delta = m_1^2 + \ldots + m_n^2$ is the so-called “non-centrality parameter”.
- Some tables/books define the non-centrality parameter as $\delta = \frac{1}{2}(m_1^2 + \ldots + m_n^2)$, so check.

χ^2_n in R

Usual set of functions: `{d,p,q,r}chisq`.

```
>     dchisq(15.3,12)
[1] 0.05196885
>     pchisq(15.3,12)
[1] 0.7745611
>     qchisq(0.99,12)
[1] 26.21697
>     qchisq(0.99,12,ncp=15)
[1] 52.15618
```

Snedecor's $\mathcal{F}_{m,n}$

- The ratio of two χ^2_m and χ^2_n independent of each other each divided by their degrees of freedom,

  $$\frac{\chi^2_m/m}{\chi^2_n/n}$$

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  follows a distribution named "Snedecor's $\mathcal{F}_{m,n}$" (after George W. Snedecor (1882 -1974)).
- Fairly complex density,

  $$f_X(x) = \frac{m^{\frac{m}{2}} n^{\frac{n}{2}} \Gamma\left(\frac{m+n}{2}\right)}{\Gamma\left(\frac{m}{2}\right) \Gamma\left(\frac{n}{2}\right)} x^{m/2-1} (n + mx)^{-(n+n)/2}$$

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- For $n > 2$, $m = n/(n-2)$ if $n > 2$ and for $n > 4$,

  $$\sigma^2 = \frac{2n^2(m+n-2)}{m(n-2)^2(n-4)}$$

Use of tables for $\mathcal{F}_{m,n}$

- Same as we did not need tables of $b(p, n)$ for $p > 0.5$, we can do with tables for the $\mathcal{F}_{m,n}$ for $\alpha < 0.5$ and obtain the rest indirectly.

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- Same as we did not need tables of $b(p, n)$ for $p > 0.5$, we can do with tables for the $\mathcal{F}_{m,n}$ for $\alpha < 0.5$ and obtain the rest indirectly.
- If $X \sim \mathcal{F}_{m,n}$, trick is to use

$$\begin{aligned} 1 - \alpha = P(X < \mathcal{F}^{\alpha}_{m,n}) &= P\left(\frac{\chi^2_m/m}{\chi^2_n/n} < \mathcal{F}^{\alpha}_{m,n}\right) \\ &= P\left(\frac{\chi^2_n/n}{\chi^2_m/m} > \frac{1}{\mathcal{F}^{\alpha}_{m,n}}\right) \end{aligned}$$

This shows,

$$\frac{1}{\mathcal{F}^{\alpha}_{m,n}} = \mathcal{F}^{1-\alpha}_{n,m}$$

Non-central versions of $\mathcal{F}_{m,n}$

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- Tables in general for only the ordinary or central case.

$\mathcal{F}_{m,n}$ in R

As usual, `{d,p,q,r}f` functions.

```
> pf(3.23, 5, 12)      # Prob left 3.23 in F(5;12)
[1] 0.9554027
> qf(0.95, 5, 12)      # Value leaving a tail of 0.
[1] 3.105875
> qf(0.99, 5, 12)      # Id. for tail of 0.01
[1] 5.064343
> qf(0.99, 5, 12, 8)   # Id. for a non-central F
[1] 11.62582
>                      # with ncp=8
```

What does the $\mathcal{F}_{m,n}$ look like? (I)

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- If both m and n large, closely concentrated around 1.

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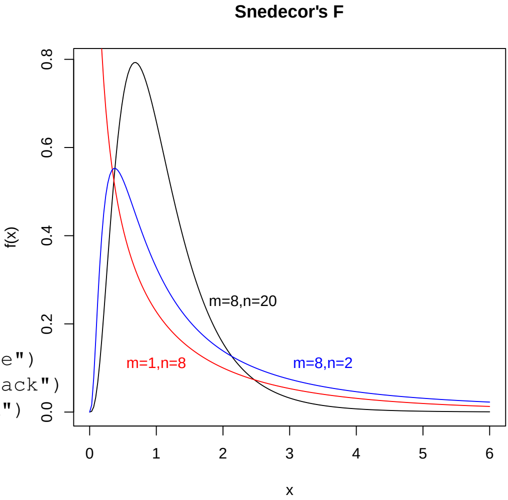
- If n not too small, shape close to scaled χ^2_m.
- If both m and n large, closely concentrated around 1.
- Right-skewed.

What does the $\mathcal{F}_{m,n}$ look like? (II)

```
> sned <- function(x) {
     df(x,m,n)
   }
> m <- 8 ; n <- 20
> curve(sned,
   from=0.0,to=6,n=200,
   ylab="f(x)",xlab="x",
   main="Snedecor's F")
> m <- 1 ; n <- 8
> curve(sned,from=0.0,col="red",
       to=6,n=200,add=TRUE)
> m <- 8 ; n <- 2
> curve(sned,from=0.0,col="blue",
       to=6,n=200,add=TRUE)
> text(3.5,0.11,"m=8,n=2",col="blue")
> text(2.3,0.25,"m=8,n=20",col="black")
> text(1.0,0.11,"m=1,n=8",col="red")
```



Student's t_n distribution

- Distribution of the ratio of independent $N(0,1)$ and $\sqrt{\chi^2_n/n}$ random variables:
$$t_n = \frac{N(0,1)}{\sqrt{\chi^2_n/n}}$$

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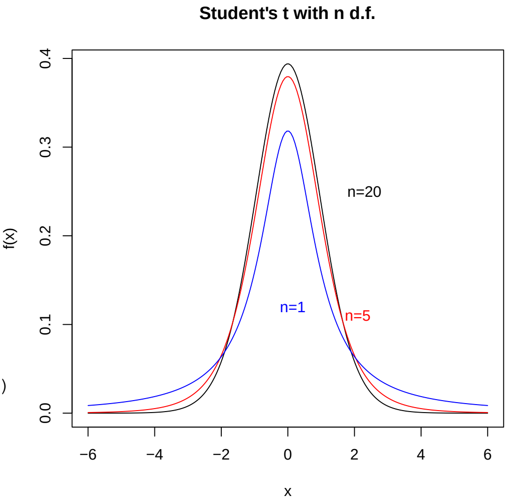
- Has density,

$$f_X(x) = \frac{\Gamma\left(\frac{n+1}{2}\right)}{\sqrt{n\pi}\,\Gamma\left(\frac{n}{2}\right)} \left(1 + \frac{x^2}{n}\right)^{-\frac{1}{2}(n+1)}$$

What does Student's t_n look like?

```
> tx <- function(x) {
     dt(x,n)
   }
> n <- 20
> curve(tx,
   from=-6,to=6,n=200,
   ylab="f(x)",xlab="x",
   main="Student's t with n d.f.")
> n <- 5
> curve(tx,from=-6,col="red",
       to=6,n=200,add=TRUE)
> n <- 1
> curve(tx,from=-6,col="blue",
       to=6,n=200,add=TRUE)
> text(0.15,0.12,"n=1",col="blue")
> text(2.3,0.25,"n=20",col="black")
> text(2.1,0.11,"n=5",col="red")
```



Moments of the t_n distribution

- Not all moments exist for all n.

Moments of the t_n distribution

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- As an striking example, when $n = 1$,

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- For greater n, higher order moments are non existent.

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- This is a *deterministic* phenomenon.

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- Individual outcomes of random events are impossible to predict, which seems to break all chances of reproducibility.

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- Therefore we state our suspicion as: “We believe $P_A(6) > P_B(6)$”, **in terms of a model.**

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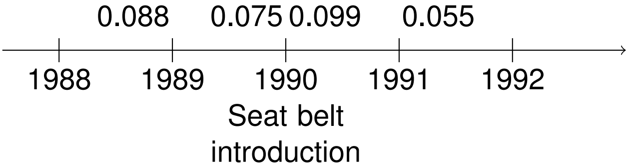
A statistician can never establish a fact for sure, only gather evidence which supports (or conflicts with) a hypothesis.

Looking only at data does not support meaningful answers

- Consider this (fictional) data on proportion of deaths in traffic accidents:



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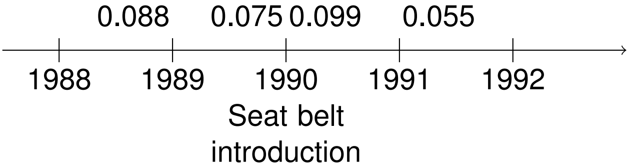

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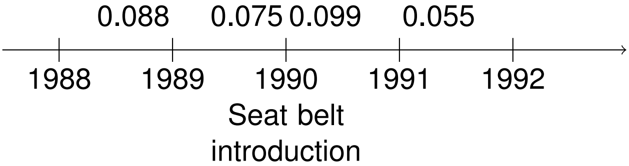

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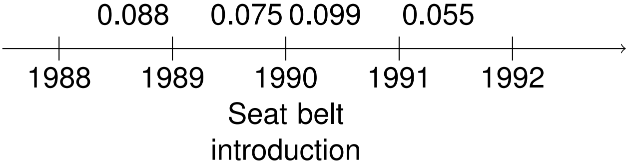

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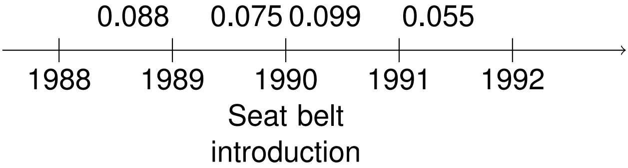

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- Simple model: $P[\mathrm{Death}] = p_0$ before, $P[\mathrm{Death}] = p_1$ after.
- *Now* we can ask ourselves: is $p_0 \neq p_1$? (Or $>$, or $<$ as the case may be.)

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- Probabilities are a model for this.
- We phrase our questions and problems in terms of what is permanent: the probabilities or the **parameters of the model.**

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Come to think of it, that purely intelectual constructions tell so much about the real world is a wonder!

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- Other problems not quite fitting in either category (e.g., serialization)
- If model is “good”, answering questions about the model will enlighten us about the real world.

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Problem in which we were asked to check if mean service time in a car repair shop was $m = 1/\lambda = 65$ minutes.

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- . . .but a more principled approach is desirable.

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- A *statistic* is a function of the sample: $S = S(\vec{X})$ or $s = s(\vec{x})$. Before the sample is taken, it is a random variable; after the sample is taken, it becomes a number (or vector of numbers)

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- With different samples, the same estimator will produce different estimates each time.

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- Least squares method is a particular case of the method of moments.

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- Usually lower order moments best (and simpler).

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- Example: $\mathcal{P}(\lambda)$, sample of n observations.

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Method of moments (II)

- Equate moments of the distribution (usually function of parameters) to sample moments.
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- Could also use,

$$\lambda + \lambda^2 = \frac{1}{n} \sum_{i=1}^{n} X_i^2$$

  Usually lower order moments best (and simpler).

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- Example: estimate m and σ^2 of $N(m, \sigma^2)$.

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- Now we need two equations:

$$\begin{aligned} m &= \frac{X_1 + X_2 + \ldots + X_n}{n} \\ \sigma^2 + m^2 &= \frac{1}{n}\sum_{i=1}^{n} X_i^2 \end{aligned}$$

from which

$$\begin{aligned} \hat{m} &= \overline{X} \\ \hat{\sigma}^2 &= \frac{1}{n}\sum_{i=1}^{n} X_i^2 - \overline{X}^2 = \frac{1}{n}\sum_{i=1}^{n}(X_i - \overline{X})^2 \end{aligned}$$

Method of moments (IV)

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- The mean is $m = \theta/2$. Therefore,

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- Not a particularly good estimator, as we will see.

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Method of moments (VI)

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- We can solve for a and r to obtain:

$$\begin{aligned} \hat{a} &= r/\overline{X} \\ \hat{r} &= \frac{\overline{X}^2}{n^{-1}\sum_{i=1}^{n} X_i^2 - \overline{X}^2} \end{aligned}$$

Method of moments (VII)

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- For instance, if we try to estimate *c* from a density

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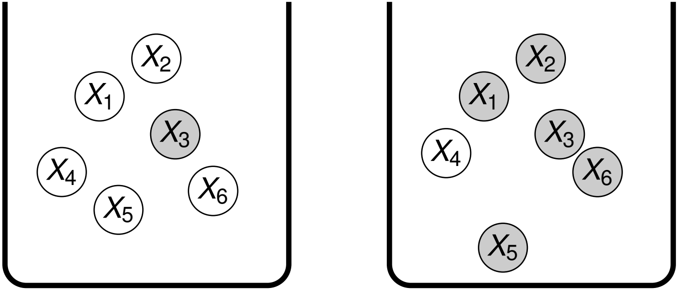
  we will get nowhere.
- Some distributions have no moments, so nothing to match.
- In case at hand, we could use a *censored* (or *trimmed* mean), like the median.

Method of maximum likelihood (I)



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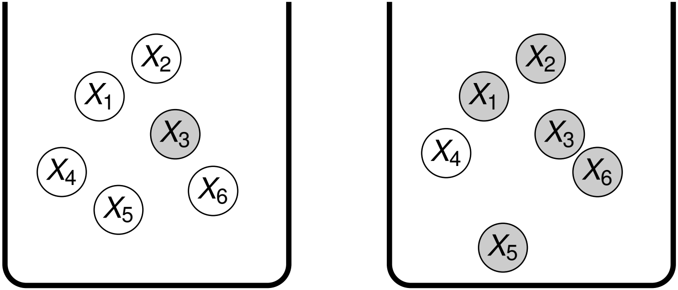

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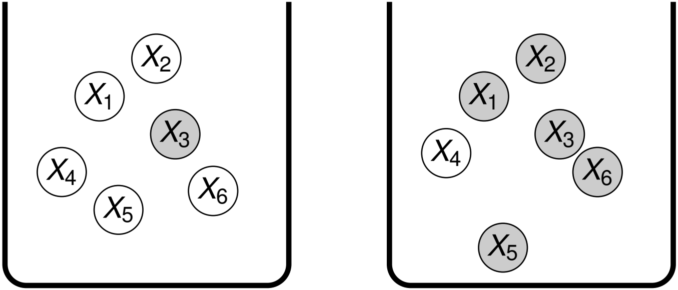

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What would be your guess?

