

Linear models

Liliana M. Dávalos
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Stony Brook University

| The State University of New York

Today's lecture

- Summarizing Bayesian results
- Linear models
 - Examples linear models
 - The Bayesian linear model
- Spatial linear models
 - The problem of space
 - How these work
- Hierarchical models
 - Why hierarchy
 - Pooling and not pooling
 - Group-level (sometimes called random) effects
 - Exercise

Summarizing Bayesian results

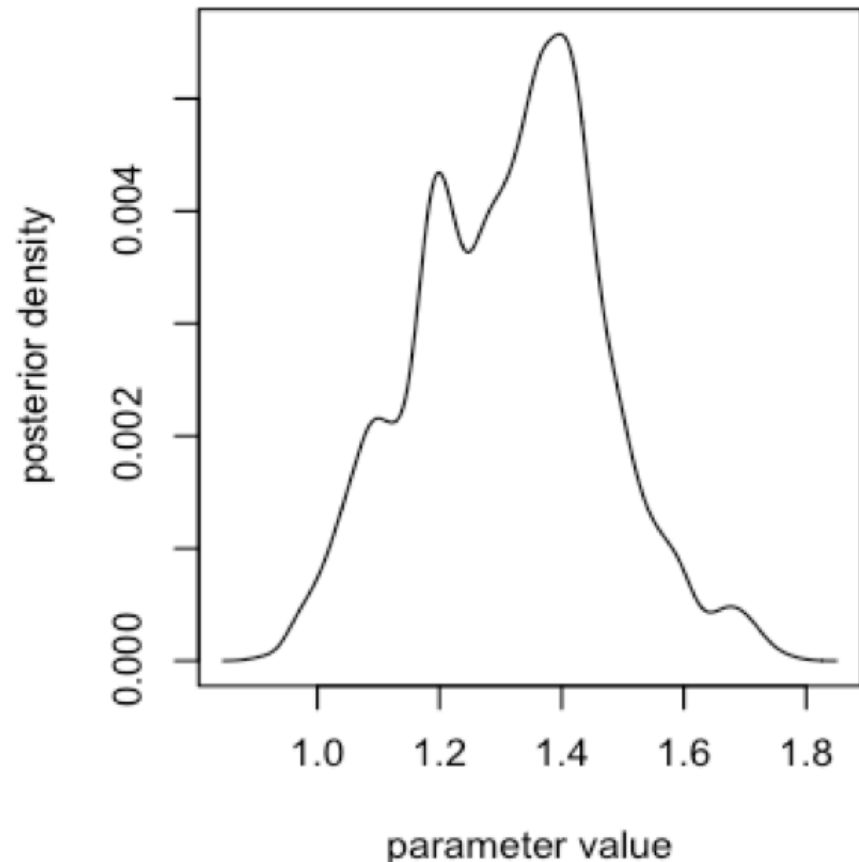


- Bayesian inference is typically about the **density** or **distribution** of the parameters of interest (rather than just a point estimate) we need new tools
- Using just the mean and variance of a parameter does not summarize the results well in all cases (e.g., multi-modality)
- Small sample inferences may be different
- Typically want to summarize intervals around the mode of the posterior with a given probability coverage

For example

- Examine the density plotted
- Would the mean and variance be enough to summarize this distribution?
- Why or why not?
- You have 3 min

A Marginal Posterior Distribution



From: Merow & Silander

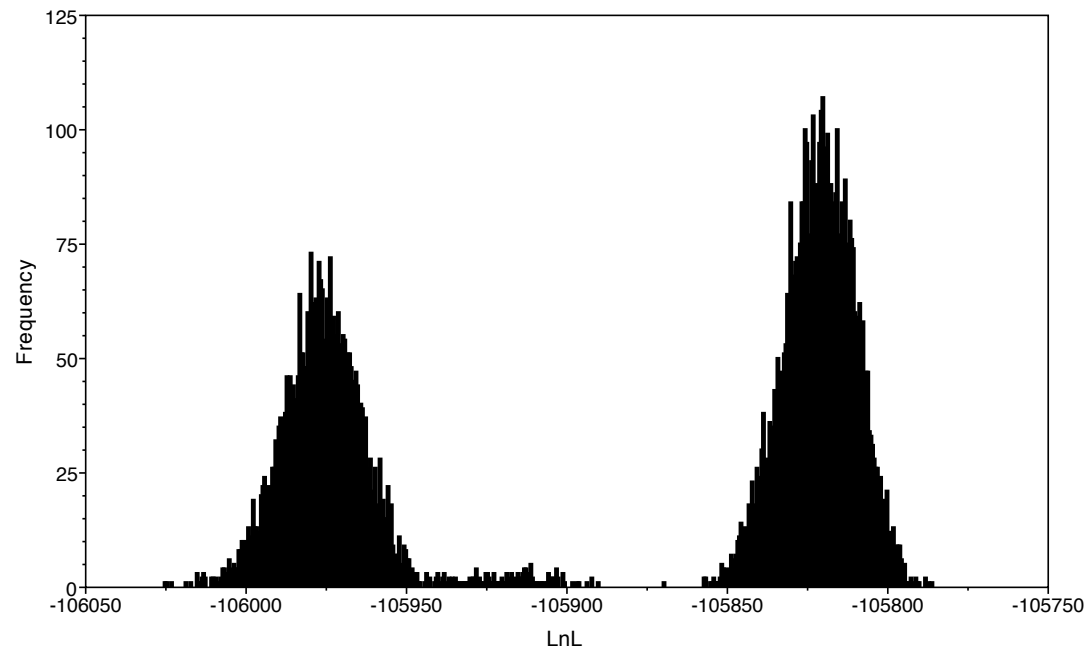
Credible intervals



- Often computed the same way as a confidence interval
- Need not be contiguous
- Definition is different
- **Credible set:** A $100(1 - \alpha)\%$ credible interval gives the region of the parameter space where the probability of covering θ is equal to $1 - \alpha$
 - Remember θ ?

Example credible interval

- Is the credible interval of this posterior distribution contiguous?
- Why or why not



Credible sets versus confidence regions



- Confidence intervals are inherently frequentist:
 - Require repeated **sampling** or **replication** of an experiment to get the region that covers the true parameter $(1 - \alpha)\%$ of the time on average
- Credible sets are a true probability statement over the parameter space of interest
- Applying the credible set definition to a confidence interval means that the coverage of the confidence interval is either zero or one

Formal definition

- A credible set, C is the subset of the posterior parameter space Θ such that the $1 - \alpha$ region satisfies

$$1 - \alpha = \int_C p(\theta | X) d\theta$$

- Note that this is a probability zero or one event with respect to a confidence interval
- This is not a unique quantity unless we center it around some measure of central tendency (mean, mode, median, etc.)

