# Estimation of Parameter Values 

Nutrition Models Workshop

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## Outline

- Nutrition models are VERY diverse
- Combination of empirical, mechanistic, dynamic and static models
- Regression, linear and nonlinear mixed models, differential equations
- Today: Main approaches for estimating parameters in a variety of models
- Some mathematical description
- Idea is for you to understand the reasoning and challenges of different approaches
- One exercise/demonstration in the end
- Fit model with two approaches


## Introduction

- Different types of models have been used for nutrition modeling
- Compartmental, regression, meta-analysis, nonlinear mixed models, .....
- One feature is common to almost all these models
- Parameters are needed to describe the system
- Quantify relationship between variables


## Introduction

- Simple example: linear regression

$$
Y_{i}=\beta_{0}+\beta_{1} x_{i}+\varepsilon_{i}
$$



- $Y_{i}$ is the response variable for the $i$ th observation
- $x_{i}$ is the predictor variable in the $i$ th observation
- $\beta_{0}$ is the intercept
- $\beta_{1}$ is the slope
- $\varepsilon_{i}$ is the error, $E\left[\varepsilon_{i}\right]=0, \operatorname{Var}\left[\varepsilon_{i}\right]=\sigma^{2}$ and $\varepsilon_{i}$ are independent
- $i=1, \ldots, n$

In matrix notation: $\quad \mathbf{y}=\mathbf{X} \boldsymbol{\beta}+\boldsymbol{\varepsilon}$

$$
\left[\begin{array}{c}
Y_{1} \\
\vdots \\
Y_{n}
\end{array}\right]=\left[\begin{array}{cc}
1 & x_{1} \\
\vdots & \vdots \\
1 & x_{n}
\end{array}\right]\left[\begin{array}{l}
\beta_{0} \\
\beta_{1}
\end{array}\right]+\left[\begin{array}{c}
\varepsilon_{1} \\
\vdots \\
\varepsilon_{n}
\end{array}\right]
$$

## Introduction

- In practice, parameter true values are unknown
- Estimators from a sample
- Parameters have to be optimal in some sense
- Least square estimators minimize squared errors
- Maximum likelihood estimators maximize the likelihood function


## Least Squares Estimators




## Least Square Estimators

- The least squares estimators minimize the square errors: $Q=\sum_{i=1}^{n}\left[Y_{i}-\left(\beta_{0}+\beta_{i} x_{i}\right)\right]^{2}$
- How do we get them???
- We can find points of minimum and maximum of a function using derivatives.


For example for $f(x)=160 x-16 x^{2}$

Set derivative to zero and "solve" for $x$ :

$$
\begin{gathered}
160-32 x=0 \\
x=5
\end{gathered}
$$

Second derivative test: - 32

## Least Squares Estimators

$$
\begin{aligned}
& \frac{\partial Q}{\partial \beta_{0}}=-2 \sum_{i=1}^{n}\left(Y_{i}-\beta_{0}-\beta_{1} x_{i}\right) \\
& \frac{\partial Q}{\partial \beta_{0}}=-2 \sum_{i=1}^{n} x_{i}\left(Y_{i}-\beta_{0}-\beta_{1} x_{i}\right)
\end{aligned}
$$

Setting these partial derivatives to zero, we construct the normal equations

$$
\begin{aligned}
& \sum_{i=1}^{n} Y_{i}=n b_{0}+b_{1} \sum_{i=1}^{n} X_{i} \\
& \sum_{i=1}^{n} X_{i} Y_{i}=b_{0} \sum_{i=1}^{n} X_{i}+b_{1} \sum_{i=1}^{n} X_{i}^{2}
\end{aligned}
$$

## Least Squares Estimators

- The least square estimators are the solutions to the normal equations

$$
\begin{aligned}
& b_{1}=\sum_{i=1}^{n}\left(x_{i}-\bar{x}\right)\left(Y_{i}-\bar{Y}\right) / \sum_{i=1}^{n}\left(x_{i}-\bar{x}\right)^{2} \\
& b_{0}=\bar{Y}-b_{1} \bar{x}
\end{aligned}
$$