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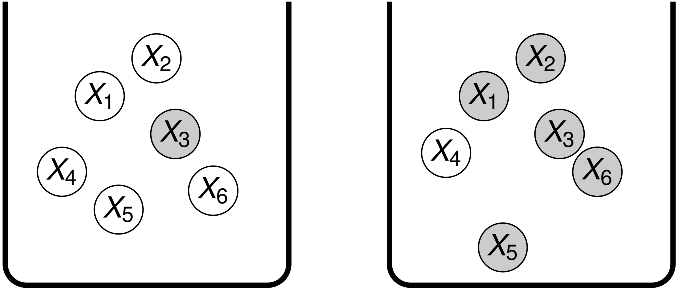

- We are allowed to sample one of the two urns, but we are not told which one it is. We pick one ball which happens to be grey

Right urn, as it can generate grey balls more easily.

Method of maximum likelihood (II)

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  When confronted to two or more states of nature which may have produced a given evidence, we choose the one(s) with optimal capability to generate such evidence.

- Both urns could generate a grey ball, but the second one does so much more easily.
- Why assume that something “strange” has happened if we can see the evidence as the outcome of something “common”?

Method of maximum likelihood (III)

- If joint density of a given sample is $f(\vec{x};\theta)$, $\theta \in \Theta$, we call *likelihood function* $f(\vec{x};\theta)$ **seen as a funcion of $\boldsymbol{\theta}$** for given $\vec{x}$.

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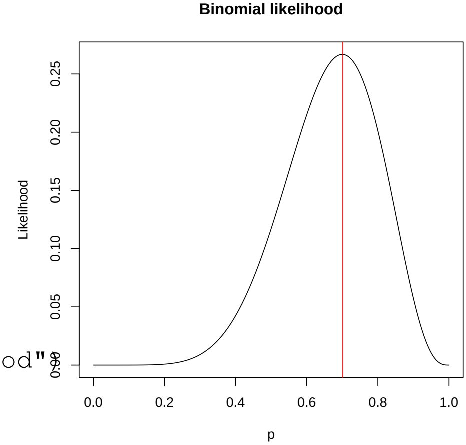
- To maximize the likelihood is tantamount to choosing the $\boldsymbol{\theta}$ which gives maximum density to the observed sample.
- Maximizing θ is *maximum likelihood estimate*, $\hat{\theta}_{MLE}$.
- $f(\vec{x};\theta)$ and $\log f(\vec{x};\theta)$ both achieve their maximum for the same value of θ. Usually easier to maximize the second.

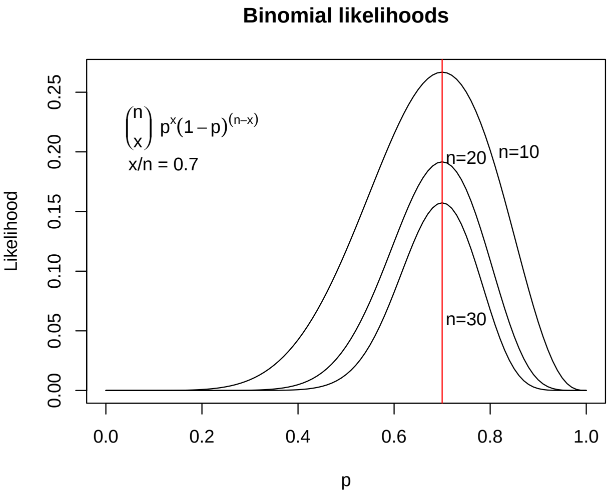
Likelihood example: binomial distribution (I)

```
> n <- 10 ; x <- 7
> binom <- function(p) {
  l <- choose(n,x) * p^x *
       (1-p)^(n-x)
  return(l)
 }
> curve(binom,from=0.00,
   to=1,n=200,
   ylab="Likelihood",
   xlab="p",
   main="Binomial likelihood")
> abline(v=x/n,col="red")
```



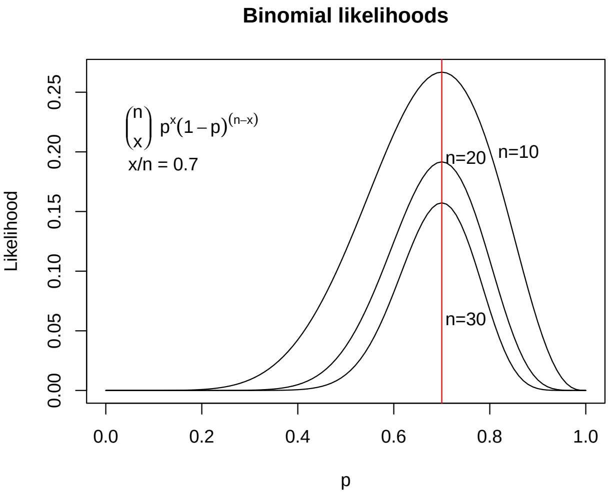
What would happen with different values of *x* and *n*?

Likelihood example: binomial (II)



Are the likelihood functions like density functions?

Likelihood example: binomial (II)



Clearly not; areas below change, not always 1.

Example: MLE of p with $x_1, x_2, \ldots, x_n$ i.i.d. $b(p)$

$$f(\vec{x}; p) = \prod_{i=1}^{n} p^{x_i}(1-p)^{1-x_i}$$

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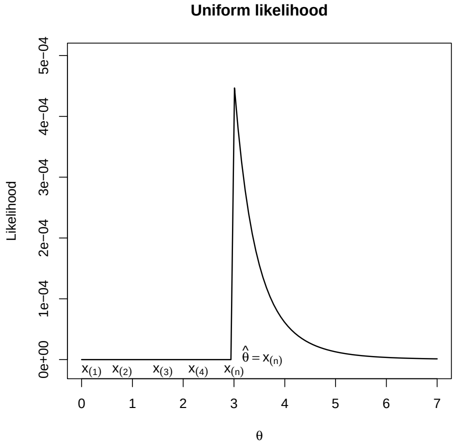

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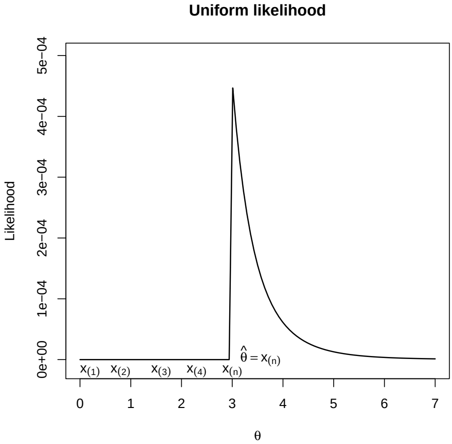

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- Not differentiable.
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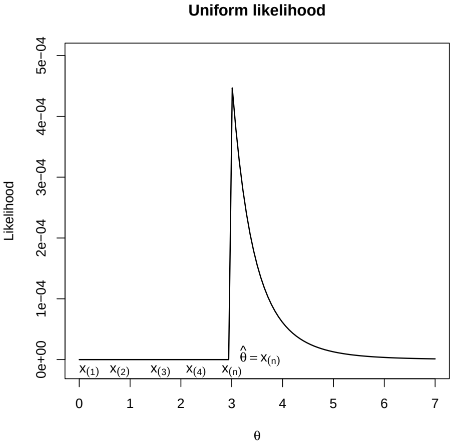

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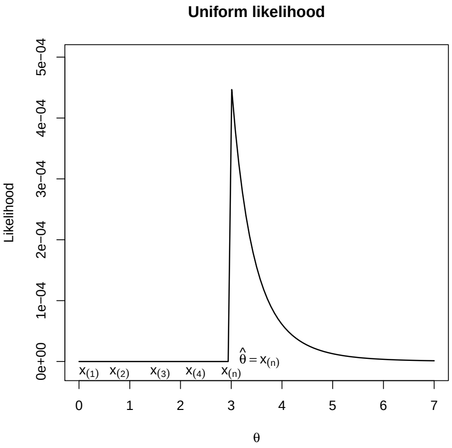

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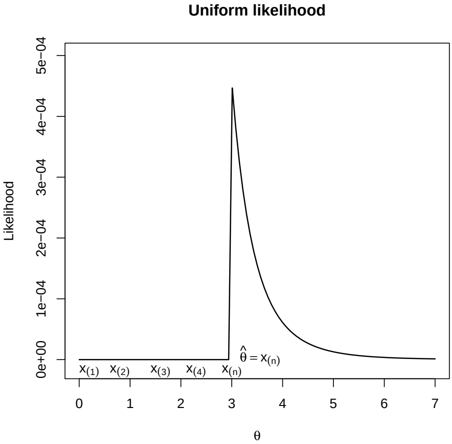

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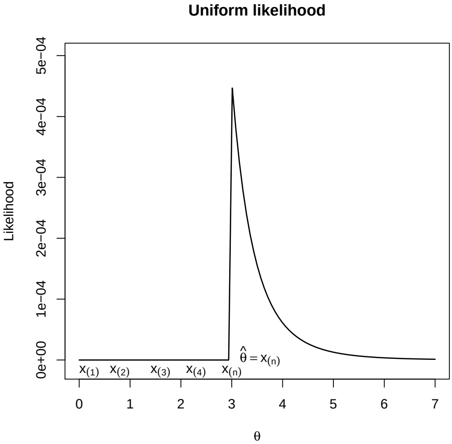

Do we need to know all $x_1, \ldots, x_n$ in order to compute the MLE?

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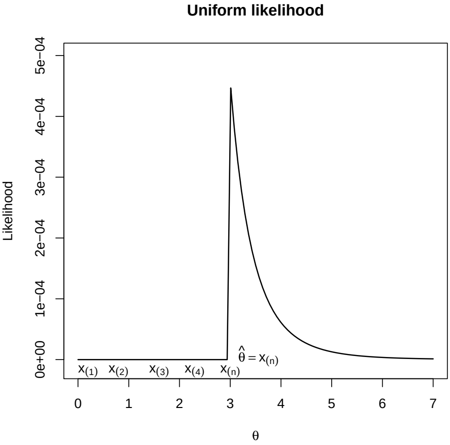

Only one ($x_{(n)}$, the largest) is necessary!

Example: MLE of a in a $\gamma(a, r)$

$$f(\vec{x}; a, r) = \prod_{i=1}^{n} \frac{a^r}{\Gamma(r)} x_i^{r-1} e^{-x_i/a} = \frac{a^{rn}}{(\Gamma(r))^n} \left(\prod_{i=1}^{n} x_i \right)^{r-1} e^{-\sum_{i=1}^{n} x_i}$$

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($\hat{r}_{MLE}$ is harder, as it involves the digamma function
$\partial \log\Gamma(r)/\partial r$.)

MLE and parameter transformations

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- Nice property. In the binomial example, $\hat{p}_{MLE} = \overline{X}/n$, and the MLE of the odds is just: $\hat{\theta}_{MLE} = \frac{\hat{p}_{MLE}}{1-\hat{p}_{MLE}}$.

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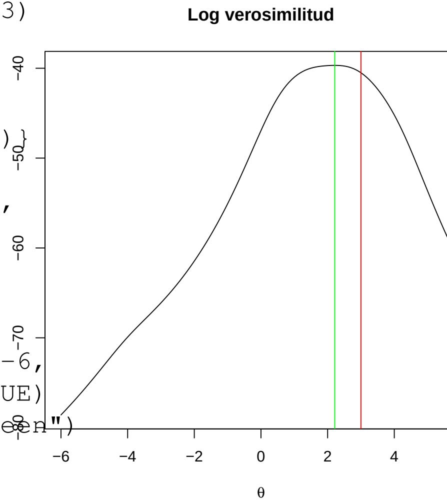
- No hope to maximize that analitycally.

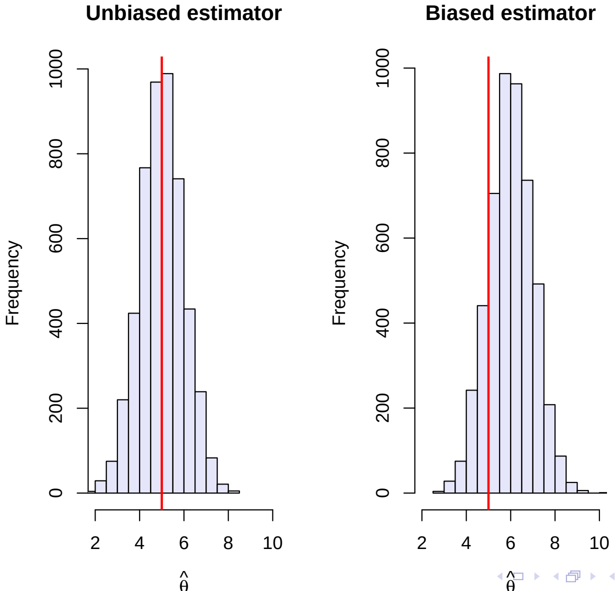
Numerical optimization

```
> x  <- rcauchy(n=15, location=3)
> thetas <- seq(from=-6,to=6,
                length.out=150)
> loglik <- function(theta) {
   sum(-log(pi*(1+(x-theta)^2)))}
> plot(thetas,
      sapply(thetas,FUN=loglik),
      type="l",ylab="",
      main="Log verosimilitud",
      xlab=expression(theta))
> abline(v=3,col="red")
> MLE <- optimize(loglik,lower=-6,
             upper=6, maximum=TRUE)
> abline(v=MLE$maximum, col="green")
```



Unbiasedness (I)

- $\hat{\theta}$ unbiased for θ means that $E[\hat{\theta}] = \theta$.