Notice

- Yesterday we used the notation

$$\Pr[\theta | D] = \frac{\Pr[D | \theta] \Pr[\theta]}{\Pr[D]}$$

- To mean the posterior distribution of θ given the data D

- Today we are using the notation

$$p(\theta | X)$$

- To mean the posterior distribution of θ given some observed variables X
- **They are the same thing**

Highest Posterior Density Regions

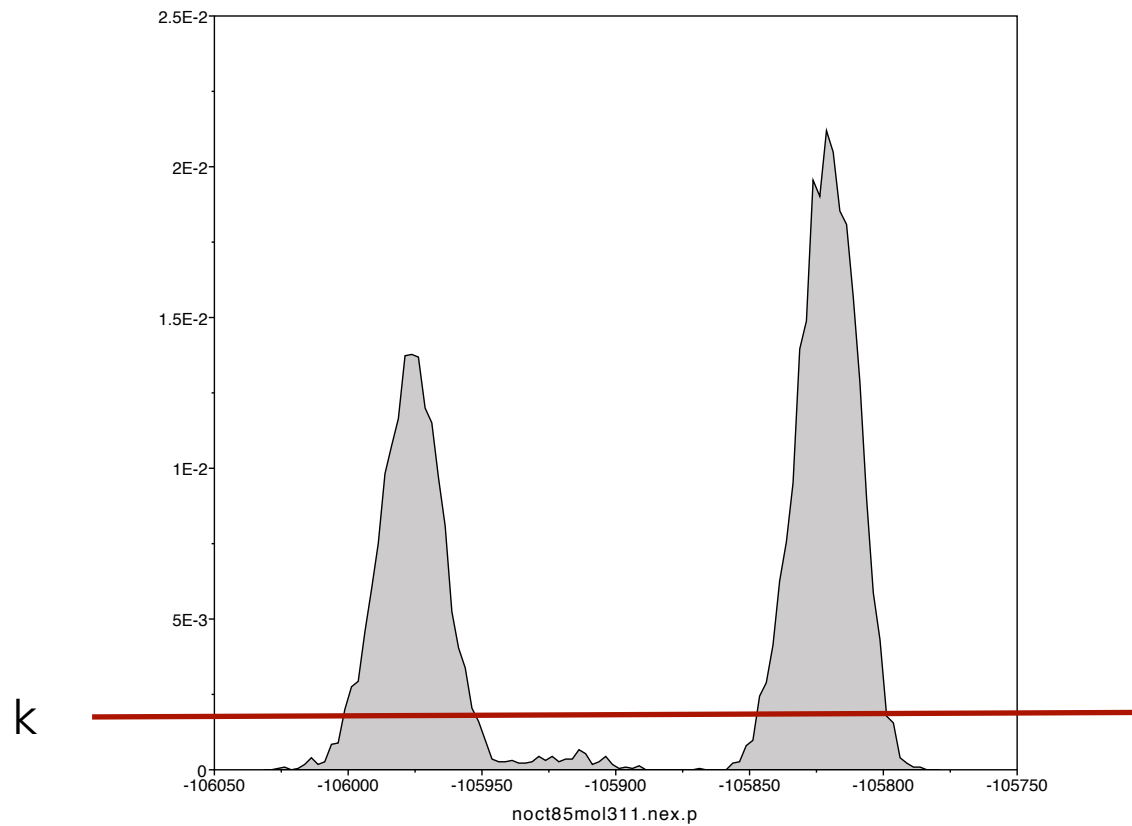


- Would like to find credible sets with the highest density — the height of the posterior pdf (**probability density function**) should be “highest” inside our credible set
- This is a generalization of the credible set defined in a previous slide
- A $100(1 - \alpha)\%$ HPD is the subset of the support of the posterior for θ where

$$C = 1 - \alpha = \{\theta : \Pr(\theta | X) \geq k\}$$

$$1 - \alpha = \int_{\theta: \Pr(\theta | X) \geq k} \Pr(\theta | X) d\theta$$

Example: bimodal HPD



Computing credible intervals



- If you know the posterior pdf of the parameter, this can be found analytically (most of the time, we don't so best avoid)
- Should consider dropping a horizontal line down the density of θ
- Can be done in R using functions in the `coda` or `hdr` packages
- Outside R, download Tracer application, visualizes posteriors, pdf, HPD

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Linear regression models

- Linear regression is, perhaps, *the* most widely used statistical modeling tool
- It addresses the following question: How does a quantity of primary interest, y , vary as (depend upon) another quantity, or set of quantities, \mathbf{x} ?

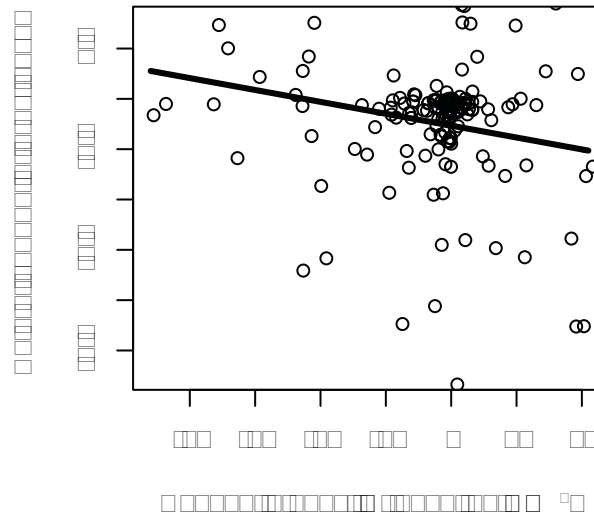


Figure 3

X and Y

- The quantity y is called the *response* or *outcome variable*
 - Some people simply refer to it as the *dependent variable*
- The variable(s) \mathbf{x} are called *explanatory variables*, *covariates* or simply *independent variables*
- In general, we are interested in the conditional distribution of y , given \mathbf{x} , parameterized as
 - $p(y | \square, \mathbf{x})$

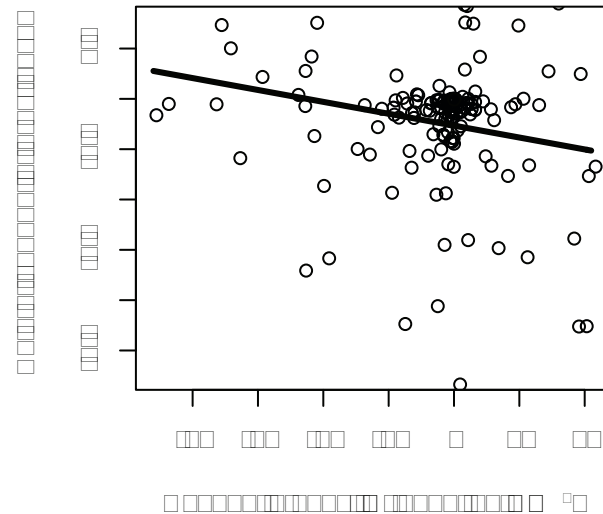


Figure 3

How linear regression works



- Typically, we have a set of units or experimental subjects $i = 1, 2, \dots, n$
- For each of these units we have measured an outcome y_i and a set of explanatory variables $\mathbf{x}'_i = (1, x_{i1}, x_{i2}, \dots, x_{ip})$
- The first element of \mathbf{x}'_i is often taken as 1 to signify the presence of an “intercept”
- In this example we have several explanatory variables up to p

Our variables

- We collect the outcome and explanatory variables into an $n \times 1$ vector and an $n \times (p+1)$ matrix:

$$y = \begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix}; X = \begin{bmatrix} 1 & x_{11} & x_{12} & \cdots & x_{1p} \\ 1 & x_{21} & x_{22} & \cdots & x_{2p} \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & x_{n1} & x_{n2} & \cdots & x_{np} \end{bmatrix} = \begin{pmatrix} x'_1 \\ x'_2 \\ \vdots \\ x'_n \end{pmatrix}$$