- The concept extends to multiple regression

$$
Q=\sum_{i=1}^{n}\left[Y_{i}-\left(\beta_{0}+\beta_{1} x_{i 1}+\beta_{p-1} x_{i, p-1}\right)\right]^{2}
$$

- General form of the least squares estimators: $\mathbf{b}=\left(\mathbf{X}^{\mathrm{T}} \mathbf{X}\right)^{-1} \mathbf{X}^{\mathrm{T}} \mathbf{Y}$


## Least Squares Estimators

- Estimates of the uncertainty associated with these parameters
- Estimator of the error's variance

$$
M S E=\frac{1}{n-p} \sum_{i=1}^{n}\left[Y_{i}-\left(b_{0}+b_{1} x_{i 1}+\cdots+b_{p-1} x_{i, p-1}\right)\right]^{2}
$$

- Estimated variance-covariance matrix of the parameters

$$
\operatorname{MSE}\left(\mathbf{X}^{\mathrm{T}} \mathbf{X}\right)^{-1}
$$

## Nonlinear Models

- So far, we can estimate parameters in linear models
- Many phenomena in biology are nonlinear
- For example, reaction velocity vs. substrate concentration in an enzymatic reaction
- Before we start with nonlinear models, let's clarify

$$
\begin{array}{ll}
Y_{i}=\frac{\theta_{1}}{1+\theta_{2} \exp \left(\theta_{3} x_{i}\right)}+\varepsilon_{i} & \text { is a nonlinear model } \\
Y_{i}=\beta_{0}+\beta_{1} x_{i}+\beta_{2} x_{i}^{2}+\varepsilon_{i} & \text { is a linear model }
\end{array}
$$

## Nonlinear Models

Michaelis-Menten Kinetics

$$
v=\frac{V_{\max }[S]}{K_{M}+[S]}
$$



## Nonlinear Regression

$$
Y_{i}=f\left(x_{i}, \boldsymbol{\theta}\right)+\varepsilon_{i}
$$

$f$ is the nonlinear function describing the relationship between $Y$ and $x$
Michaelis-Menten example: $\quad y_{i}=\frac{V_{\max } x_{i}}{K_{M}+x_{i}}+\varepsilon_{i} \quad \Rightarrow f\left(x_{i}, \boldsymbol{\theta}\right)=\frac{V_{\max } x_{i}}{K_{M}+x_{i}}$

- $y_{i}$ is the reaction rate for the th observation
- $x_{i}$ is the associated substrate concentration
$\boldsymbol{\theta}=\left(V_{\max }, K_{M}\right)^{\mathrm{T}}$ are the parameters to be estimated
- $\varepsilon_{i}$ is the error, $\mathrm{E}\left[\varepsilon_{i}\right]=0, \operatorname{Var}\left[\varepsilon_{i}\right]=\sigma^{2}$ and independent
- $i=1, \ldots, n$


## Least Squares Estimators

- For the simple linear regression model, least squares minimize

$$
Q=\sum_{i=1}^{n}\left[Y_{i}-\left(\beta_{0}+\beta_{1} x_{i}\right)\right]^{2}
$$

- For the nonlinear regression, the idea is the same: minimize

$$
Q=\sum_{i=1}^{n}\left[Y_{i}-f\left(x_{i}\right)\right]^{2}
$$

## Least Squares Estimators

- Solution to the normal equations are often difficult to obtain analytically
- Numerical Algorithms
- For example, Gauss-Newton
- Require initial values to initialize numerical procedures


## Gauss-Newton

- Default in PROC NLIN and nls ()
- Approximate the nonlinear model with linear terms
- Taylor series expansion and least squares as for linear regression
- Denote the least squares estimates $\mathbf{g}$ and the initial values $\mathbf{g}^{(0)}=\left(g_{0}^{(0)}, g_{1}^{(0)}, \cdots, g_{p-1}^{(0)}\right)$
- Approximation around starting values:

$$
f\left(x_{i}, \boldsymbol{\theta}\right) \approx f\left(x_{i}, \mathbf{g}^{(0)}\right)+\sum_{k=0}^{p-1}\left[\frac{\partial f\left(x_{i}, \boldsymbol{\theta}\right)}{\partial \theta_{k}}\right]_{\theta=g^{(0)}}\left(\theta_{k}-g_{k}^{(0)}\right)
$$