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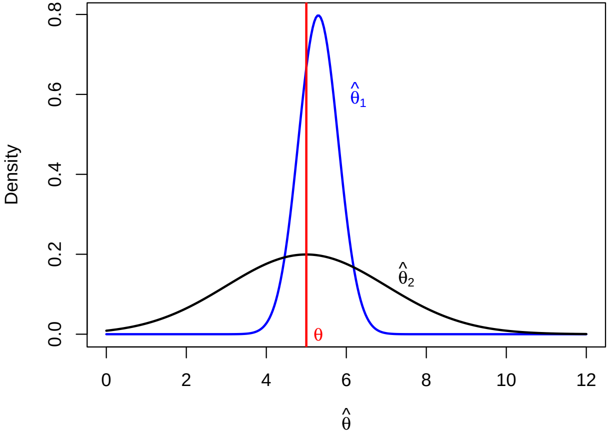

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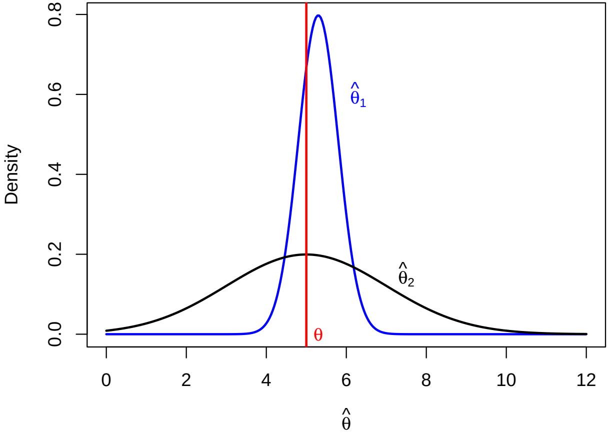

Which one would you prefer?

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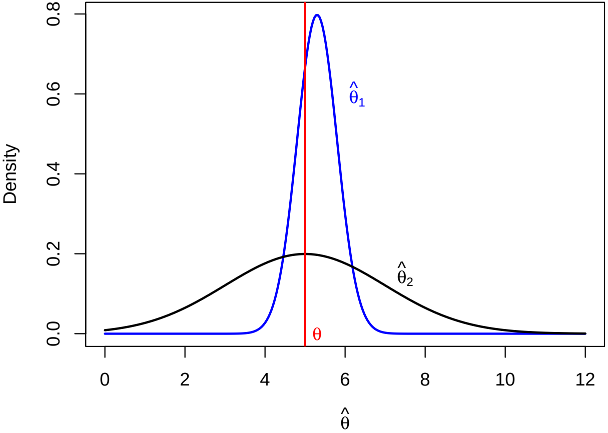

If squared error loss, $E|\hat{\theta} - \theta|^2$, we might prefer $\hat{\theta}_1$, even if

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- In general, if g is a non-linear function,

$$E[\hat{\theta}] = \theta \quad \not\Rightarrow \quad E[g(\hat{\theta})] = g(\theta)$$

A digression: Jensen’s inequality

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- **Example:** $g(x) = 1/x$ is convex, so

$$E[g(\overline{X})] = E[1/\overline{X}] \geq 1/E[\overline{X}] = g\left(E[\overline{X}]\right)$$

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What implicit assumption does MSE about gravity of estimation error?

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"Twice as large, four times as bad." Arbitrary, mathematically convenient.

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- Quite often MLE is biased, although in general it is asymptotically unbiased.

Consistency (I) (reminder: probability limits)

- We say that the limit in probability of a sequence or random variables $\{Z_n\}$ is Z if for any $\epsilon > 0$, $\eta > 0$ there is N such that for $n > N$:

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- Compare with usual notion of limit in mathematical analysis.
- Usual notation is $Z_n \overset{p}{\to} Z$ or $\text{plim}(Z_n) = Z$.

Consistency (II)

- $\hat{\theta}_n$ denotes an estimator of θ based on a sample of size n. For instance, we might have

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- In general, consistency is the very least we ask for. (We want to be rewarded for our effort in sampling!)

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How can we have consistency and not unbiasedness?

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- We can usually show consistency by using:
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  2. Tchebychev inequality.
- Consistency does not imply unbiasedness.

Think of $\hat{\theta}_n$ taking the true value θ with probability $1 - \frac{1}{n}$ and the value n with probability $\frac{1}{n}$.

Consistency vía Tchebychev inequality

Example: consistency of $\hat{\lambda} = \overline{X}$ as estimator of λ of a $\mathcal{P}(\lambda)$.

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- Make your pick of $1 - \eta$ as close to 1 as desired; whatever the implied k, we only have to choose n large enough to make ϵ as small as we wish.

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- Therefore, it is clear that $\hat{\theta}_{MLE} \xrightarrow{p} \theta$.

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- If both variance and bias decrease to zero, we also have consistency.

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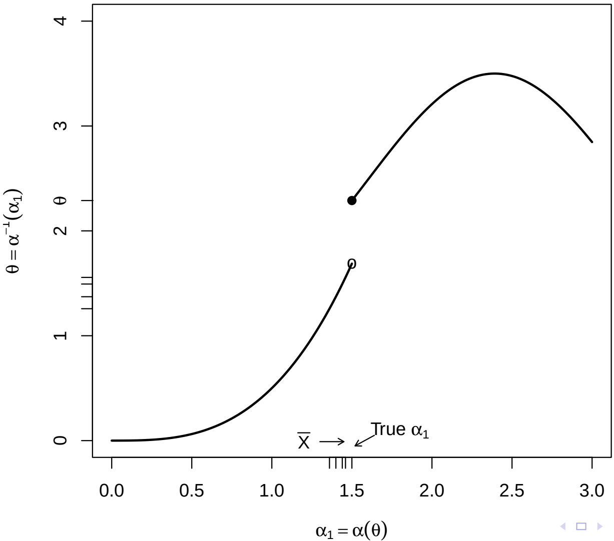
- Notice: if $\alpha_q^{-1}()$ were not continuous, $\overline{X}$ could be very close of m and $\alpha_q^{-1}(\overline{X})$ **not** close to $\alpha_q^{-1}(m) = \theta$.

Consistency of moment estimators (II)

An illustration of what happens:



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- Example: (artificial). In a $\mathcal{P}(\lambda)$,

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  would be consistent (but pretty bad for sample sizes n below 10^5!).
- Consistency is reassuring, but we need to check for realistic sample sizes (often through simulation).

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- Want to exclude of consideration those estimators which only work in certain circumstances.
- Requiring unbiasedness is one way of excluding of consideration estimators such as $\hat{\theta}_*$.

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- Assume Var(θ_*) were the lowest attainable. Then, any estimator with efficiency 1 relative to $\hat{\theta}_*$ will be called **efficient**.

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- If we neglect some observations, as in $\hat{m}_2 = \frac{X_1 + \ldots + X_3}{3}$ the variance is $\frac{1}{3}$.
- The efficiency of $\hat{m}_2$ relative to $\hat{m}_1$ is:

$$\frac{\mathrm{Var}(\hat{m}_1)}{\mathrm{Var}(\hat{m}_2)} = \frac{3}{5}$$

Efficiency: a less trivial example

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- We might tolerate this loss of efficiency to protect ourselves against a heavy tail distribution (like Cauchy).

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  this is the celebrated Cramer-Rao lower bound.
- $I(\theta)$ is the so-called Fisher information contained in one observation, and is defined as:

  $$I(\theta) = E\left(\frac{\partial \log f(X;\theta)}{\partial \theta}\right)^2$$

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- If we average the derivative over possible values of X we have Fisher information.

Efficient estimators and the Cramer-Rao bound

- Under regularity conditions, if

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- We *know* what the optimum is before we start.
- No fear that there is a better estimator that just didn't occur to us!

The Cramer-Rao bound: historical notes

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- The original publications date of 1945 (Rao) and 1946 (Cramer).

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- Failure of these conditions render unusable the Cramer-Rao bound.

A trick to compute the Cramer-Rao bound.

- It turns out that

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- Usually best the second derivative, but sometimes looking at the first we can easily compute its mean value.

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$$\mathrm{Var}(\hat{\lambda}) \geq \frac{1}{n\frac{1}{\lambda}} = \frac{\lambda}{n}$$

so $\overline{X}$ is optimal in the unbiased class.

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- In that case, taking the derivative of

$$\left(\frac{X-\lambda}{\lambda}\right)$$

  would have readily given us $1/\lambda$.

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- The CR bound is then,

$$\mathrm{Var}(\hat{p}) \geq \frac{1}{n\frac{1}{p(1-p)}} = \frac{p(1-p)}{n}$$

and $\hat{p} = \overline{X}$ is efficient.

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- Hence, estimators with efficiency 1 as defined previously, may not exist.
- In general, the MLE reaches the CR lower bound, at least asymptotically.

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- Loose idea: when a statistic “squeezes all the juice” out of a sample, it is sufficient.
- We have to formalize this “squeezing” property.

The concept of sufficiency (II)

- If given a statistic $S = S(\vec{X})$ the conditional density (or probability)
$$f(\vec{X}|S) = \frac{f_{\vec{X}}(\vec{X};\theta)}{f_S(S;\theta)}$$
is independent of θ, $S(\vec{X})$ is said to be **sufficient** for θ.

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- Motivation: if once we know $S = S(\vec{X})$ the density (or probability) of the sample values does not depend on θ, *knowing those individual sample values cannot be of help in determining* θ*.*

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$$f(\vec{X}|S) = \frac{f_{\vec{X}}(\vec{X};\theta)}{f_S(S;\theta)}$$
is independent of θ, $S(\vec{X})$ is said to be **sufficient** for θ.
- Motivation: if once we know $S = S(\vec{X})$ the density (or probability) of the sample values does not depend on θ, *knowing those individual sample values cannot be of help in determining* θ*.*
- All information about θ is then contained in $S = S(\vec{X})$.

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\end{aligned}
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- Therefore, S (or any other 1-1 function of S) is sufficient for λ.

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- *Given* $X_{(1)}, \ldots, X_{(n)}$, any order is equally likely, with probability $1/n!$, whichever the parameter(s) of the distribution may be.
- Therefore, $X_{(1)}, \ldots, X_{(n)}$ is always a sufficient statistic, although of little interest (it doesn't "compact" information).

The factorization theorem (I)

- If we can decompose the joint density (or probability) as a product,
$$f_{\vec{X}}(\vec{X};\theta) = g(S(\vec{X});\theta) \times h(\vec{X})$$
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- Quite easy to prove.
- Quite practical; we only have to see which function (or functions) of the sample “carry with them” the parameter θ.

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- Clearly, $S = X_1 + \ldots + X_n$ is sufficient.

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as a function of θ**,** we only need $g(S(\vec{X});\theta)$;
- The term $h(\vec{X})$ is just a constant in the likelihood function.

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- No further reduction is possible.

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- $p \Longrightarrow q$ and $\neg q \Longrightarrow \neg p$ are logically equivalent. ($\neg$ above stands for negation:)
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- When testing hypothesis, we rely on a softened versions of this equivalence.

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  2. ...or else the null hypothesis is not true to begin with.
- As statisticians, we go with the second option.

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- Alternative approaches (like the one advocated by the Bayesian school) give more clues on how to learn.

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How would you phrase the hypothesis in items 1 and 2 above?

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1) $\Theta_0 = 0$, $\Theta = \mathcal{R}$. 2) $\Theta_0 = \{(x, y) : x = y\}$, $\Theta = \mathcal{R}^2$

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- What is “rare”? Problem dependent.

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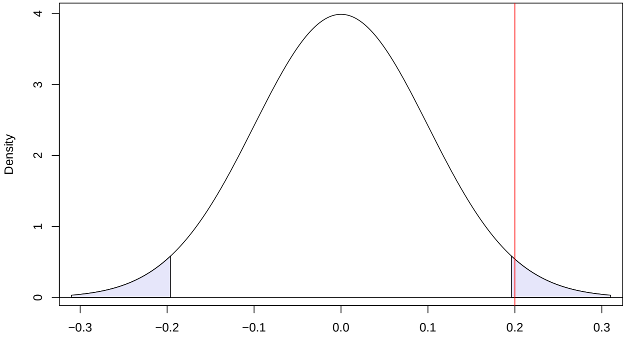
- The probability of the critical region when H_0 is true, is called the significance level.

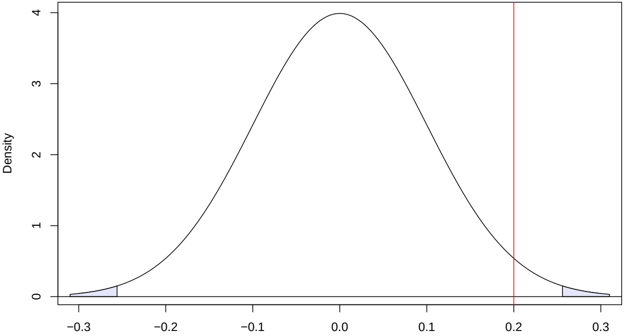
The anatomy of a hypothesis test (IV)

At the stated level of significance (5%), we would reject H_0.



The anatomy of a hypothesis test (V)

With a different level of significance (1%), we would **not** reject H_0.



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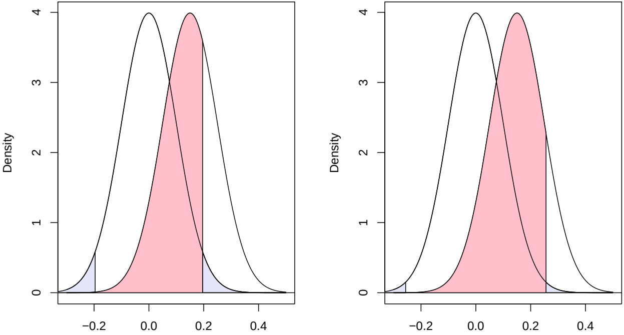
- Not rejecting H_0 when it is false is called *Type II* error, and its probability is denoted by β.