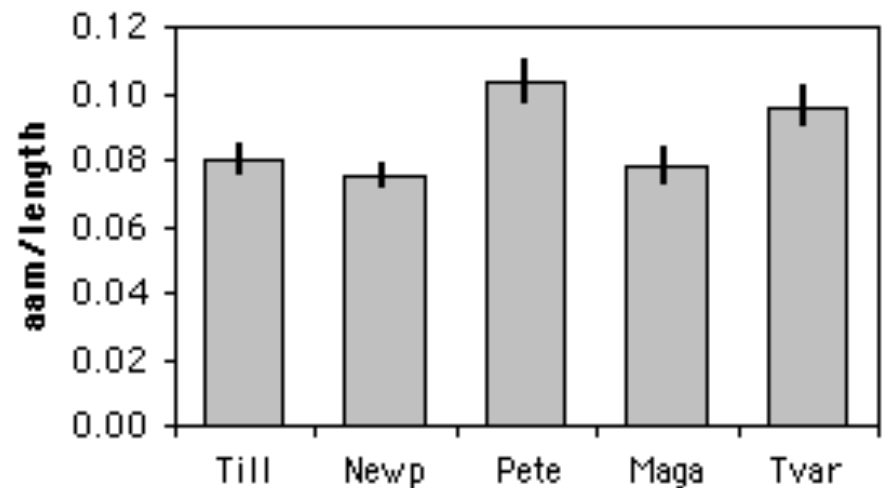
Importance linear model



- The linear model is the most fundamental of all serious statistical models underpinning:
 - ANOVA: y_i is continuous, x_{ij} 's are all categorical
 - REGRESSION: y_i is continuous, x_{ij} 's are continuous
 - ANCOVA: y_i is continuous, x_{ij} 's are continuous for some j and categorical for others

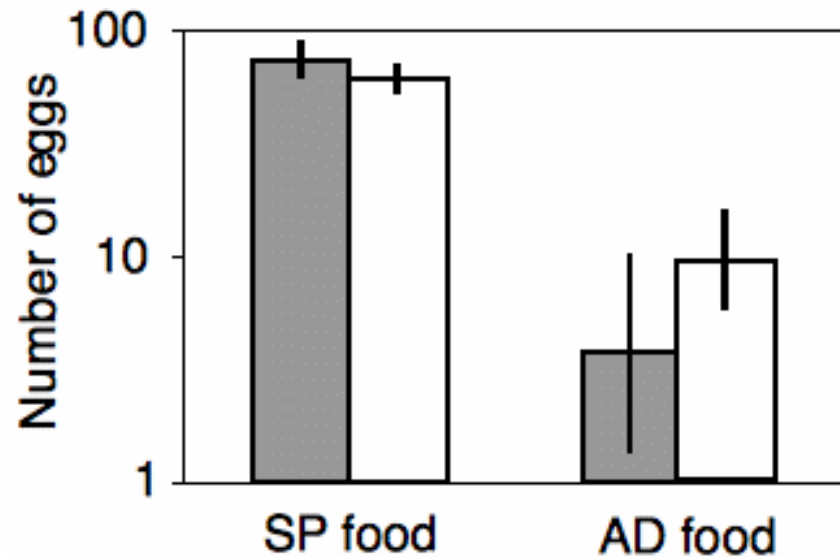
Example one-way anova

- Length of the anterior adductor muscle scar divided by total length in *Mytilus trossulus*
- Means \pm one standard error are shown for five locations.



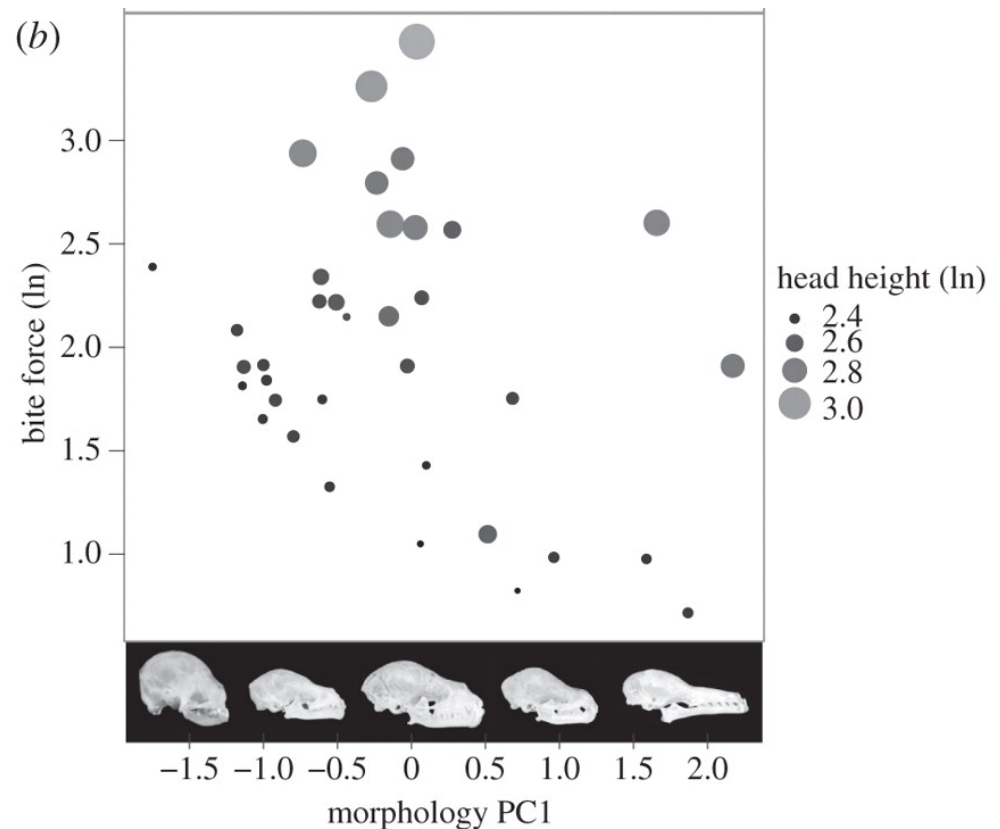
Two-way anova

- Mean total numbers of eggs of females from the SP strain (gray bars) and AD strain (white bars)
- Values are mean \pm SEM
- Adapted from Fig. 4 of Shimoji and Miyatake [2002]