## Gauss-Newton

- Model approximation

$$
Y_{i}-f\left(x_{i}, \mathbf{g}^{(0)}\right) \approx \sum_{k=0}^{p-1}\left[\frac{\partial f\left(x_{i}, \boldsymbol{\theta}\right)}{\partial \theta_{k}}\right]_{\theta=g^{(0)}}\left(\theta_{k}-g\right)_{k}^{(0)}+\varepsilon_{i}
$$

- It is a linear model!
- Estimate parameters by least squares: $\mathbf{b}^{(0)}=\left(\mathbf{D}^{(0) \mathrm{T}} \mathbf{D}^{(0)}\right)^{-1} \mathbf{D}^{(0) \mathrm{T}} \mathbf{Y}^{(0)}$
- Update: $\mathbf{g}^{(1)}=\mathbf{g}^{(0)}+\mathbf{b}^{(0)}$


## Gauss-Newton

- Evaluation criteria: $S S E^{(0)}=\sum_{i=1}^{n}\left(Y_{i}-f_{i}^{(0)}\right)^{2}$
- Start the process again with $\mathbf{g}^{(1)}$ as the initial values
- Repeat procedure until $S S E^{(s+1)}-S S E^{(s)}$ is negligible
- Estimate of error's variance: $M S E=\sum_{i=1}^{n}\left[Y_{i}-f\left(x_{i}, \mathbf{g}\right)\right]^{2} / n-p$
- Other methods available, e.g. Nelder-Mead and Marquardt


## Compartmental Models

- Traditionally used in nutritional modeling
- Roots on pharmacokinetics and differential calculus



## Compartmental Models

- Functional forms described in terms of differential equations
- Instead of the "integrated form"
- Strategy for parameter estimation
- Expected mean represented by a compartmental model $f$
- If $f$ cannot be obtained analytically, it has to be solved numerically
- Euler, Runge-Kutta4, Isoda
- Can use nonlinear least squares but have to numerically solve $f$ at iteration
- Modern software estimate using maximum likelihood


## Maximum Likelihood Estimation

- Another strategy for parameter estimation
- For regression models with independent $\varepsilon_{i} \sim N\left(0, \sigma^{2}\right)$, estimators coincide with least squares estimators
- Estimators maximize the likelihood function
- Parameter values that are in best agreement with the data


## Maximum Likelihood Estimation



$$
p\left(y \mid \mu, \sigma^{2}\right)=\frac{1}{\sqrt{2 \pi \sigma^{2}}} \exp \left(-\frac{(y-\mu)^{2}}{2 \sigma^{2}}\right)
$$

- $p\left(y \mid \mu \sigma^{2}\right)$ is the density function: How likely $y$ is at each value
- The likelihood function is: $L\left(\mu, \sigma^{2} \mid y_{1}, \ldots, y_{n}\right)=p\left(y_{1} \mid \mu, \sigma^{2}\right) \times \ldots \times p\left(y_{n} \mid \mu, \sigma^{2}\right)$
- "How likely the whole data is with that set of parameters values"
- MLE: "maximize the likelihood of getting the observed data"


## Maximum Likelihood Estimation

- Linear Regression Example: $Y_{i}=\beta_{0}+\beta_{1} x_{i}+\varepsilon_{i}$

$$
L\left(\beta_{0}, \beta_{1}, \sigma^{2} \mid y_{1}, \ldots, y_{n}\right)=\left(\frac{1}{\sqrt{2 \pi \sigma^{2}}}\right)^{n} \exp \left[-\frac{1}{2 \sigma^{2}} \sum_{i}\left(y_{i}-\beta_{0}-\beta_{1} x_{i}\right)^{2}\right]
$$

- It is easier to work with the log-likelihood

$$
\log L\left(\beta_{0}, \beta_{1}, \sigma^{2} \mid y_{1}, \ldots, y_{n}\right)=-\frac{n}{2} \log (2 \pi)-\frac{n}{2} \log \left(\sigma^{2}\right)-\frac{1}{2 \sigma^{2}} \sum_{i}\left(y_{i}-\beta_{0}-\beta_{1} x_{i}\right)^{2}
$$