Trade-off between Type I and II errors - Ilustration



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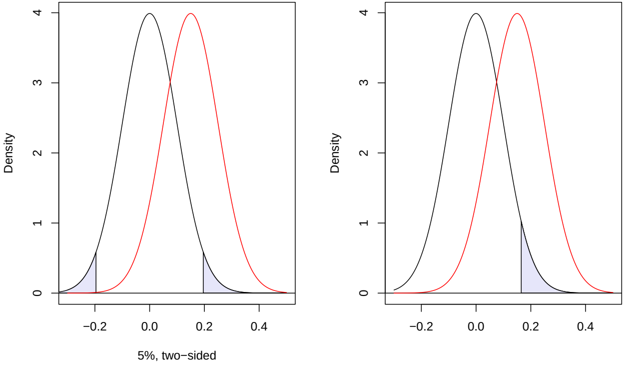
- Sometimes, we have a clear idea of what the "competing" hypothesis is, and in this case we want to use that information.

Testing against an alternative H_a

If we test H_0 against an alternative H_a, a one-sided critical region makes more sense.



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- In other cases, a unique most powerful test may not exist.

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x	0	1	2	3	4	5
$P(x; \theta_0)$	0.60	0.26	0.05	0.04	0.04	0.01
$P(x; \theta_a)$	0.10	0.15	0.10	0.25	0.30	0.10

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How would you choose a critical region of size $\alpha = 0.05$ with maximum power?

The Neyman-Pearson theorem (I)

- After fixing the significance level α, what critical region would give better power against a simple alternative?
- Let's consider testing $H_0 : \theta = \theta_0$ vs. $H_a : \theta = \theta_a$:

x	0	1	2	3	4	5
$P(x;\theta_0)$	0.60	0.26	0.05	0.04	0.04	0.01
$P(x;\theta_a)$	0.10	0.15	0.10	0.25	0.30	0.10

Picking $x = 4$ and $x = 5$, for a total power of 0.40.

The Neyman-Pearson theorem (II)

- The intuition is that we want our critical region to be made of points x with high ratio

  $$\frac{f(x;\theta_a)}{f(x;\theta_0)}$$

  where $f(x;\theta_0)$ is the density under the null and $f(x;\theta_a)$ is the density under the alternative.

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  where $f(x;\theta_0)$ is the density under the null and $f(x;\theta_a)$ is the density under the alternative.
- Neyman-Pearson theorem: *The most powerful test of given size α for $H_0 : \theta = \theta_0$ against the alternative $H_a : \theta = \theta_a$ has critical region of the form:*

$$C_\alpha = \left\{ \vec{x} : \frac{f(\vec{x};\theta_a)}{f(\vec{x};\theta_0)} > k_\alpha \right\}$$

  for a constant k_α which depends on α.

The Neyman-Pearson theorem - Proof (I)

- Consider the critical region

$$C_\alpha = \left\{ \vec{x} : \frac{f(\vec{x};\theta_a)}{f(\vec{x};\theta_0)} > k_\alpha \right\}$$

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- Subtracting $\delta = \int_{C\cap A} f(\vec{x};\theta_0)d\vec{x}$ in both sides:

$$\int_{C\cap A^c} f(\vec{x};\theta_0)d\vec{x} = \int_{A\cap C^c} f(\vec{x};\theta_0)d\vec{x} = \alpha - \delta \geq 0$$

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How do we know $\alpha - \delta \geq 0$?

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Because $C \cap A \subseteq C$.

The Neyman-Pearson theorem - Proof (II)

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$$\int_C f(\vec{x};\theta_a)d\vec{x} - \int_A f(\vec{x};\theta_a)d\vec{x}$$

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$$\int_C f(\vec{x};\theta_a)d\vec{x} - \int_A f(\vec{x};\theta_a)d\vec{x}$$

- Inside C we have $f(\vec{x};\theta_a) > kf(\vec{x};\theta_0)$ and outside $f(\vec{x};\theta_a) \leq kf(\vec{x};\theta_0)$. The difference of powers is:

$$\begin{aligned}
\int_C f(\vec{x};\theta_a)d\vec{x} &- \int_A f(\vec{x};\theta_a)d\vec{x} \\
&= \int_{C\cap A^c} f(\vec{x};\theta_a)d\vec{x} - \int_{A\cap C^c} f(\vec{x};\theta_a)d\vec{x} \\
&\geq k\int_{C\cap A^c} f(\vec{x};\theta_0)d\vec{x} - k\int_{A\cap C^c} f(\vec{x};\theta_0)d\vec{x} \\
&= k(\alpha-\delta) - k(\alpha-\delta) = 0
\end{aligned}$$

Neyman-Pearson example (I)

- In a large company, the number of workers not showing up for work is Poisson-distributed. Workers claim that $\lambda = 1$, while management claims $\lambda = 2$. They check four days and obtain 1, 0, 2, and 2 workers not showing up for work.

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  1. Obtain the most powerful critical region to test the workers hypothesis (H_0) against the management's at a 0.05 significance level.
  2. What is the power of the test?
- We have:

$$\begin{aligned}
f(\vec{x}; \lambda = 1) &= \prod_{i=1}^{4} \frac{e^{-1} 1^{x_i}}{x_i!} = \frac{e^{-4}}{\prod_{i=1}^{4} x_i!} \\
f(\vec{x}; \lambda = 2) &= \prod_{i=1}^{4} \frac{e^{-2} 2^{x_i}}{x_i!} = \frac{e^{-8} 2^{\sum_{i=1}^{4} x_i}}{\prod_{i=1}^{4} x_i!}
\end{aligned}$$

Neyman-Pearson example (II)

- From Neyman-Pearson, the most powerful critical region of size α is of the form:

$$\begin{aligned} C_\alpha &= \left\{\vec{x} : \frac{f(\vec{x}; \lambda = 2)}{f(\vec{x}; \lambda = 1)} > k_\alpha\right\} \\ &= \left\{\vec{x} : \frac{e^{-8} 2^{\sum_{i=1}^{4} x_i}}{e^{-4}}\right\} \\ &= \left\{\vec{x} : e^{-4} 2^{\sum_{i=1}^{4} x_i} > k_\alpha\right\} \end{aligned}$$

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- Taking logs and bringing all constants into k'_α:

$$C_\alpha = \left\{ \vec{x} : \sum_{i=1}^{4} x_i > k'_\alpha \right\}$$

Neyman-Pearson example (III)

- We now know **the form** of C_α

$$C_\alpha = \left\{ \vec{x} : \sum_{i=1}^{4} x_i > k'_\alpha \right\}$$

- Have no clue about what the value of k'_α is, but know $\sum_{i=1}^{4} x_i \sim \mathcal{P}(\lambda = 4)$ when H_0 is true.
- For C_α to have size $\alpha = 0.05$, the constant must be a value exceeded with probability no greater than α when sampling a $\mathcal{P}(\lambda = 4)$ distribution. Resorting to tables (or R) gives us:

```
> ppois(0:8,lambda=4)
[1] 0.01832 0.09158 0.23810 0.43347 0.62884
[6] 0.78513 0.88933 0.94887 0.97864
```

- $[8, \infty)$ would be a critical region for $S = \sum_{i=1}^{4} x_i$ quite close to $\alpha = 0.05$; $[9, \infty)$ would have $\alpha = 0.02136$.

Neyman-Pearson and sufficiency (I)

- Do we loose something by using Neyman-Pearson's theorem?
- We decide between H_0 and H_a as if only the likelihood ratio (LR) matters.
- Might be justified if the LR were a sufficient statistic.
- It is! In a sense, it is the "smallest" sufficient statistic.
- We prove a simplified version next.

Neyman-Pearson and sufficiency (II)

- Consider the simple case where $\Theta = \{\theta_0, \theta_1\}$ and both distributions $F_X(x;\theta)$ have commen support.
- The, the likelihood ratio

$$R(\vec{x}) = \frac{f_{\vec{X}}(\vec{x};\theta_0)}{f_{\vec{X}}(\vec{x};\theta_1)}$$

  is a sufficient statistic.
- To prove sufficiency we have to show that

$$f_{\vec{X}}(\vec{x}|R(\vec{x}) = r;\theta_0) = f_{\vec{X}}(\vec{x}|R(\vec{x}) = r;\theta_1)$$

Neyman-Pearson and sufficiency (III)

$$\begin{aligned}
f_{\vec{X}}(\vec{x}|R(\vec{x}) = r; \theta_0) &= \frac{f_{\vec{X}}(\vec{x}; \theta_0)}{\int_{R(\vec{X})=r} f_{\vec{X}}(\vec{x}; \theta_0) d\vec{x}} = \frac{r f_{\vec{X}}(\vec{x}; \theta_1)}{\int_{R(\vec{X})=r} r f_{\vec{X}}(\vec{x}; \theta_1) d\vec{x}} \\
&= \frac{f_{\vec{X}}(\vec{x}; \theta_1)}{\int_{R(\vec{X})=r} f_{\vec{X}}(\vec{x}; \theta_1) d\vec{x}} = f_{\vec{X}}(\vec{x}|R(\vec{x}) = r; \theta_1)
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Some quirks of hypothesis testing (I)

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- If evidence is not strong, the null is the surviving hypothesis, whichever it happens to be!
- The null should be provisionally established knowledge, put to test. How we arrive to that knowledge, there is no telling.
- Alternative approaches (like bayesian inference) treat conjectures in a more symmetric way.

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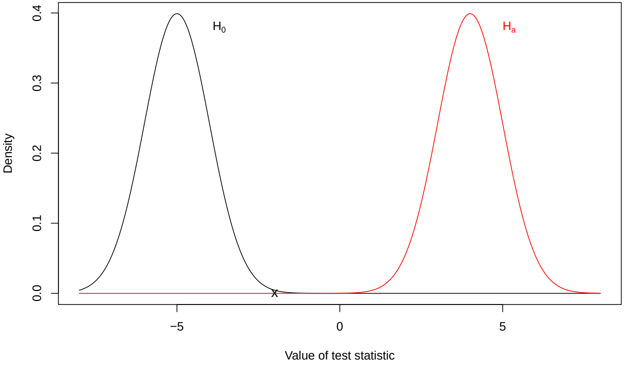
- That H_0 is rejected **does not mean that H_a should be accepted.**



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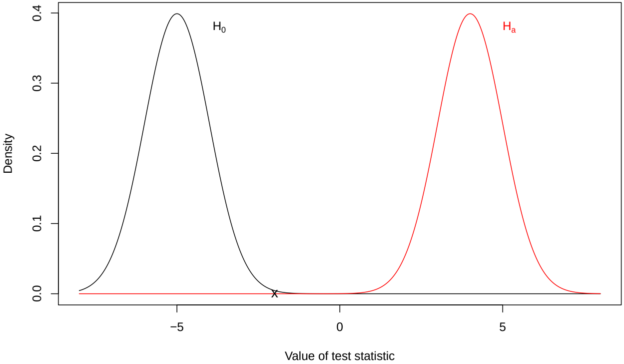

- An observation at X is evidence against H_0 but much more so against H_a. In such situation, we should revise our hypothesis and admit that other possibilities might exist.

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- Under the frequentist approach, no way to deal with this.

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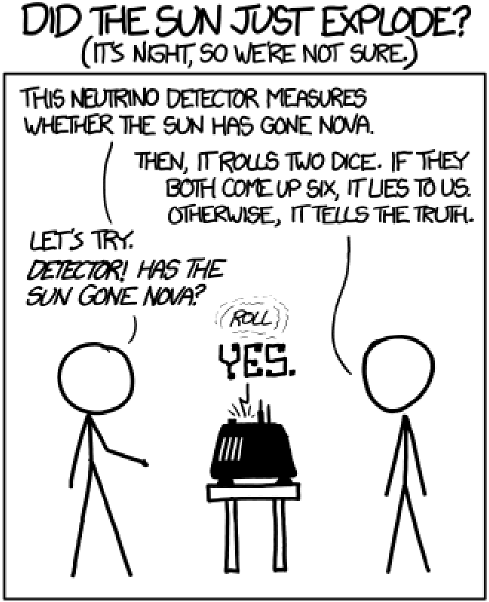
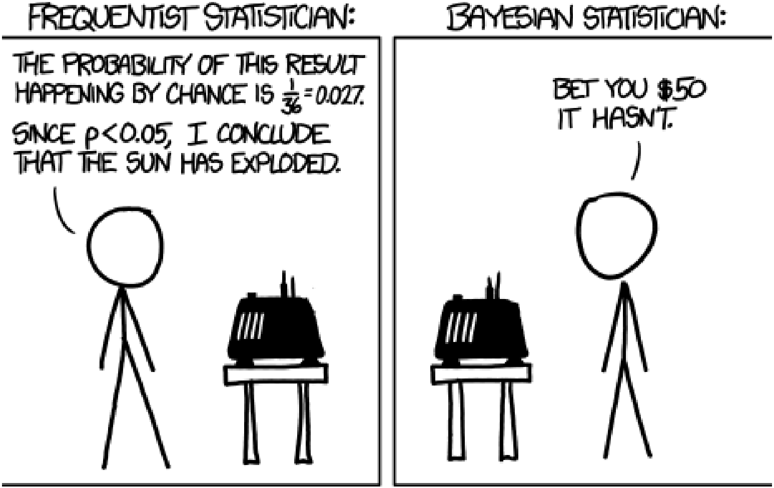


Some quirks of hypothesis testing (IV)



`https://xkcd.com/1132/`

Goodness-of fit problems

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  3. Do intervals between accidents at work appear to follow an exponential distribution? *(one parameter to be estimated)*
- In all these cases, we have data and we want to test adequacy of a given distribution, possibly not fully especified (= some parameter has to be estimated).

