#### Philip Leifeld

GV903: Advanced Research Methods, Week 11



# 1. Conceptual Introduction

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- We can come up with linear models for other outcome distributions, like binary or Poisson-distributed data and plug them in.
- In fact, we can use any distribution as an underlying population process.

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- ► Easy: take the product of all individual probabilities because the probabilities are independent from each other.
- We can leverage this idea for forming a likelihood function, too.

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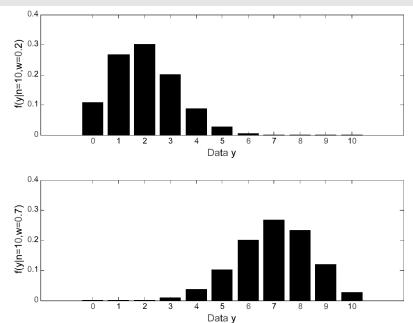
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- ► The two are in principle identical, except you ask the other way around. What is the model, given the observed data? Rather than what are the expected data, given a known model?

# Example: Binomial Distribution

# Binomial Sampling, n = 10 and w = 0.2 or w = 0.7



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Binomial probability function:

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I. e., we insert the probability parameter first and then get the expected observations.

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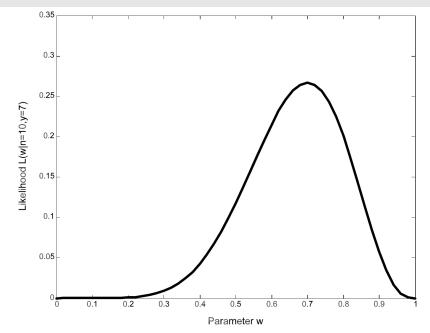
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Binomial likelihood function for w = 0.7: L(w | n = 10, y = 7) = f(y = 7 | n = 10, w)

$$= \frac{10!}{7!3!} w^7 (1 - w)^3 \quad (0 \le w \le 1).$$

I. e., now we insert the observations first and then solve for the parameter  $\boldsymbol{w}$ .

#### The Likelihood Function for w = 0.7



# 3. MLE: The General Procedure

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4. Take the second derivative to verify this is a maximum, not a minimum:

$$\frac{\partial^2 \ln L(w|y)}{\partial w_i^2} < 0.$$

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$$\frac{d^2 \ln L(w \mid n = 10, y = 7)}{dw^2} = -\frac{7}{w^2} - \frac{3}{(1 - w)^2}$$
$$= -47.62 < 0$$

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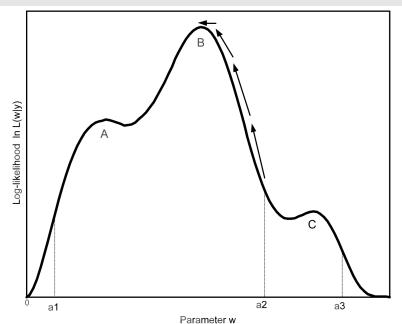
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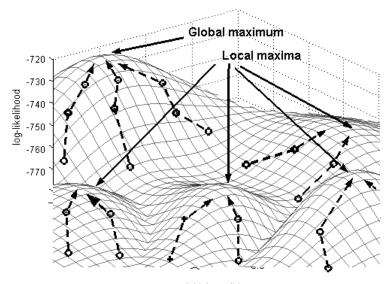
An optimization algorithm needs to find the maximum, for example Newton-Raphson or BFGS.