- To find parameters that maximize the likelihood we...
- Take the derivative with respect to each parameter and set to zero. Also need second derivative test


## Mixed Models

- Modern mixed modeling relies heavily on likelihood methods
- Extension of (non)linear models with both fixed and random effects
- Probably the "type" of model you need to analyze your data or construct your nutrition model
- There's a whole workshop on mixed models in this meeting


## Nonlinear Mixed Models

- Nonlinear functional forms
- Michaelis-Menten, logistic, exponential, Gompertz, ...
- Random effects that "enter the model" nonlinearly
- Allow you to model nonlinear clustered, logitudinal data
- Records from the same animal, treatment means from the same study


## Nonlinear Mixed Models

$$
y_{i j}=f\left(x_{i j}, \boldsymbol{\theta}_{i}\right)+\varepsilon_{i j}
$$

- $y_{i j}$ is the $j$ th record on the ith "subject" or cluster
- $x_{i j}$ is the associated predictor variable
- $\boldsymbol{\theta}_{i}$ is the vector of subject specific parameters

- $\varepsilon_{i j}$ is the random error $\sim N\left(0, \sigma^{2}\right)$


## Nonlinear MM Maximum Likelihood

- There is more than one source of variability
- Between subjects and within subjects
- To represent the generative process of the data we need to take both into account
- Joint density of the response and the random effects


## Maximum Likelihood

- For the linear regression


$$
p\left(y \mid \mu, \sigma^{2}\right)=\frac{1}{\sqrt{2 \pi \sigma^{2}}} \exp \left(-\frac{(y-\mu)^{2}}{2 \sigma^{2}}\right)
$$

- The likelihood function is: $L\left(\mu, \sigma^{2} \mid y_{1}, \ldots, y_{n}\right)=p\left(y_{1} \mid \mu, \sigma^{2}\right) \times \ldots \times p\left(y_{n} \mid \mu, \sigma^{2}\right)$
- For the nonlinear mixed model, we need to compute the marginal density of the responses: $p\left(\mathbf{y} \mid \boldsymbol{\beta}, \sigma^{2}, \Psi\right)=\int p\left(\mathbf{y} \mid \mathbf{b}, \boldsymbol{\beta}, \sigma^{2}\right) p(\mathbf{b} \mid \Psi) d \mathbf{b}$


## Maximum Likelihood

- Bad news from a estimation perspective
- The likelihood function to estimate the parameters requires integrating the joint density with respect to the random effects
- The integral often does not have a closed form expression
- Approximation of the likelihood function


## Exercise

- Let's go back to the compartmental model

$$
\left\{\begin{array}{l}
\frac{d y_{1}}{d t}=-k_{a} y_{1} \\
\frac{d y_{2}}{d x}=k_{a} y_{1}-k_{e} y_{2}
\end{array}\right.
$$

- $y_{1}$ is the amount of drug in the gut compartment
- $y_{2}$ is the amount of drug in the blood compartment
- $k_{a}$ is the absorption rate $(1 / \mathrm{hr})$
- $k_{e}$ is the elimination rate $(1 / \mathrm{hr})$


## Exercise

- Data from Davidian and Giltinan (1995)
- 12 subjects received a single oral dose of theophylline
- Anti-asthmatic drug
- Single oral dose at time zero
- Measurements of blood concentrations of drug at 11 time points over a 25 hour period


## Exercise



## Exercise

- We only observe data from the second compartment
- The differential equation for the second compartment can actually be solved analytically
- We will estimate the parameters in two different ways
- Analytical solutions: nonlinear mixed model
- Numerical solutions for differential equations in a mixed model framework


## Exercise

- The analytical solution to the second differential equation is

$$
C(t)=\frac{\text { Dose } k_{e} k_{a}}{C l\left(k_{a}-k_{e}\right)}\left[\exp \left(-k_{e} t\right)-\exp \left(-k_{a} t\right)\right]
$$