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- k is the number of classes, p the number of parameter estimated, if any.

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- Howto choose the class boundaries? Good question.
- Usually no particular alternative: a pure significance test.
- Critical region: right tail.

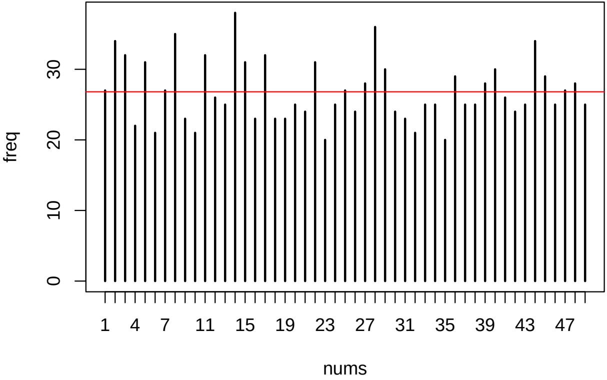
Example - I

```
> primitiva[1:3,1:8]
       Fecha Semana N1 N2 N3 N4 N5 N6
1 01/01/2009      1  4  8 12 25 34 46
2 03/01/2009      1  9 11 21 30 31 44
3 08/01/2009      2  7 17 27 28 29 44
> nums <- as.matrix(primitiva[,3:8])
> freq <- table(nums)
> sum(freq)            # How many numbers seen?
[1] 1314
> e <- sum(freq) / 49  # Expected each under H0
> e
[1] 26.82
```

Example -II

The absolute frequencies of each number are:

```
> plot(freq)
> abline(h=e,col="red")
```



Example -III

- Question is now to decide whether the departures from the expected number of appearances is enough to reject H_0 (=”all numbers equally likely”).

Example - IV

- R has a standard function which does the same at once.

```
>  result <- chisq.test(x=freq,p=rep(1/49,49))
>  result
        Chi-squared test for given probabiliti

data:  freq
X-squared = 34, df = 48, p-value = 0.9
```

Example - V

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- For instance, you might have in the case shown:

O_i	E_i	$(O_i - E_i)$	$(O_i - E_i)^2$	$(O_i - E_i)^2/E_i$
27	26.81633	0.183673	0.03373	0.001258
34	26.81633	7.183673	51.60516	1.924394
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
25	26.81633	-1.816327	3.29904	0.123023
			$Z =$	33.6865

Chi square test with estimated parameters (I)

- Data: deaths by horse kick in 200 army corps years.

DEATHS	OBSERVED CASES
0	109
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- The hypothesis does not uniquely fix the distribution.
- The MLE of λ is:

$$\hat{\lambda} = \frac{0 \times 109 + 1 \times 65 + 2 \times 22 + 3 \times 3 + 4 \times 1}{200} = 0.61$$

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we would compute E_1 (the expected number of cases with 0 deaths) as: $200 \times 0.5433509 = 108.67$.

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  we would compute E_1 (the expected number of cases with 0 deaths) as: $200 \times 0.5433509 = 108.67$.
- Likewise for the remaining E_i cells.

Chi square test with estimated parameters (III)

- Now we have:

O_i	E_i	$(O_i - E_i)$	$(O_i - E_i)^2$	$\frac{(O_i - E_i)^2}{E_i}$
109	108.67017	0.32983	0.10879	0.00100
65	66.28881	-1.28881	1.66102	0.02505
22	20.21809	1.78191	3.17522	0.15704
3	4.11101	-1.11101	1.23434	0.30025
1	0.62693	0.37307	0.13918	0.22200
			$Z =$	0.70537

Chi square test with estimated parameters (IV)

- We now compare Z with a chi-square with **3** degrees of freedom ($k - p - 1 = 5 - 1 - 1 = 3$):

  ```
  > 1 - pchisq(0.70537,df=3)
  [1] 0.8719
  ```

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- For example, we may have:

Gender	Right-handed	Left-handed	Total
Male	43	9	52
Female	44	4	48
Total	87	13	100

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- Definition can be generalized to different number of dimensions
- For example, we may have:

Gender	Right-handed	Left-handed	Total
Male	43	9	52
Female	44	4	48
Total	87	13	100

- The row and column totals are referred as the *margins.*

Sampling schemes (I)

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- …or we may fix the row margin or the column margin.
- In the first case we speak of *multinomial sampling*, in the second of *product multinomial sampling.*
- Why should we care? Marginal probabilities can only be estimated from “free” margins.

Sampling schemes (II)

- Consider the following case: we pick a sample of 1000 persons and cross-classify them according to ethnic origin and whether they suffered in the last winter from common cold. Want to test relative vulnerability.

Race	Had cold	Didn't have cold	Total
Whites	801	104	905
Non-whites	83	12	95
Total	884	116	1000

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Whites	801	104	905
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Total	884	116	1000

- We may estimate the proportion of whites as 905/1000 = 0.905 and the overall prevalence of cold as 0.884

Sampling schemes (III)

- Suppose though we are sampling a population with a tiny proportion of non-whites. We might end up with a table such as:

Race	Had cold	Didn't have cold	Total
Whites	891	108	999
Non-whites	1	0	1
Total	892	108	1000

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Whites	891	108	999
Non-whites	1	0	1
Total	892	108	1000

- We end up with a table in which non-whites are almost (or totally) absent.

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Non-whites	1	0	1
Total	892	108	1000

- We end up with a table in which non-whites are almost (or totally) absent.
- Non-white sample far too small to investigate the matter of interest.

Sampling schemes (IV)

- What we need instead is to sample both races separately, say 500 each:

Race	Had cold	Didn't have cold	Total
Whites	398	102	500
Non-whites	403	97	500
Total	801	199	1000

Sampling schemes (IV)

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Race	Had cold	Didn't have cold	Total
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- *Then* we are assured to have enough observations in each group.

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- Marginal totals do not estimate anything now: the row totals are fixed by design.

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- Both hypothesis are tested conditional on the margins, and the results are exactly the same for a given table, no matter how it was sampled.
- Why conditionally on the margins? It is the distribution of counts inside the table what is indicative of independence (or homogeneity), *not* how many people of each race we look at.

Testing independence (I)

- Consider,

Race	Had cold	Didn't have cold	Total
Whites	801	104	905
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Total	884	116	1000

and assume it was obtained fixing only $N = 1000$.

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- The hypothesis of interest is $H_0 : p_{ij} = p_{i.} \times p_{.j}$
- $\hat{p}_{11} = 0.884 \times 0.905$, and $E_{11} = 1000 \times 0.884 \times 0.905$. Similarly for the rest.

Testing independence (II)

Race	Had cold	Didn't have cold	Total
Whites	801	104	905
Non-whites	83	12	95
Total	884	116	1000

- Apparently, we estimate 4 parameters p_{ij} for the 4 cells.

Testing independence (II)

Race	Had cold	Didn't have cold	Total
Whites	801	104	905
Non-whites	83	12	95
Total	884	116	1000

- Apparently, we estimate 4 parameters p_{ij} for the 4 cells.
- Conditionally on the margins, only two parameters are free, and need to be counted.

Testing independence (III)

O_{ij}	E_{ij}	$(O_{ij} - E_{ij})$	$(O_{ij} - E_{ij})^2$	$\frac{(O_{ij}-E_{ij})^2}{E_{ij}}$
801	800.02	0.98	0.9604	0.00120
83	83.98	-0.98	0.9604	0.01144
104	104.98	-0.98	0.9604	0.00915
12	11.02	0.98	0.9604	0.08715
			$Z =$	0.10894

- The expected values are computed as $E_{ij} = Np_{ij} = Np_{i.}p_{.j}$.

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- For instance, $800.02 = 1000 \times 0.884 \times 0.905$.

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- The expected values are computed as $E_{ij} = Np_{ij} = Np_{i.}p_{.j}$.
- For instance, $800.02 = 1000 \times 0.884 \times 0.905$.
- Degrees of freedom are $k - p - 1 = 4 - 2 - 1 = 1$. So we have to compare 0.10894 with the quantiles of a χ^2_1 distribution.

Testing independence (IV)

- We can easily construct the table:

```
> ColdRace <- matrix(c(801,83,104,12),2,2)
> ColdRace <- as.table(ColdRace)
> colnames(ColdRace) <-  c("Cold","Not-Cold")
> rownames(ColdRace) <-  c("Whites","Non-white
> ColdRace
          Cold Not-Cold
Whites     801      104
Non-whites  83       12
```

Testing independence (V)

Function `loglin` fits, among many other things, the independence model:

```
> result   <- loglin(ColdRace,margin=list(1,2),fit
2 iterations: deviation 0
> result$pearson
[1] 0.1089
> result$df
[1] 1
```

Testing independence (VI)

- The E_{ij} approach quite well O_{ij}:

```
> result$fit
                 Cold Not-Cold
Whites         800.02   104.98
Non-whites      83.98    11.02
```

Testing homogeneity (I)

- Consider again,

Observed counts ($= O_i$)

Race	Had cold	Didn't have cold	Total
Whites	801	104	905
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- We are testing the hypothesis $H_0 : p_{1j} = p_{2j}$ for all j.
- Under H_0, $\hat{p}_{.j} = n_{.j}/n_{..}$ is a sensible estimate of $p_{.j}$, common to all i.

Testing homogeneity (II)

- The results are exactly the same, only they are arrived at in a different manner.

Expected counts ($= E_i$)

Race	Had cold	Didn't have cold	Total
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- The E_{1j} in the first row are computed as $905 \times \hat{p}_{.j}$
- The E_{2j} in the second row are computed as $95 \times \hat{p}_{.j}$

Testing homogeneity (III)

- $$Z_1 = \sum_{j=1}^{2} \frac{(O_{1j} - E_{1j})^2}{E_{1j}}$$

  for the cells in the first row would be distributed as $\chi^2_{k-1} = \chi^2_1$ if no parameters were estimated and the $p_{.j}$ used were the correct p_{1j}.

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  woud be χ^2_1.
- $Z = Z_1 + Z_2$ would be distributed as a χ^2_2, but we have to subtract **1** parameter $p_{.1}$ estimated (why not also $p_{.2}$?).
- **The same** statistic Z follows **the same** distribution under H_0 than in the case of independence.

General rule

- When testing either independence or homogeneity in an $r \times s$ contingency table, in both cases we form

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- The resulting value of Z is (under the null hypothesis of independence or homogeneity) distributed as:

$$\chi^2_{(r-1)(s-1)}$$

- H_0 should be rejected if Z falls in the α right tail of said distribution (alternatively: if the probability to the right of Z in a $\chi^2_{(r-1)(s-1)}$ is "small").

Fisher's exact test (I)

- Consider again our table,

Race	Had cold	Didn't have cold	Total
Whites	n_{11}	n_{12}	$n_{1.}$
Non-whites	n_{21}	n_{22}	$n_{2.}$
Total	$n_{.1}$	$n_{.2}$	$N = n_{..}$

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Total	$n_{.1}$	$n_{.2}$	$\mathrm{N} = n_{..}$

- For given $p_{11}, p_{21}, p_{12}, p_{22}$ its probability would be:

$$\frac{N!}{n_{11}!n_{12}!n_{21}!n_{22}!} p_{11}^{n_{11}} p_{21}^{n_{21}} p_{12}^{n_{12}} p_{22}^{n_{22}}$$

Fisher's exact test (II)

- The probabilities that N is distributed as it is in the row and column margins are respectively:

$$\frac{N!}{n_{1.}!n_{2.}!}p_{1.}^{n_{1.}}p_{2.}^{n_{2.}} \qquad \frac{N!}{n_{.1}!n_{.1}!}p_{.1}^{n_{.1}}p_{.2}^{n_{.2}}$$

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- Conditional on the margins, the probability of a given table is:

$$\frac{\left(\frac{N!}{n_{11}!n_{12}!n_{21}!n_{22}!}p_{11}^{n_{11}}p_{21}^{n_{21}}p_{12}^{n_{12}}p_{22}^{n_{22}}\right)}{\left(\frac{N!}{n_{1.}!n_{2.}!}p_{1.}^{n_{1.}}p_{2.}^{n_{2.}}\right)\left(\frac{N!}{n_{.1}!n_{.2}!}p_{.1}^{n_{.1}}p_{.2}^{n_{.2}}\right)}$$

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- Under the null hypothesis $p_{ij} = p_{i.}p_{.j}$ all nuisance parameters cancel!

Fisher's exact test (III)

- All we are left with for the probability of a given table is:

$$\frac{\left(\dfrac{N!}{n_{11}!n_{12}!n_{21}!n_{22}!}\right)}{\left(\dfrac{N!}{n_{1.}!n_{2.}!}\right)\left(\dfrac{N!}{n_{.1}!n_{.2}!}\right)}$$

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- Can compute the probability of each table under the null $H_0 : p_{ij} = p_{i.}p_{.j}$ and check whether what we have observed is very unlikely.

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- The denominator is always the same.
- Can compute the probability of each table under the null $H_0 : p_{ij} = p_{i.}p_{.j}$ and check whether what we have observed is very unlikely.
- Unfeasible for large tables.