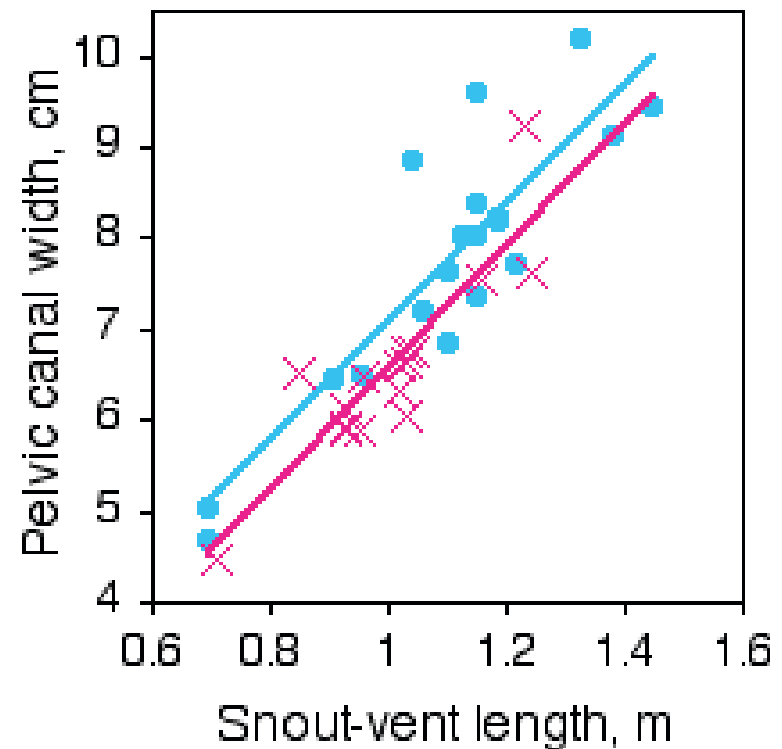
Example regression

- Morphology PC1 as a predictor of \ln bite force (b , mean coefficient = -0.327 ± 0.007)
- From Dumont, Dávalos et al 2012



Example ancova

- Pelvic canal width vs. snout-vent length in the American alligator
- Blue circles and line are males; pink X's and line are females
- From Prieto-Marquez et al. 2007



Think, pair, share

- Let's discuss for 2 min with neighbor
 - Propose a **linear** model you want to build using Bayesian methods
 - What is the **dependent** variable?
 - What is the **independent** variable(s)?
 - Does it involve anova, regression, or ancova?

$$y = \begin{pmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{pmatrix}; X = \begin{bmatrix} 1 & x_{11} & x_{12} & \cdots & x_{1p} \\ 1 & x_{21} & x_{22} & \cdots & x_{2p} \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & x_{n1} & x_{n2} & \cdots & x_{np} \end{bmatrix} = \begin{pmatrix} x'_1 \\ x'_2 \\ \vdots \\ x'_n \end{pmatrix}$$

Bayesian linear model

- The Bayesian linear model is given by:

$$y_i | \mu_i, \sigma^2, \mathbf{X} \stackrel{ind}{\sim} N(\mu_i, \sigma^2); i = 1, 2, \dots, n;$$

$$\mu_i = \beta_0 + \beta_1 x_i + \dots + \beta_p x_{ip} = \mathbf{x}_i' \boldsymbol{\beta}; \boldsymbol{\beta} = (\beta_0, \beta_1, \dots, \beta_p);$$

$$\boldsymbol{\beta}, \sigma^2 | \mathbf{X} \sim p(\boldsymbol{\beta}, \sigma^2 | \mathbf{X})$$

- Unknown parameters include the regression parameters and the variance, i.e. $\boldsymbol{\theta} = \{\boldsymbol{\beta}, \sigma^2\}$
- $p(\boldsymbol{\beta}, \sigma^2 | \mathbf{X}) \equiv p(\boldsymbol{\theta} | \mathbf{X})$ is the joint *prior* on the parameters. We assume \mathbf{X} is observed *without error* and all inference is conditional on \mathbf{X}
- We suppress dependence on \mathbf{X} in subsequent notation

Bayesian linear model



- Specifying $p(\beta, \sigma^2)$ completes the model
- All inference proceeds from $p(\beta, \sigma^2 | \mathbf{y})$

- With no prior information, we specify

$$p(\beta, \sigma^2) \propto \frac{1}{\sigma^2} \quad \text{Or its equivalent} \quad p(\beta) \propto 1; p(\log(\sigma^2)) \propto 1$$

- The above is **NOT** a probability density (they do not integrate to any finite number)
- So why is it that we are even discussing them?
- Even if the priors are *improper*, as long as the resulting posterior distributions are valid we can still conduct legitimate statistical inference on them

Practical questions

- Look at yesterday's jags model
- Or as in:

- What is the prior on σ^2 ?

$$p(\beta) \propto 1; p(\log(\sigma^2)) \propto 1$$

- What is the prior on β ?

- Was the prior specified as in:

$$p(\beta, \sigma^2) \propto \frac{1}{\sigma^2}$$

Computing the posterior distribution



- Strategy: Factor the **joint** posterior distribution for β and σ^2 as:

$$p(\beta, \sigma^2 | y) = p(\beta | \sigma^2, y) \times p(\sigma^2 | y)$$

- The *conditional posterior* distribution of β , given σ^2 :

$$\beta | \sigma^2, y \sim N(\hat{\beta}, \sigma^2 V_\beta)$$

- where, using some algebra, one finds: $\hat{\beta} = (X'X)^{-1}X'y$
- and $V_\beta = (X'X)^{-1}$

Computing the posterior distribution



- The *marginal posterior* distribution of σ^2 : Let $k = (p + 1)$ be the number of columns of \mathbf{X}

$$\sigma^2 | y \sim IG\left(\frac{n-k}{2}, \frac{(n-k)s^2}{2}\right),$$

- Where

$$s^2 = \frac{1}{n-k} (y - \mathbf{X}\hat{\beta})'(y - \mathbf{X}\hat{\beta})$$

- is the classical unbiased estimate of σ^2 in the linear regression model

Questions

- What are the columns of \mathbf{X} ?
- Why are we interested in the marginal posterior? (As opposed to the joint posterior)?
- Given that $s^2 \propto \frac{1}{n-k}$
- what can we do to reduce variance in our models?

Computing the posterior distribution 2



- The *marginal posterior* distribution $p(\beta \mid \mathbf{y})$, averaging over σ^2 , is *multivariate t* with $n - k$ degrees of freedom
- But we rarely use this fact in practice
- Instead, we *sample* from the posterior distribution

Algorithm for sampling from the posterior distribution



- We draw samples from $p(\beta, \sigma^2 | \mathbf{y})$ by executing the following steps:
- Step 1: Compute $\hat{\beta}$ and \mathbf{V}_{β}
- Step 2: Compute s^2
- Step 3: Draw M samples from $p(\sigma^2 | \mathbf{y})$:

$$\sigma^{2(j)} \sim IG\left(\frac{n-k}{2}, \frac{(n-k)s^2}{2}\right), j = 1 \dots M$$

- Step 4: For $j = 1, \dots, M$, draw $\beta^{(j)}$ from $p(\beta | \sigma^{2(j)}, \mathbf{y})$:

$$\beta^{(j)} \sim N\left(\hat{\beta}, \sigma^{2(j)} \mathbf{V}_{\beta}\right)$$

From: Banerjee & Finley 2013

Sampling from the posterior distribution



- The marginal distribution of each individual regression parameter β_j is a non-central univariate t_{n-p} distribution

- In fact,

$$\frac{\beta_j - \hat{\beta}_j}{s\sqrt{V_{\beta;jj}}} \sim t_{n-p}$$

- The 95% credible interval for each β_j is constructed from the quantiles of the t -distribution
- This exactly coincides with the 95% classical confidence intervals, but the interpretation is direct: the probability of β_j falling in that interval, given the observed data, is 0.95