- As a nonlinear mixed model

$$
\begin{gathered}
C_{i j}=\frac{\operatorname{Dose}_{i} k_{e} k_{a, i}}{C l_{i}\left(k_{a, i}-k_{e}\right)}\left[\exp \left(-k_{e} t_{i j}\right)-\exp \left(-k_{a, i, t} t_{i j}\right)\right]+\varepsilon_{i j} \\
\varepsilon_{\varepsilon_{i j} \sim N\left(0, \sigma^{2}\right) \text { and }\left[\begin{array}{l}
C l_{i} \\
k_{a, i}
\end{array}\right] \sim N\left(\left[\begin{array}{cc}
0 \\
0
\end{array}\right],\left[\begin{array}{cc}
\sigma_{c l}^{2} & 0 \\
0 & \sigma_{k_{i}}^{2}
\end{array}\right]\right)}=\text {. }
\end{gathered}
$$

## Exercise

- All three parameters must be positive
- Reparameterize model with parameters on a log scale

$$
C(t)=\frac{\text { Dose } \exp \left(l k_{e}+l k_{a}-l C l\right)}{\exp \left(l k_{a}\right)-\exp \left(l k_{e}\right)}\left\{\exp \left[-\exp \left(l k_{e}\right) t\right]-\exp \left[-\exp \left(l k_{a}\right) t\right]\right\}
$$

where

$$
l k_{e}=\log \left(k_{e}\right) \quad, \quad l k_{a}=\log \left(k_{a}\right) \quad \text { and } \quad l C l=\log (C l)
$$

## Exercise

- First method
- Fit nonlinear mixed model in R


## Exercise

- Second method
- Nonlinear mixed model but solve differential equations numerically: Isoda solver

$$
\left\{\begin{array}{l}
\frac{d y_{1}}{d t}=-k_{a} y_{1} \\
\frac{d y_{2}}{d x}=k_{a} y_{1}-k_{e} y_{2} \\
y_{1}(0)=\text { Dose } \\
y_{2}(0)=0
\end{array}\right.
$$

- Observation Equation: $\quad C(t)=\frac{y_{2}(t)}{C l} k_{e}$


## Bayesian Inference

- Combines prior information with new data: update of knowledge
- All parameters are treated as random variables
- Prior distributions for parameters
- Inference is based on the posterior distribution
- Bayes theorem

Prior: beta(52.22,9.52); Data: B(50,25); Posterior: beta(77.22,34.52)


## Bayesian Inference

- Inference based on posterior
- Combines prior information with the observed data
- Particularly suited for models built with many parameters that good biological knowledge is available
- Many freely software available
- Including with differential equations "solvers"
- We don't have to have a known or tractable posterior: Markov Chain Monte Carlo (MCMC)


## Example of a Multivariate Nonlinear Model

- From Strathe et al. (2012). J. Agri. Sci. 150:764-774



## Example for a Multivariate Nonlinear Model

$$
\begin{array}{ll}
\text { Multivariate Model: } & P D=\frac{P D_{\max }}{B W_{P D \max }} B W \cdot \log \left(\frac{B W_{P D \max } \cdot \exp (1)}{B W}\right) \\
L D & =k_{f}\left(M E-a \cdot B W^{b}-P D / k_{p}\right)
\end{array}
$$

## Priors from literature

partial etticiencies $\mathrm{k}_{\mathrm{p}}$ and $\mathrm{k}_{\mathrm{f}}$

| $k_{f}$ | $k_{p}$ | Reference |
| :--- | :--- | :--- |
| $0.72-0.88$ | $0.52-0.63$ | Strathe et al. (2010a)* |
| 0.75 | 0.56 | van Milgen et al. (2000)* |
| $0.77-0.82$ | $0.58-0.60$ | van Milgen \& Noblet (1999)* |
| 0.84 | 0.62 | Noblet et al. (1999) $\dagger$ |
| 0.76 | 0.54 | NRC (1998) $\dagger$ |
| 0.60 | 0.52 | Tess et al. (1984) $\dagger$ |
| 0.74 | 0.56 | ARC (1981) $\dagger$ |

Credible Intervals for the Posterior

$$
\begin{array}{lll}
b & 0.60(0.56-0.66) & 0.61(0 \\
k_{p} & 0.59(0.53-0.65) & 0.58(0 \\
k_{f} & 0.78(0.72-0.85) & 0.76(0
\end{array}
$$

From Strathe et al. (2012). J. Agri. Sci. 150:764-774