Fisher's exact test (IV)

- Function to do it in R. Useful for small tables; no approximations. Will fail for large tables.

```
>  fisher.test(ColdRace)
         Fisher's Exact Test for Count Data

data:  ColdRace
p-value = 0.7
alternative hypothesis: true odds ratio is not
95 percent confidence interval:
 0.5346 2.1400
sample estimates:
odds ratio
     1.113
```

Fisher's exact test (V)

Table: Accidents 1970-2009 of european airlines involving loss of life

Airline	Flights	Accs	Airline	Flights	Accs
Aer Lingus	1200000	0	Icelandair	390000	0
Air France	5900000	8	Lufthansa	7300000	4
Alitalia	3900000	3	KLM	2400000	3
Austrian Airlines	750000	0	Olympic Airways	1800000	3
Braathens	1350000	1	Sabena	1600000	0
British Airways	8270000	3	SAS	5400000	2
British Midland	1030000	1	Swiss/Swissair	3200000	5
easyJet	760000	0	TAP Air Portugal	850000	3
Finnair	1700000	0	Turkish Airlines	2100000	10
Iberia	4500000	4	Virgin Atlantic	150000	0

Fisher’s exact test (VI)

- When counts are very small, the chi square approximation may be bad, and Fisher’s test is required.

```
> chisq.test(accidentes)
        Pearson's Chi-squared test

data:  accidentes
X-squared = 56, df = 19, p-value = 2e-05
```

Fisher’s exact test (VII)

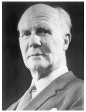
- It is not feasible to compute ALL tables, simulation is performed instead.

```
> fisher.test(accidentes,
              simulate.p.value=TRUE,
              B=10000)
        Fisher's Exact Test for Count Data wit
        simulated p-value (based on 10000 repl

data:  accidentes
p-value = 0.002
alternative hypothesis: two.sided
```

Historical notes

Egon Pearson



C.R.Rao

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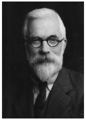

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Student's *t*

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Likelihood,
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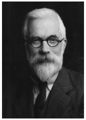

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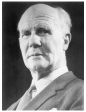

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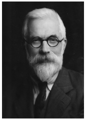

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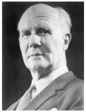

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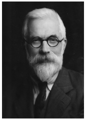

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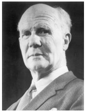

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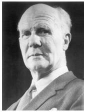
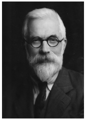


C.R.Rao

K.Pearson

W.S.Gosset

R.A.Fisher



J.Neyman

H.Cramér

1900
Method moments, χ^2 tests

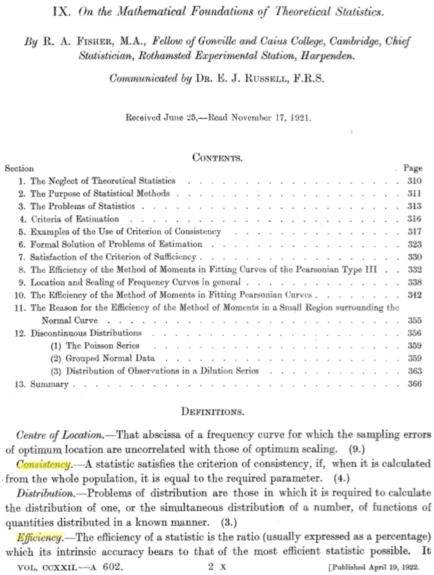
1908
Student's t

1921
Likelihood, sufficiency, efficiency

1933
NP lemma, power, UMP tests

1945
CR inequality

Earlier notions were defined differently



IX. *On the Mathematical Foundations of Theoretical Statistics.*

By R. A. Fisher, M.A., *Fellow of Gonville and Caius College, Cambridge, Chief Statistician, Rothamsted Experimental Station, Harpenden.*

Communicated by Dr. E. J. Russell, F.R.S.

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Contents.

Definitions.

Centre of Location.—That abscissa of a frequency curve for which the sampling errors of optimum location are uncorrelated with those of optimum scaling. (9.)

Consistency.—A statistic satisfies the criterion of consistency, if, when it is calculated from the whole population, it is equal to the required parameter. (4.)

Distribution.—Problems of distribution are those in which it is required to calculate the distribution of one, or the simultaneous distribution of a number, of functions of quantities distributed in a known manner. (3.)

Efficiency.—The efficiency of a statistic is the ratio (usually expressed as a percentage) which its intrinsic accuracy bears to that of the most efficient statistic possible. It

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- Normal distribution is a useful model in many situations.
- Why? Central Limit Theorem.
- Even when the the distribution of a random variable is not normal, normal theory based tests are surprisingly adequate.
- By “adequate” is meant that significance levels (α) and power ($1 - \beta$) are close to theoretical values.
- Several of these tests first introduced by Fisher, put on a firmer ground by the Neyman-Pearson lemma.

$H_0 : m = m_0$ with $X \sim N(m, \sigma^2)$ and σ^2 known (I)

- We have $\overline{X} \sim N(m_0, \sigma^2/n)$ and therefore:

$$T = \frac{\overline{X} - m_0}{\sigma/\sqrt{n}} \sim N(0,1)$$

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$$\text{Prob}\left\{-z_{\alpha/2} \leq T \leq z_{\alpha/2}\right\} = 1 - \alpha$$

- We would reject H_0 at the significance level α if $|T| > |z_{\alpha/2}|$.

$H_0 : m = m_0$ with $X \sim N(m, \sigma^2)$ and σ^2 known (II)

- If we expect departures from H_0 to be of the form $m > m_0$ or $m < m_0$ we would adjust the critical region accordingly:

$$\begin{aligned} m > m_0 &\implies \text{Reject if } T > z_\alpha \\ m < m_0 &\implies \text{Reject if } T < -z_\alpha \end{aligned}$$

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- Makes sense when looking at the test statistic $T = \dfrac{\overline{X} - m_0}{\sigma/\sqrt{n}}$; would also be the answer given by the Neyman and Pearson theorem for a simple alternative.
- "Reject if $|T| > |z_{\alpha/2}|$" is just a compromise when no clear alternative.

A digression: confidence intervals

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- The “likely” region is the confidence interval.
- This does **not** extend to tests with a prescribed alternative H_a.
- When we have a H_a, the critical region may be one-sided, not the complement of the confidence interval.

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- For given m, the greater n, the farther away from 0 is the mean of the test statistic.

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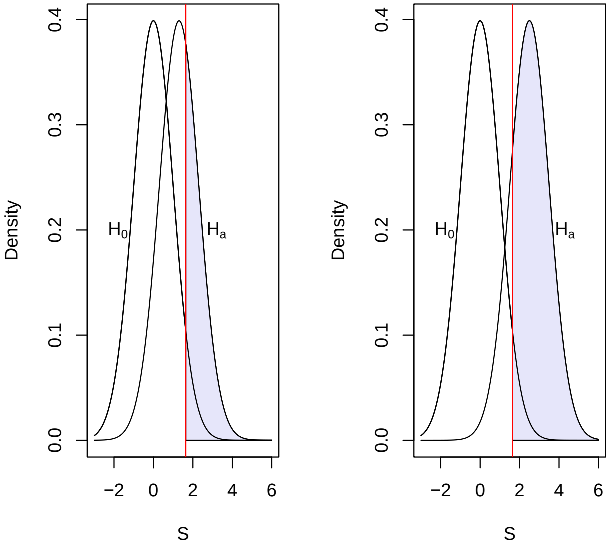

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- Key fact:

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- This paves the way to eliminating the nuisance parameter σ^2 by *studentization*.

$H_0 : m = m_0$ with $X \sim N(m, \sigma^2)$ and σ^2 unknown (II)

- The ratio,

$$T = \frac{\frac{\sqrt{n}(\overline{X}-m_0)}{\sigma}}{\sqrt{\frac{nS^2/\sigma^2}{n-1}}} \quad = \quad \frac{(\overline{X}-m_0)}{S}\sqrt{n-1} \quad \sim \quad \frac{N(0,1)}{\sqrt{\frac{\chi^2_{n-1}}{n-1}}}$$

  when $H_0 : m = m_0$ is true.

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- Decision rule: "Reject H_0 if $|T| > t_{\alpha/2;n-1}$."

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- Decision rule: "Reject H_0 if $|T| > t_{\alpha/2;n-1}$."
- Again, we take critical regions of full α size to the right or to the left, if alternative is one-sided.

Example: $H_0 : m_0 = 2, \sigma^2 = 1$ known

- Let the sample be:

```
> x <- c(2.2,3.4,2.9,3,1.6,3,3.1,3.6,1.9)
> length(x)                        #  sample size
[1] 9
> T <- sqrt(9) * ( mean(x) - 2 ) / 1
> T
[1] 2.233
> qnorm(0.975)                     #  leaves tails of
[1] 1.96
```

- In this case, we would reject.

Example: $H_0 : m_0 = 2$, $\sigma^2 = 1$ unknown

- Now, we would compute

```
> T <- sqrt(9-1) * ( mean(x) - 2 ) / sqrt( 8 *
> T
[1] 3.257
> qt(0.975,df=8)          # so reject
[1] 2.306
> var(x)
[1] 0.4703
> sum( (x-mean(x))^2 ) / 9
[1] 0.418
> ( 8 * var(x) / 9 )     # var command uses (n-1
[1] 0.418
```

$H_0 : \sigma^2 = \sigma_0^2$ with $X \sim N(m, \sigma^2)$

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- Critical region $[0, \chi^2_{n-1;1-\alpha/2}] \cup [\chi^2_{n-1;\alpha/2}, \infty)$, unless we have an alternative $H_a : \sigma^2 < \sigma_0^2$ or $H_a : \sigma^2 > \sigma_0^2$

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- Critical region $[0, \chi^2_{n-1;1-\alpha/2}] \cup [\chi^2_{n-1;\alpha/2}, \infty)$, unless we have an alternative $H_a : \sigma^2 < \sigma_0^2$ or $H_a : \sigma^2 > \sigma_0^2$
- In the first case the critical region would be $[0, \chi^2_{n-1;1-\alpha}]$, in the second $[\chi^2_{n-1;\alpha}, \infty)$

$H_0 : m_1 - m_2 = m_1^* - m_2^*$ with X, Y normal, variances known (I)

- The commonest test by far is that of $H_0 : m_1 - m_2 = 0$, but we present the test generally.

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- We have,

$$\overline{X} - \overline{Y} \quad \sim \quad N\left(m_1 - m_2, \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}\right)$$

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- Hence, under H_0,

$$\frac{\overline{X} - \overline{Y} - (m_1^* - m_2^*)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n}}} \sim N(0, 1)$$

$H_0 : m_1 - m_2 = m_1^* - m_2^*$ with X, Y normal, variances known (II)

- Therefore, under H_0,

$$\text{Prob}\left\{-z_{\alpha/2} \leq \frac{\overline{X} - \overline{Y} - (m_1^* - m_2^*)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}} \leq z_{\alpha/2}\right\} = 1 - \alpha$$

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- The critical region for the test statistic is made of the two $\alpha/2$ tails, unless we have reason to expect the deviance to be one-sided.

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- Using the crucial assumption that $\sigma_1^2 = \sigma_2^2 = \sigma^2$ we can construct a test statistic which does not depend on σ^2 .

$H_0 : m_1 - m_2 = m_1^* - m_2^*$ with X, Y normal, variances $\sigma_1^2 = \sigma_2^2$ unknown (II)

- Using $\sigma_1^2 = \sigma_2^2 = \sigma^2$

$$\frac{\frac{\overline{X}-\overline{Y}-(m_1-m_2)}{\sigma\sqrt{\frac{1}{n_1}+\frac{1}{n_2}}}}{\frac{1}{\sigma}\sqrt{\frac{n_1 S_1^2+n_2 S_2^2}{n_1+n_2-2}}} \quad \sim \quad t_{n_1+n_2-2}$$

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- Cancelling the nuisance parameter σ we end up with:

$$\frac{\overline{X} - \overline{Y} - (m_1 - m_2)}{\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}\sqrt{\frac{n_1 S_1^2+n_2 S_2^2}{n_1+n_2-2}}} \sim t_{n_1+n_2-2}$$

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- Assumption $\sigma_1^2 = \sigma_2^2$ crucial, otherwise an open question (so-called Behrens-Fisher problem).

$H_0 : \sigma_1^2/\sigma_2^2 = \sigma_{1*}^2/\sigma_{2*}^2$ with X, Y normal (I)

- With respective sample sizes n_1 and n_2, we have:

$$\frac{n_1 S_1^2}{\sigma_1^2} \sim \chi^2_{n_1-1} \qquad \frac{n_2 S_2^2}{\sigma_2^2} \sim \chi^2_{n_2-1}$$

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- Clearly both statistics are independent, so

$$\frac{n_1 S_1^2 \sigma_2^2 (n_2 - 1)}{n_2 S_2^2 \sigma_1^2 (n_1 - 1)} \sim \mathcal{F}_{n_1-1, n_2-1}$$

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- It the hypothesis H_0 is true, replacing σ_1^2, σ_2^2 by their hypothetical values would give a test statistic with the distribution shown.

General ideas

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- Tests for the difference of means are quite sensitive to different variances: the requirement $\sigma_1^2 = \sigma_2^2$ cannot be dispensed with.

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- Our test statistic is $\overline{x} - \overline{y}$. Need something to compare to.
- If we arrange the observations as:

  $$x_1, \ldots, x_{n_1}, y_1, \ldots, y_{n_2}$$

  $\overline{x} - \overline{y}$ is just the difference of the averages of the first n_1 and subsequent n_2 observations.

Permutation tests (II)

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- Sampling is usually done by permuting the original sample, hence the name.

Testing $H_0 : m = m_0$ with no normality (I)

- For "large" n (=sample size), use normal theory tests. "Large" is $n \geq 30$ (if σ^2 is known) and $n \geq 100$ (if it is not).

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- For the particular case of $\overline{X}$ we have:

$$\text{Prob}\left\{|\overline{X} - m| < \frac{k\sigma}{\sqrt{n}}\right\} \geq 1 - \frac{1}{k^2}$$

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- Therefore, replacing k by $1/\sqrt{\alpha}$ we have:

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- This distribution-free method gives tests less powerful (and confidence intervals wider) than the normal theory tests.