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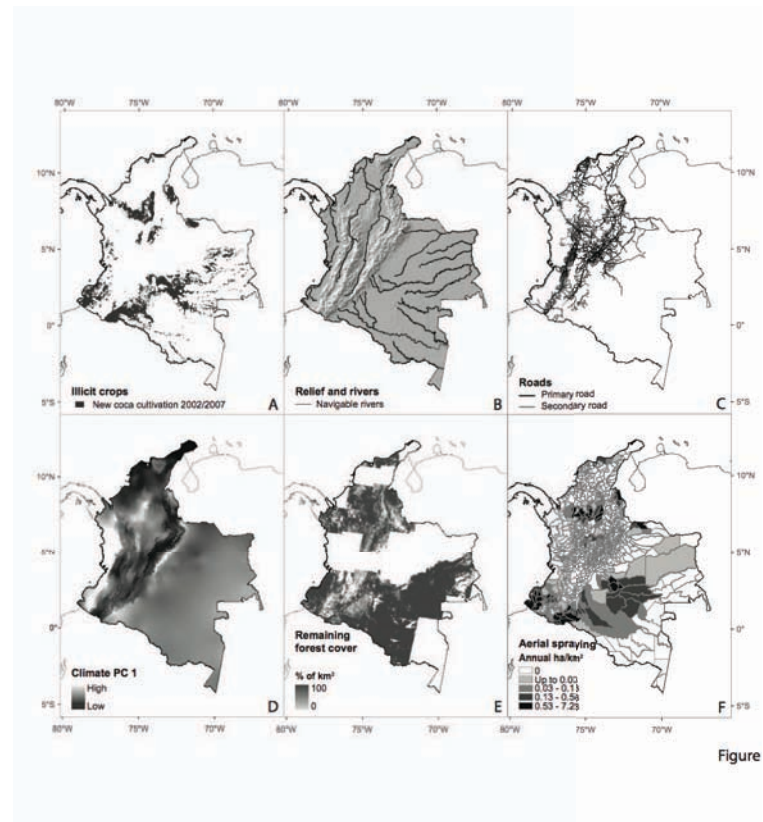
The first law of geography

- First law of geography:
- *"Everything is related to everything else, but near things are more related than distant things."*
Tobler 1970



Quick discussion

- Which one of the variables on the right shows the most aggregated spatial pattern?
- Which one shows the least?
- How important do you think these spatial patterns are for modeling this landscape?



Figure

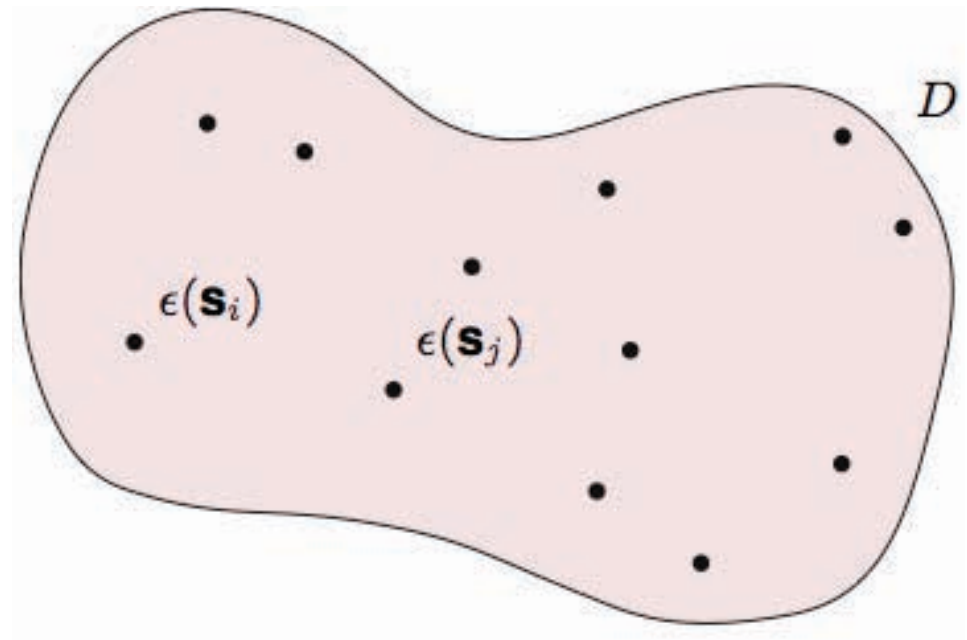
Spatial models



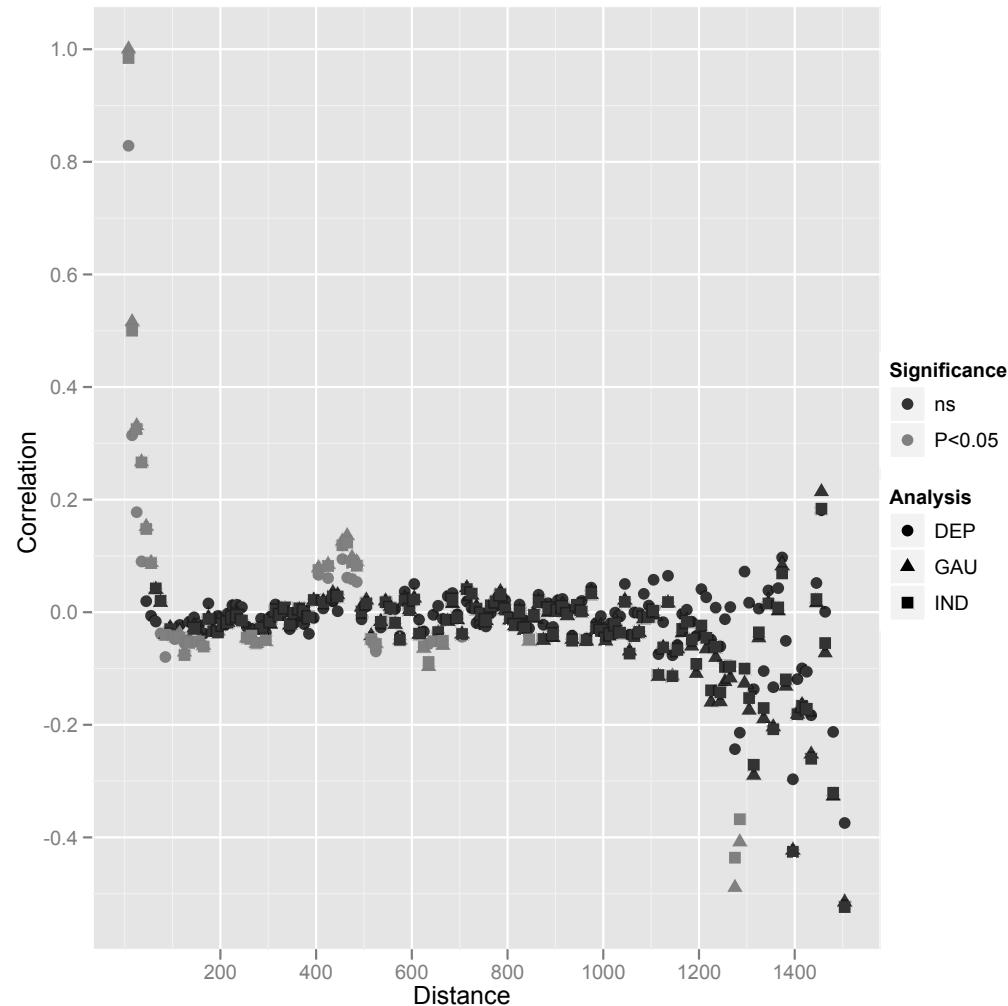
- Point-level modeling refers to modeling of spatial data collected at locations referenced by coordinates (e.g., lat- long, Easting-Northing)
- **Fundamental concept:** Data from a spatial process $\{Y(\mathbf{s}) : \mathbf{s} \in D\}$, where D represents some landscape
- **Example:** $Y(\mathbf{s})$ is a pollutant level at site \mathbf{s}
- **Conceptually:** Pollutant level exists at all possible sites
- **Practically:** Data will be a partial realization of a spatial process – observed at $\{s_1, \dots, s_n\}$
- **Statistical objectives:** Inference about the process $Y(\mathbf{s})$; predict at new locations