# Iterative Optimization to Find the MLE

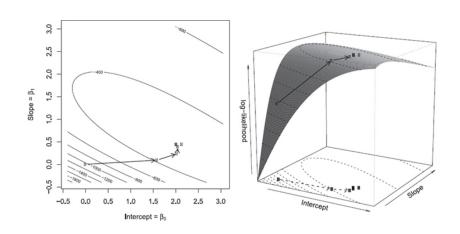


#### Multidimensional Likelihood and Local Maxima

Source: Akbar et al 2019: Statistical Analysis of Wireless Systems Using Markov Models



## Newton-Raphson Optimization for Linear Models



# 4. Example: Sample Mean

Following the exposition in Scott Long (1997)

You should know the PDF of the normal distribution (here with  $\sigma=1$  fixed):

$$f(y_i | \mu, \sigma = 1) = \frac{1}{\sqrt{2\pi}} \exp\left(\frac{-(y_i - \mu)^2}{2}\right)$$

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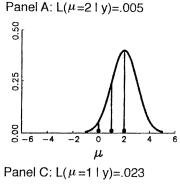
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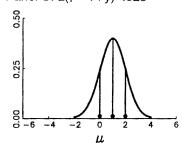
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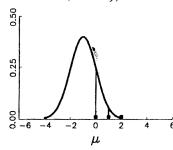
Let's say the three observed values are 0, 1, and 2. We can take a few "guesses" of  $\mu$  and evaluate the likelihood...

# Four Guesses of $\mu$ : $\mu = 1$ Maximizes the Likelihood

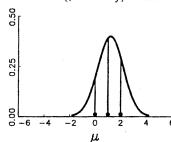




Panel B:  $L(\mu = -1 \text{ l y}) = .0001$ 



Panel D:  $L(\mu = 1.2 \text{ l y}) = .022$ 



# 5. Re-Interpreting the Linear Model

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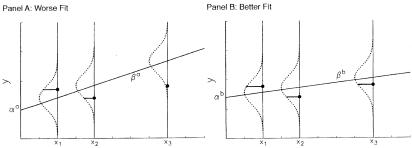
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The corresponding likelihood function (i. e., for all data):

$$L(\alpha, \beta, \sigma | \mathbf{y}, \mathbf{X}) = \prod_{i=1}^{N} \frac{1}{\sigma} \phi \left( \frac{y_i - [\alpha + \beta x_i]}{\sigma} \right)$$

Take the log (note how this replaces product by sum operator):

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We can now compute the first and second derivative to maximize this likelihood. This will yield  $\hat{\beta}$  and  $\hat{\sigma}$ .

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This extends seamlessly to the multiple regression case with more IVs (see Ward/Ahlquist p. 13 for additional simplification):

$$\ln L(\boldsymbol{\beta}, \sigma | \mathbf{y}, \mathbf{X}) = \sum_{i=1}^{N} \ln \frac{1}{\sigma} \phi \left( \frac{y_i - \mathbf{x}_i \boldsymbol{\beta}}{\sigma} \right)$$

We can now compute the first and second derivative to maximize this likelihood. This will yield  $\hat{\beta}$  and  $\hat{\sigma}$ .

We can do this analytically for the linear model. (In most cases, we would need an optimization algorithm.)

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Think of this as the multivariate version of the second derivative for testing for a maximum of the log likelihood.

A small value for the diagonal  $\beta$  entry, for example, indicates that the likelihood is changing slowly when  $\beta$  changes, which means the maximum is hard to find with respect to  $\hat{\beta}$  and the variance is large.

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# 6. MLE in R

Binomial likelihood function with y heads, n trials,  $\pi$  probability:

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Corresponding log likelihood:

```
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```

Write this as an R function:

```
binomial.loglikelihood <- function(prob, y, n) {
   loglikelihood <- y*log(prob) + (n-y)*log(1-prob)
   return(loglikelihood)
}</pre>
```

Use the optim function to optimize the likelihood given fixed y, n:

#### This yields a list object with several slots:

```
$par
[1] 0.4300015
$value
[1] -68.33149
$counts
function gradient
      13
$convergence
[1] 0
$message
NULL
$hessian
           [,1]
[1,] -407.9996
```

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```
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[1] 0.4300015
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      13
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           [,1]
[1,] -407.9996
par lists the estimated \pi parameter.
```

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```
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      13
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$message
NULL
$hessian
           [,1]
[1,] -407.9996
```

value shows the log-likelihood of our final solution.

This yields a list object with several slots:

```
$par
[1] 0.4300015
$value
[1] -68.33149
$counts
function gradient
      13
$convergence
[1] 0
$message
NULL
$hessian
           [,1]
[1,] -407,9996
```

counts shows how often optim called the function and gradient.

This yields a list object with several slots:

```
$par
[1] 0.4300015
$value
[1] -68.33149
Scounts
function gradient
      13
$convergence
[1] 0
$message
NULL
$hessian
           [.1]
[1,] -407.9996
```

convergence: 0 means successfully converged to maximum.

This yields a list object with several slots:

```
$par
[1] 0.4300015
$value
[1] -68.33149
Scounts
function gradient
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$convergence
[1] 0
$message
NULL
$hessian
           [.1]
[1,] -407.9996
```

message: Messages from the function during optimization.

This yields a list object with several slots:

```
$par
[1] 0.4300015
$value
[1] -68.33149
$counts
function gradient
      13
$convergence
[1] 0
$message
NULL
$hessian
           [,1]
[1,] -407.9996
```

hessian: Hessian matrix (here: only one parameter).

We can now proceed to compute the standard error(s): sqrt(diag(solve(-test\$hessian)))

#### MIF in R.

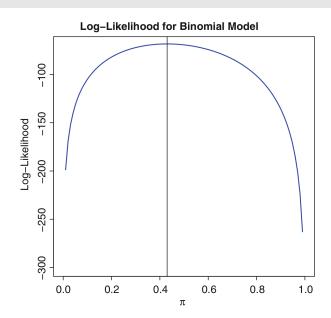
We can now proceed to compute the standard error(s):

```
sqrt(diag(solve(-test$hessian)))
```

Only one parameter. It's easy to plot the likelihood function:

```
ruler <- seq(0,1,0.01)
loglikelihood <- binomial.loglikelihood(ruler, y=43, n=100)
plot(ruler, loglikelihood, type="l", lwd=2, col="blue",
    xlab=expression(pi),ylab="Log-Likelihood",ylim=c(-300,-70),
    main="Log-Likelihood for Binomial Model")
abline(v=.43)</pre>
```

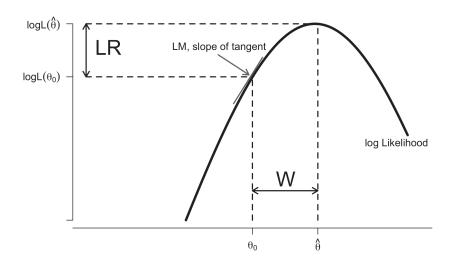
#### MLE in R: The Likelihood Function



# 7. Diagnostics and Goodness of Fit

# MLE Diagnostics

Likelihood Ratio Test, Wald Statistic, and LM Test



This is the MLE analogue of the F test.

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$$LR(\boldsymbol{\theta}_R, \boldsymbol{\theta}_G \mid \mathbf{x}) = -2\log \frac{\mathcal{L}(\boldsymbol{\theta}_R \mid \mathbf{x})}{\mathcal{L}(\boldsymbol{\theta}_G \mid \mathbf{x})}$$

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It follows a  $\chi^2_{q-r}$  distribution with g-r degrees of freedom.

A similar diagnostic is the *model deviance*, the log-likelihood difference between a model and a saturated model (with as many parameters as observations). It is sometimes used to compute the difference between residual deviance and null deviance.

#### AIC and BIC

The most common goodness-of-fit measures for MLE are AIC and BIC.

Akaike Information Criterion (AIC):

$$AIC = -2\log\hat{\mathcal{L}} + 2k$$

Bayesian Information Criterion (BIC):

$$BIC = -2\log \hat{\mathcal{L}} + k\log n$$

where k is the number of parameters and n is the number of observations.

Both measures penalise the inclusion of additional parameters.

Smaller values are "better". Only use for model comparison with the same data! Never interpret the absolute value of AIC or BIC!

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- MLE will allow us to look at models for various outcome distributions in the spring, such as binary, count, and ordinal DVs. This is called *generalized linear model* (GLM).
- ► The MLE framework is also the starting point for Bayesian statistics (not covered in this module).