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$(\overline{X} \pm z_{\alpha/2} s/\sqrt{n})$

The case of a proportion (II)

Example:

- In a sample of 500 parts from a very large batch, 33 are found to be defective. Would the hypothesis $H_0 : p = 0.04$ be rejected against an alternative $H_a : p > 0.04$? $(\alpha = 0.05)$.

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  the critical region would be to the right.
- Replacing $\overline{X}$ by $33/500$ we get a value for the test statistic of 2.97, well inside a critical region of size $\alpha = 0.01$. So we would reject H_0 at said level of significance.

The case of a proportion (III)

Example (continued):

- If we were asked to estimate by interval the true p with confidence $1-\alpha=0.99$, we could use:

$$\frac{(\overline{X}-p)}{\sqrt{\frac{0.0667\times 0.9333}{500}}}\approx N(0,1)$$

The case of a proportion (III)

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- If we were asked to estimate by interval the true p with confidence $1 - \alpha = 0.99$, we could use:

$$\frac{(\overline{X} - p)}{\sqrt{\dfrac{0.0667 \times 0.9333}{500}}} \approx N(0, 1)$$

- Then,

$$\mathrm{Prob}\left\{\overline{X} - 2.5758\sqrt{\frac{0.06222}{500}} \leq p \leq \overline{X} + 2.5758\sqrt{\frac{0.06222}{500}}\right\} \approx 0$$

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- The confidence interval would thus be (0.0666 ± 0.0287)
- Replacing s^2 by the upper bound of $p(1 - p) = 0.25$ would be *very* conservative here.

Testing differences of means

- We state without proof the following approximate results:

$$\begin{aligned}
\frac{\overline{X} - \overline{Y} - (m_1 - m_2)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}} &\approx N(0,1) \qquad (n_1 \geq 30, n_2 \geq 30) \\
\frac{\overline{X} - \overline{Y} - (m_1 - m_2)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} &\approx N(0,1) \qquad (n_1 \geq 100, n_2 \geq 100)
\end{aligned}$$

- Those approximate distributions can be used in the construction of test statistics or confidence intervals.

Testing differences of proportions

- The results in the previous slide can be specialized to the case of two proportions. In that case,

$$\begin{aligned} \overline{X} &= \frac{Z_1}{n_1} \qquad m_1 = p_1 \\ \overline{Y} &= \frac{Z_2}{n_2} \qquad m_2 = p_2 \\ \frac{\frac{Z_1}{n_1} - \frac{Z_2}{n_2} - (p_1 - p_2)}{\sqrt{\frac{p_1 q_1}{n_1} + \frac{p_2 q_2}{n_2}}} &\approx N(0,1) \end{aligned}$$

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How would we construct a confidence interval for $(p_1 - p_2)$?

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$$\left(\frac{Z_1}{n_1} - \frac{Z_2}{n_2}\right) \pm z_{\alpha/2} \sqrt{\frac{p_1 q_1}{n_1} + \frac{p_2 q_2}{n_2}}$$

The OC (“operating characteristic”) curve (I)

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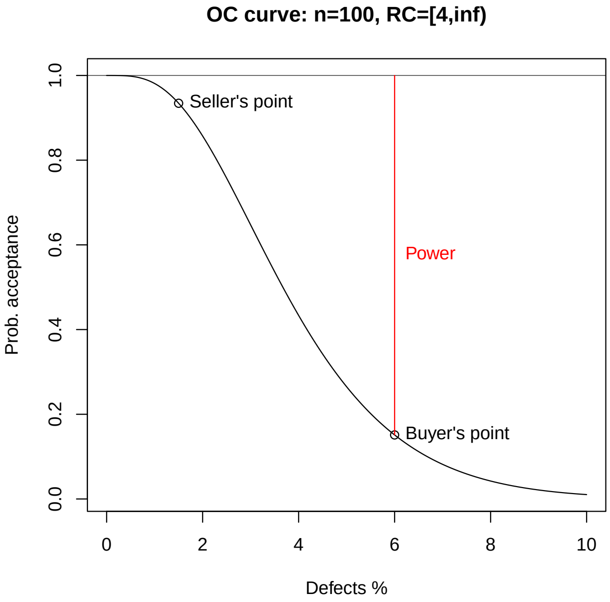
- The performance of a test of H_0 against a set of alternatives usually described by the OC curve: it gives the probability of non-rejection of H_0 for both the null and a range of alternatives.
- Common in specification of industrial quality sampling protocols.
- The conflicting interests of buyer and seller are specified in two points, through which the the curve is forced to pass.

The OC (“operating characteristic”) curve (II)



Paired comparisons (I)

- When performing the classical t-test we assume *independent* observations.
- Sometimes, this is clearly not the case. A different test would be indicated: one possibility is the **paired comparisons test**.

Paired comparisons (II)

- Consider the following data on weight at birth of male babies:

Mother	First	Second
A	3.800	4.150
B	2.400	2.755
C	2.750	2.900
D	1.800	1.990
Average	2.687	2.949

- It doesn't make much sense to assume independence between babies in the first and secon column.
- We may notice that second babies are always heavier; this has probability $1/16$ of happening under the null hypothesis of equal weights.

Paired comparisons (III)

- If weights had the same mean for babies of the same mother, difference of weight should have mean zero.

Mother	**First**	**Second**	**First−Second**
A	3.800	4.150	−0.350
B	2.400	2.755	−0.355
C	2.750	2.900	−0.150
D	1.800	1.990	−0.190
Average	2.687	2.949	−0.261

- This suggests one way of testing which accounts for dependence.

Paired comparisons (IV)

```
> First  <- c(3.80, 2.40, 2.75, 1.80)
> Second <- c(4.150, 2.755, 2.900, 1.990)
> t.test(x=First,y=Second)
        Welch Two Sample t-test

data:  First and Second
t = -0.43, df = 6, p-value = 0.7
alternative hypothesis: true difference in means i
95 percent confidence interval:
 -1.764  1.241
sample estimates:
mean of x mean of y
    2.688     2.949
```

Paired comparisons (V)

```
> t.test(x=First,y=Second, paired=TRUE)
        Paired t-test

data:  First and Second
t = -4.9, df = 3, p-value = 0.02
alternative hypothesis: true mean difference is no
95 percent confidence interval:
 -0.43094 -0.09156
sample estimates:
mean difference
        -0.2613
```

Sampling of independent observations

- We have been assuming samples

  $$X_1, X_2, \ldots, X_n$$

  made of independent observations.
- This makes sense:
  - When we sample an infinite population: seeing one value does not affect the probability of seeing the same or another value.
  - When we sample with replacement.
- With finite populations without replacement, what we see affects the probability of what is yet to be seen.

Finite versus infinite populations (I)

- With infinite populations, precision depends only on sample size.
- Usually, standard error of estimation is $\sqrt{\frac{\sigma^2}{n}}$ where n is sample size and σ^2 the population variance.
- If estimator is **consistent** we approach (but never quite hit with certainty) the true value of the parameter.

Finite versus infinite populations (II)

- If population is finite of size N, we could inspect all units and estimate anything with certainty:

  $$\hat{m} = \frac{X_1 + X_2 + \ldots + X_n}{n}$$

  would verify $m = \hat{m}$ if $n = N$.
- All parameters can, in principle, be known with certainty!
- With $n \neq N$,
  - If $n/N \approx 0$, independent sampling good approximation.
  - If $n/N \gg 0$, we have to take into account that we are looking at a substantial portion of the population.

An overview of things to come

We will see:

- What makes sampling without replacement more complex.
- What relationship there is among independent and non-independent sampling.
- What other types of sampling exist.

The central approximation

- Requirement: replacement or "large" population size N.
- If n is "large" and $X_1, \ldots, X_n$ "near" independent,

$$\overline{X} = \frac{X_1 + \ldots + X_n}{n} \sim N(m, \sigma^2/n)$$

- Then,

$$\text{Prob}\left(\overline{X} - z_{\alpha/2}\sqrt{\frac{\sigma^2}{n}} \leq m \leq \overline{X} + z_{\alpha/2}\sqrt{\frac{\sigma^2}{n}}\right) = 1 - \alpha$$

Estimation of the population total

- Since $T = Nm$, we just have multiply by N the extremes of the interval for m.
- Hence,

$$\text{Prob}\left(N\overline{X} - Nz_{\alpha/2}\sqrt{\frac{\sigma^2}{n}} \leq T \leq N\overline{X} + Nz_{\alpha/2}\sqrt{\frac{\sigma^2}{n}}\right) = 1 - \alpha$$

Estimation of a proportion

- If X_i is a binary variable, $\overline{X}$ is the sample proportion.
- We have $\overline{X} \sim N(p, pq/n)$
- Usual estimate of variance is $\hat{p}(1-\hat{p})/n$.
- Sometimes we use a (conservative) estimate: $pq \leq 0.25$, hence a bound for σ^2 is $0.25/n$.

Sampling error with confidence $1 - \alpha$.

- From
$$\mathrm{Prob}\left(\overline{X} - z_{\alpha/2}\sqrt{\frac{\sigma^2}{n}} \leq m \leq \overline{X} + z_{\alpha/2}\sqrt{\frac{\sigma^2}{n}}\right) = 1 - \alpha$$
we see that we will be off the true value m by less than $z_{\alpha/2}\sqrt{\frac{\sigma^2}{n}}$ with probability $1 - \alpha$.
- This is called the “$1 - \alpha$ (sampling) error”.
- “Sampling error” also used to mean standard deviation of the estimate.

Finding the required sample size n

- **Example:** What n do we need so that with confidence 0.95 the error in the estimation of a proportion is less than 0.03?
- **Solution:** Error is less than $z_{\alpha/2}\sqrt{\frac{\sigma^2}{n}}$ with confidence $1-\alpha$.
- Confidence 0.95 means $z_{\alpha/2} = 1.96$
- Want $0.03 > 1.96\sqrt{\frac{\sigma^2}{n}}$. Worst case scenario is $\sigma^2 = 0.25$.
- Therefore, $n > \frac{(1.96)^2 \times 0.25}{0.03^2} = 1067.11$ will do. Will take $n = 1068$.

Interesting facts (I)

- Under independent sampling required sample size depends only on variance and precision required.
- Questions like: "Is a sample of 4% enough?" are badly posed.
- $n = 400$ (4% of a population with $N = 10000$) insufficient to give a precision of 0.03 with confidence 0.95.
- … but $n = 3000$ (0.3% of a population with $N = 1000000$) vastly enough!

Interesting facts (II)

- As long as populations are large detail is expensive!
- To estimate a proportion in the CAPV with the precision stated requires about $n = 1068$.
- To estimate the same proportion for each of the three Territories with the same precision, requires three times as large a sample!
- Subpopulation estimates have much lower precision than those for the whole population.

Estimation of the mean (I)

- In independent sampling,

$$\begin{aligned} E[\overline{x}] &= E\left[\frac{X_1 + \ldots + X_n}{n}\right] \\ &= \frac{m + m + \ldots + m}{n} = \frac{nm}{n} = m \end{aligned}$$

- $E[X_i] = m$ irrespective of what other values are in the sample.
- Without replacement, distribution of X_i depends on what other values are already present in the sample.
- The same result as for independent sampling is true!

Estimation of the mean (II)

- **Theorem 1** In a finite population of size N with $m = \sum_{i=1}^{N} y_i/N$, for samples $Y_1, \ldots, Y_n$ without replacement of size $n < N$ we have:

$$E[\overline{Y}] = m$$

- **Proof**
  - $Y_1, Y_2, \ldots, Y_n$ are the elements of the sample.
  - $y_1, y_2, \ldots, y_N$ are the elements of the population.

Estimation of the mean (III)

- There are $\binom{N}{n} = \frac{N!}{(N-n)!n!}$ different samples.
- Of those, $\binom{N-1}{n-1}$ contain each of the values $y_1, y_2, \ldots, y_N$.
- Clearly,

$$\sum (Y_1 + Y_2 + \ldots + Y_n) = \binom{N-1}{n-1}(y_1 + y_2 + \ldots + y_N)$$

where the sum in the left is taken over all $\binom{N}{n}$ different samples. Dividing by $\binom{N}{n}$ finishes the proof.

Estimation of the mean (IV)

- Indeed,

$$\begin{aligned} \frac{\sum(Y_1+Y_2+\ldots+Y_n)}{\binom{N}{n}} &= \frac{\binom{N-1}{n-1}(y_1+y_2+\ldots+y_N)}{\binom{N}{n}} \\ &= \frac{n}{N}(y_1+y_2+\ldots+y_N) \end{aligned}$$

- Therefore,

$$E[\overline{Y}] = \frac{\sum(Y_1+\ldots+Y_n)/n}{\binom{N}{n}} = \frac{(y_1+\ldots+y_N)}{N} = E[\overline{y}] = m$$

The indicator variable method

- We have

  $$(Y_1 + Y_2 + \ldots + Y_n) = (y_1 Z_1 + y_2 Z_2 + \ldots y_N Z_N)$$

  where Z_i is a binary variable which takes value 1 if y_i belongs to a given sample.
- The probability of that happening is n/N. Then,

  $$E[(Y_1 + Y_2 + \ldots + Y_n)] = \frac{n}{N}(y_1 + y_2 + \ldots y_N),$$

  which again gives the previous result $E[\overline{Y}] = \overline{y} = m$.

Population variance an quasi-variance

- They are defined as:

$$\sigma^2 = \frac{\sum_{i=1}^{N}(y_i - \overline{y})^2}{N} \qquad \tilde{\sigma}^2 = \frac{\sum_{i=1}^{N}(y_i - \overline{y})^2}{N-1}$$

- Similarly for sample analogues:

$$s^2 = \frac{\sum_{i=1}^{n}(Y_i - \overline{Y})^2}{n} \qquad \tilde{s}^2 = \frac{\sum_{i=1}^{n}(Y_i - \overline{Y})^2}{n-1}$$

- Turns out some formulae are simpler in terms of quasi-variances.