Simple linear model

- $Y(\mathbf{s}) = \mu(\mathbf{s}) + \epsilon(\mathbf{s})$
- Assumptions regarding $\epsilon(\mathbf{s})$:
- $\epsilon(\mathbf{s}) \stackrel{iid}{\sim} N(0, \sigma^2)$
- $\epsilon(\mathbf{s}_i)$ and $\epsilon(\mathbf{s}_j)$ are uncorrelated for all $i \neq j$

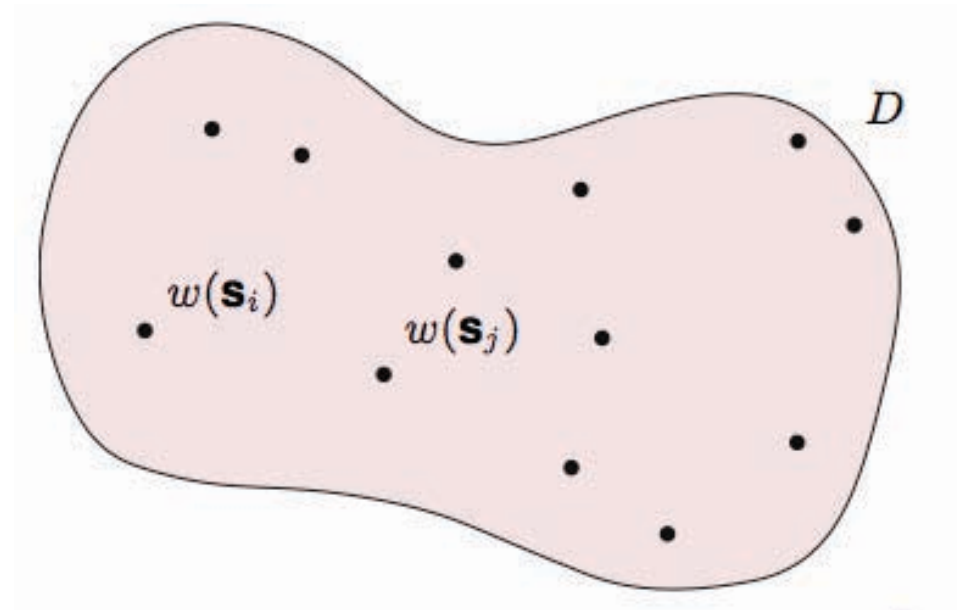


What does spatial autocorrelation look like?



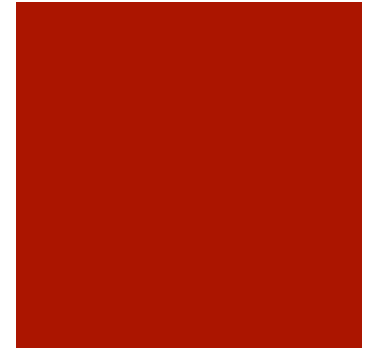
Spatial Gaussian process

- Let $\mathbf{w} = [w(\mathbf{s}_i)]_{i=1}^n$, then
- $\mathbf{w} \sim N(\mathbf{0}, \sigma^2 R(\Phi))$,
- Where
- $R(\Phi) = [\Phi(\Phi; \|\mathbf{s}_i - \mathbf{s}_j\|)]_{i,j=1}^n$



Realization of a Gaussian process

ϕ is the distance decay of the spatial process

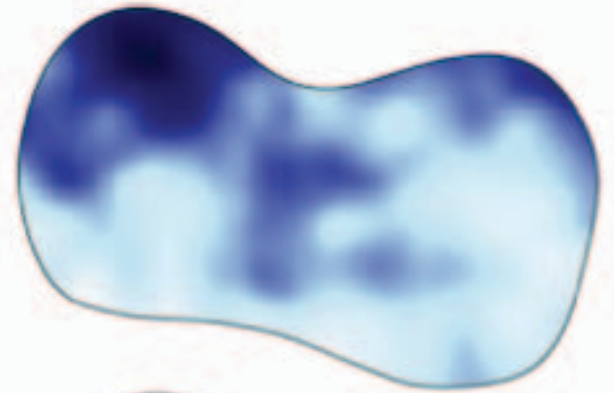


- Changing ϕ and holding $\sigma^2 = 1$:
- $\mathbf{w} \sim N(\mathbf{0}, \sigma^2 R(\phi))$,
- Where $R(\phi) = [\rho(\phi; |\mathbf{s}_i - \mathbf{s}_j|)]_{i,j=1}^n$
- Correlation model for $R(\phi)$: e.g., exponential decay
- $\rho(\phi; t) = \exp(-\phi t)$ if $t > 0$
- Other **valid** models e.g., Gaussian, Spherical, Matérn
- **Effective range**, $t_0 = \ln(0.05)/\phi \approx 3/\phi$

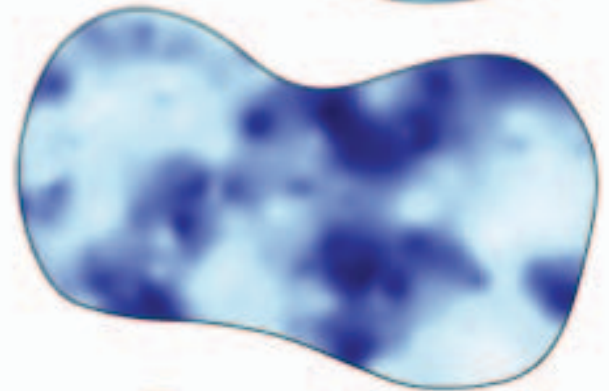
Realization of a Gaussian process

- **Effective range,**
 $t_0 = \ln(0.05)/\kappa \approx 3/\kappa$

□ small



□ medium



□ large



Simple linear model + random spatial effects



- $Y(\mathbf{s}) = \mu(\mathbf{s}) + w(\mathbf{s}) + \varepsilon(\mathbf{s})$
- Response: $Y(\mathbf{s})$ at some site
- Mean: $\mu = \mathbf{x}^T(\mathbf{s}) \beta$
- Spatial random effects: $w(\mathbf{s}) \sim \overset{\text{GP}}{GP}(0, \sigma^2 \rho(\phi; |\mathbf{s}_1 - \mathbf{s}_2|))$
- Non-spatial variance: $\varepsilon(\mathbf{s}) \overset{iid}{\sim} N(0, \tau^2)$
 - Non spatial variance is here

This is the
• Gaussian
process

Hierarchical modeling

- First stage:

$$y \mid \beta, w, \tau^2 = \prod_{i=1}^n N(Y(s_i) \mid xT(s_i)\beta + w(s_i), \tau^2)$$

- Second stage:

$$w \mid \sigma^2, \phi \sim N(0, \sigma^2 R(\phi))$$

- Third stage: priors on $\Omega = (\beta, \tau^2, \sigma^2, \phi)$

To summarize, the parameters we want are:



- β = regression coefficients
- τ^2 = residual variance
- σ^2 = spatial variance
- ϕ = decay of spatial dependence
- Together, σ^2 and ϕ define the spatial weights, \mathbf{w}
- Usually we want to look at the surface of spatial weights to see if there are any latent patterns
 - (e.g., indications of a missing variable)

Colorado data illustration

- Modeling temperature:
507 locations in Colorado
- Simple spatial regression
model:

$$Y(s) = \mathbf{x}^T(s)\beta + w(s) + \varepsilon(s)$$

$$w(s) \sim GP(0, \sigma^2 \rho(\cdot; \phi, \nu));$$

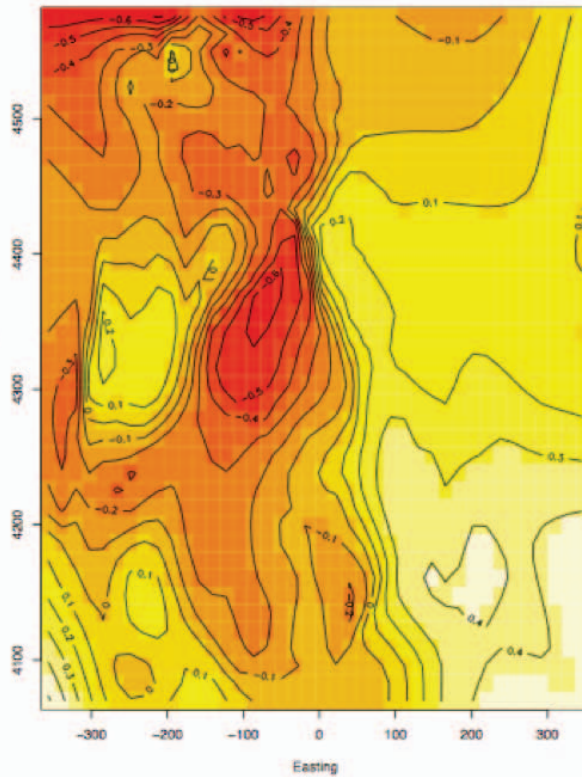
$$\varepsilon(s) \stackrel{iid}{\sim} N(0, \tau^2)$$

Parameters	50% (2.5%, 97.5%)
intercept	2.827 (2.131, 3.866)
[elevation]	-0.426 (-0.527, -0.333)
precipitation	0.037 (0.002, 0.072)
σ^2	0.134 (0.051, 1.245)
ϕ	7.39E-3 (4.71E-3, 51.21E-3)
Range	278.2 (38.8, 476.3)
τ^2	0.051 (0.022, 0.092)

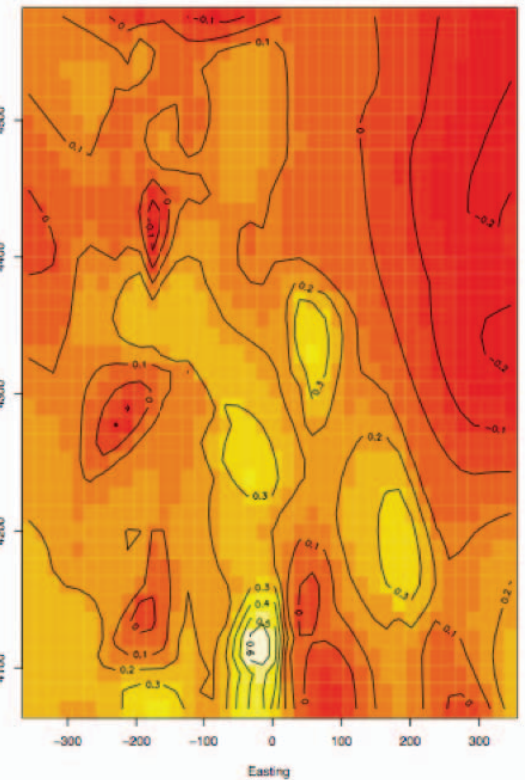
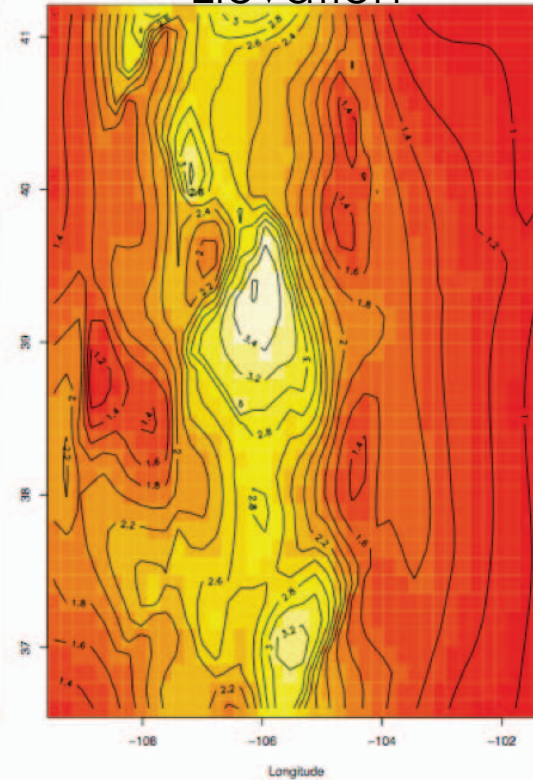
Spatial model example



Elevation



Residual without elevation



Residual with elevation

Spatial random effects



- Spatial random effects can:
 - Account for spatial autocorrelation (samples aren't independent)
 - Ensure that your regression coefficients aren't contorted to accommodate patterns that aren't actually related to the predictor
 - Identify spatial patterns in residuals that are related to omitted predictors

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Why use hierarchical models?



- Account for sources of uncertainty/variability
 - Account for individual-level and group-level variation when estimating group-level coefficients
 - Classical models require averaging over individual-level variation
- Borrow strength across groups (minimize effects of small sample sizes in some groups)

Group-level coefficients



- Group-level effects absorb variation that's NOT related to the fixed effects so you potentially get lower bias for estimates of population-level effects
- Group-level effects pick up unmeasured variation
- It's probably never worse than non-hierarchical models because the worst case is that you find among group variation to be irrelevant

A note about terms

- Hierarchical models are often called *mixed effects models*
 - Mixed effects = fixed + random effects
 - Fixed effects: coefficients that apply to all observations
 - Random effects: coefficients that apply to individual clusters
 - Problem is “fixed” and “random” are used with various meanings in statistics and social science

Note continued



- I follow Andrew Gelman and call these models *hierarchical*
 - Hierarchical models = population-level effects + group-level effects
 - Population-level: affecting all observations
 - Group-level: affecting only observations in a given cluster
- You will see how this works later

What is a hierarchical model?