Variance of $\overline{Y}$ (I)

- **Theorem 2** In a finite population of size N, the estimator $\overline{Y}$ of $m = \sum_{i=1}^{N} y_i/N$ based on a sample of size $n < N$ without replacement $Y_1, \ldots, Y_n$ has variance:

$$\mathrm{Var}[\overline{Y}] = \frac{\tilde{\sigma}^2}{n}\left(1 - \frac{n}{N}\right)$$

- Factor

$$\left(1 - \frac{n}{N}\right)$$

  usually called “finite population correction factor” or “correction factor”.

Variance of $\overline{Y}$ (II)

- **Remarks:**
- It is the same expression as in independent random sampling with i) σ^2 replaced by $\tilde{\sigma}^2$, and ii) corrected with the factor $(1 - n/N)$.
- If $n = N$, the variance $\text{Var}(\overline{Y})$ is 0 (why?).
- Formula covers middle ground between infinite populations ($n/N = 0$) and census sampling ($n/N = 1$).

Variance of $\overline{Y}$ (III)

- **Proof**

$$\begin{aligned}\mathrm{Var}(\overline{Y}) &= \mathrm{Var}\left(\frac{y_1 Z_i + \ldots + y_N Z_N}{n}\right)\\ &= \frac{1}{n^2}\left[\sum_{i=1}^{N} y_i^2 \mathrm{Var}(Z_i) + \sum_{i=1}^{N}\sum_{j\neq i} y_i y_j \mathrm{Cov}(Z_i, Z_j)\right]\end{aligned}$$

- We only need expressions for $\mathrm{Var}(Z_i)$ and $\mathrm{Cov}(Z_i, Z_j)$.

Variance of $\overline{Y}$ (IV)

- Since Z_i is binary with probability n/N,

$$\mathrm{Var}(Z_i) = (n/N)(1 - n/N).$$

- But $\mathrm{E}[Z_i Z_j] = P(Z_i = 1, Z_j = 1) = \frac{n(n-1)}{N(N-1)}$, so

$$\mathrm{Cov}(Z_i, Z_j) = \frac{n(n-1)}{N(N-1)} - \left(\frac{n}{N}\right)^2 = -\frac{n(1-n/N)}{N(N-1)}$$

- Replacing in expression for $\mathrm{Var}(\overline{Y})$ will lead to result.

Variance of $\overline{Y}$ (V)

$$\begin{aligned}
\mathrm{Var}(\overline{Y}) &= \frac{1}{n^2}\left[\sum_{i=1}^{N} y_i^2 \underbrace{\mathrm{Var}(Z_i)}_{(n/N)(1-n/N)} + \sum_{i=1}^{N}\sum_{j\neq i} y_i y_j \underbrace{\mathrm{Cov}(Z_i, Z_j)}_{-\frac{n(1-n/N)}{N(N-1)}}\right] \\
&= \frac{1}{n^2}\left(\frac{n}{N}\right)\left(1-\frac{n}{N}\right)\left[\sum_{i=1}^{N} y_i^2 - \frac{1}{N-1}\sum_{i=1}^{N}\sum_{j\neq i} y_i y_j\right]
\end{aligned}$$

- Will rewrite expression in brackets.

Variance of $\overline{Y}$ (VI)

- Remark that,

$$\begin{aligned}\sum_{i=1}^{N}(y_i - m)^2 &= \sum_{i=1}^{N} y_i^2 - \frac{\left(\sum_{i=1}^{N} y_i\right)^2}{N} \\ &= \frac{N-1}{N}\left[\sum_{i=1}^{N} y_i^2 - \sum_{i=1}^{N}\sum_{j\neq i}\frac{y_i y_j}{N-1}\right]\end{aligned}$$

- The expression in square brackets in th r.h.s is therefore $\frac{N}{N-1}\sum_{i=1}^{N}(y_i - m)^2$.

Variance of $\overline{Y}$ (VII)

- We are now done!

$$
\begin{aligned}
\mathrm{Var}(\overline{Y}) &= \frac{1}{n^2}\left(\frac{n}{N}\right)\left(1-\frac{n}{N}\right)\underbrace{\left[\sum_{i=1}^{N} y_i^2 - \frac{1}{N-1}\sum_{i=1}^{N}\sum_{j\neq i} y_i y_j\right]}_{\frac{N}{N-1}\sum_{i=1}^{N}(y_i-m)^2} \\
&= \frac{1}{n}\left(1-\frac{n}{N}\right)\frac{\sum_{i=1}^{N}(y_i-m)^2}{N-1} \\
&= \left(1-\frac{n}{N}\right)\frac{\tilde{\sigma}^2}{n}
\end{aligned}
$$

Sample size for given precision (I)

- The $(1-\alpha)$ error is

$$\delta = z_{\alpha/2}\sqrt{\frac{\tilde{\sigma}^2}{n}(1-n/N)}$$

- Solving for n we obtain

$$n = \frac{N z_{\alpha/2}^2 \tilde{\sigma}^2}{N\delta^2 + \tilde{\sigma}^2 z_{\alpha/2}^2}$$

- In terms of the variance, it can be written as:

$$n = \frac{N z_{\alpha/2}^2 \sigma^2}{(N-1)\delta^2 + \sigma^2 z_{\alpha/2}^2}$$

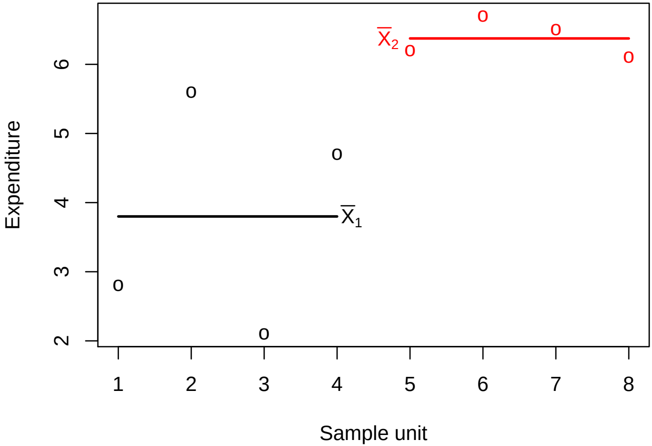
Sample size for given precision (II)

- $\tilde{\sigma}^2$ or σ^2 are required.
- We either replace an upper bound or conservative estimation for σ^2.
- Failing that, we estimate σ^2 or $\tilde{\sigma}^2$.
- Turns out $\tilde{s}^2$ is an unbiased estimate for $\tilde{\sigma}^2 \ldots$
- $\ldots$yet the difference between $\tilde{\sigma}^2$ and σ^2 or $\tilde{s}^2$ and s^2 is so small in practice that they are used interchangeably.

Why strata?

- Sometimes we know something about the composition of the population, knowledge that can be put to use.
- **Example:** We might know that males and females have different spending in e.g. tobacco or cosmetics.
- To estimate average spending, it makes sense to sample males and females, and combine the estimations.
- Sometimes, the target quantity might be similar, but the variance quite different. Also makes sense to differentiate.

Example 1



- Makes sense to estimate mean in each subpopulation

Definitions and notation

- We assume the population is divided in h strata. Total size is $N = N_1 + N_2 + \ldots + N_h$.
- The i-th stratum has a mean $m_i = \frac{1}{N_i} \sum_{j=1}^{N_i} y_{ij}$ and variance $\sigma_i^2 = \frac{1}{N_i} \sum_{j=1}^{N_i} (y_{ij} - m_i)^2$.
- Clearly,

$$\begin{aligned} m &= \sum_{i=1}^{h} \left(\frac{N_i}{N} \right) m_i \\ \sigma^2 &= \sum_{i=1}^{h} \frac{N_i}{N} \sigma_i^2 + \sum_{i=1}^{h} \frac{N_i}{N} (m_i - m)^2 \end{aligned}$$

Estimation of the mean

- The estimator of the mean when sampling without replacement the whole population has variance $\frac{\tilde{\sigma}^2}{n}(1 - n/N)$.
- Similarly, the estimation of the mean of each stratum has variance $\sigma_i^2 = \frac{\tilde{\sigma}_i^2}{n}(1 - n_i/N_i)$.
- The variance of the global mean reconstituted from the estimated means of the strata is

$$\sigma_*^2 = \sum_{i=1}^{h} \left(\frac{N_i}{N}\right)^2 \frac{\tilde{\sigma}_i^2}{n_i}(1 - n_i/N_i)$$

Does the estimation of *m* improve?

- Yes. If we sample each stratum in proportion to its size (i.e., $n_i/N_i = n/N$ for all i), then:

$$\frac{\tilde{\sigma}^2}{n}(1 - n/N) - \sigma_*^2 = \left(1 - \frac{n}{N}\right) \sum_{i=1}^{h} \left(\frac{N_i}{N}\right) \left[\frac{N_i - 1}{N - 1} - \frac{N_i}{N}\right] \frac{\tilde{\sigma}_i^2}{n_i} + \left(1 - \frac{n}{N}\right) \frac{1}{n} \sum_{i=1}^{h} \frac{N_i}{N - 1}(m_i - m)^2$$

- Marked Improvement when the m_i's very different.

Optimal allocation (I)

- It makes little sense to spend sampling effort for homogeneous strata.
- After all, if a stratum is perfectly homogeneous, looking at a single observation is enough.
- Let $w_i = N_i/N$. If we can spend C, we should minimize

$$F = \sum_{i=1}^{h} w_i^2 \frac{\tilde{\sigma}_i^2}{n_i} + \lambda \left(\sum_{i=1}^{h} c_i n_i - C \right)$$

- First term, variance neglecting finite population correction.
- Second term, restriction on total sampling cost, assuming c_i cost per unit sampled in stratum i.

Optimal allocation (II)

- Taking derivatives w.r.t. n_i ($i = 1, \ldots, h$) and equating to zero, we obtain

$$\frac{\partial F}{\partial n_i} = \frac{w_i^2 \tilde{\sigma}_i^2}{-n_i^2} + \lambda c_i = 0$$

- From that expression we get,

$$n_i \propto \frac{N_i \tilde{\sigma}_i}{N\sqrt{c_i}}$$

- Therefore enough to allocate n_i proportional to right hand side..
- Intuition: sample more **big** strata and **disperse** strata; sample less strata where sampling is relatively more **costly**.

Optimal allocation (III)

- But, how to determine n_i?
- We know

$$n_i = k \frac{N_i \tilde{\sigma}_i}{N \sqrt{c_i}}$$

- Further,

$$C = \sum_{i=1}^{h} c_i n_i = k \sum_{i=1}^{h} \frac{N_i \tilde{\sigma}_i \sqrt{c_i}}{N}$$

- Therefore,

$$n_i = \underbrace{\frac{NC}{\sum_{i=1}^{h} N_i \tilde{\sigma}_i \sqrt{c_i}}}_{\color{red}{k}} \times \frac{N_i \tilde{\sigma}_i}{N \sqrt{c_i}}$$

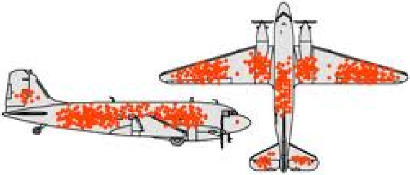
Abraham Wald on sample selection

Abraham Wald (1902-1950)

- Hungarian-born. Graduated (Ph.D. Mathematics) from University of Vienna, 1931.
- Fled to the USA in 1938, as Nazi persecution intensified in Austria.
- Important contributions to the war effort as statistician (notably sequential analysis)
- Was consulted about aircraft armoring.

What Wald saw that the others did not

- *Mark hits in B-29 bombers as they come back.*



- Pretty obvious! Will armor the most beaten areas.
- *I didn't tell you to do that!*
- Do you want us to protect the areas with no hits?
- *That's exactly what I suggest!*

Sample selection is ubiquitous!

- If you ask for volunteers in a field study, no chance you will get a truly random sample.
- Never do!
- Do not let the survey taker choose the units.
- A random sample is not a “grab set”.
- Build a census, randomize properly, address the chosen units and no others.

Methods of sampling that you should be aware of

- Multi-step sampling and conglomerate sampling
- Systematic sampling
- If you use systematic sampling (every n-th unit with random start), make sure no periodicities exist that will destroy randomness.

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- Central limit theorem (CLT) establishes convergence in distribution to a normal in many circumstances.
- If

  $$\varphi_{X_n}(u) \longrightarrow \varphi_X(u)$$

  and $\varphi_X(u)$ is continuous at $u = 0$, then $X_n \xrightarrow{d} X$ (or, equivalently, $F_{X_n}(x) \longrightarrow F_X(x)$ in all continuity points of $F_X(x)$).

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- ...but not in the usual "mathematics" sense.
- When we say that e.g. $a_n = 1/n$ converges to 0 we mean that for large enough n, $a_n \approx 0$.
- No matter how small ϵ, n can always be found such that $|a_n - 0| < \epsilon$.

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- Tchebycheff's inequality is a simple way to show convergence in probability in many cases.

Convergence in probability via Tchebychev inequality (I)

- Consider the simple case where $Z_n \sim (m, \sigma^2/n)$. This happens for instance with the binomial frequency $(X_1 + \ldots + X_n)/n$ with $m = p$ and $\sigma^2 = pq$.

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- Make your pick of $1 - \eta$ as close to 1 as desired; whatever the implied k, we only have to choose n large enough to make ϵ as small as we wish.

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  ensures $Z_n \xrightarrow{p} m$.
- Common mean and variance going to zero is a sufficient condition for convergence in probability (to the common mean) of a random sequence.

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- It also implies weak convergence.

Books and Monographies I