- Hierarchical models are used when the data are structured in groups. e.g. demographically, temporally, spatially
- Different (but related) parameters are used for each group
- These group-level parameters can be interpreted to describe group-level differences for predictors we DIDN'T measure

Groups



- Types of groups
 - Clustered data: when modeling individual plant growth and comparing among populations, some observations are made on individuals (e.g. stem length) while some are made on populations (e.g. temperature, soil)
 - E.g., fit a matrix demographic model and use population random effects on probability of seedling survival
 - Repeated measures data: Time effects - e.g. in a mark recapture model survival might vary by year
 - Spatial effects – in a species distribution model, latent, spatially autocorrelated patterns – cells are more like their neighbors

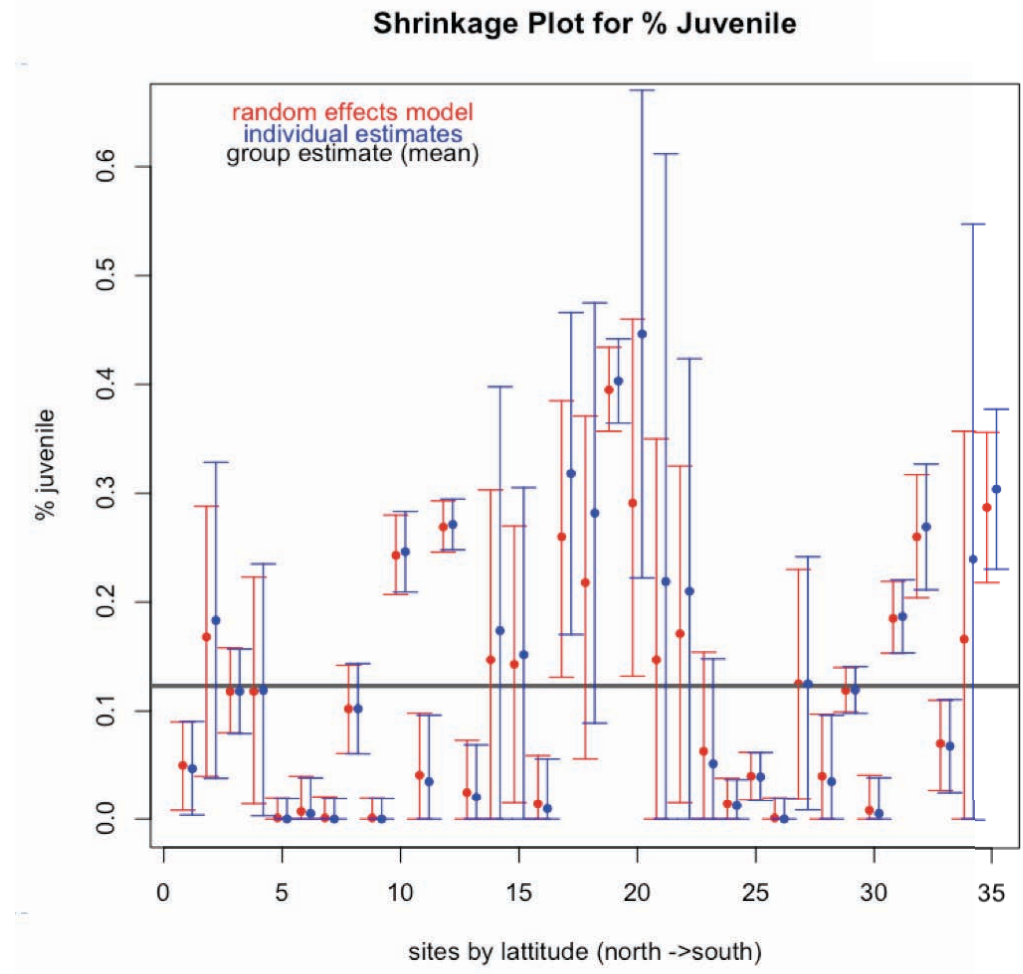
How to model hierarchical parameters?



- Consider the three alternatives for modeling groups
 - Pool all groups together
 - Ignore latent differences
 - Ignore autocorrelation (observations not independent)
- Model each group separately
 - What about small groups?
 - Many more parameters to estimate
 - Ignores latent similarity
- Model each group hierarchically
 - Groups are similar but different
 - Intermediate number of parameters

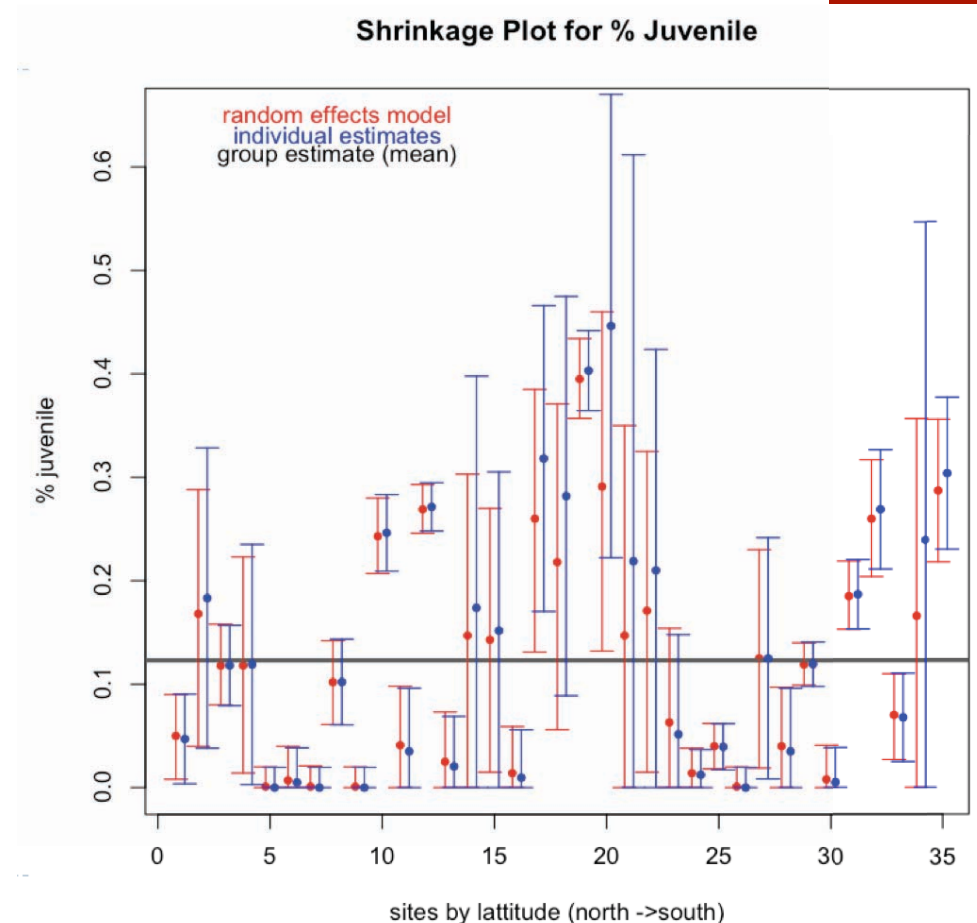
Comparison of pooling alternatives

- Proportion of juvenile aloe in 35 populations spanning the species' range
- Multiple samples from each population
- Combined estimates across samples from different years to estimate the variance in each population



Questions

- Which estimates are closest to the observations?
- Name 1 advantage of the group estimate
 - Name 1 disadvantage
- Name 1 advantage of the individual estimates
 - Name 1 disadvantage



Hierarchical regression



- Regressions have intercept and slope terms
- Hierarchical regressions have different intercepts or slopes (or both) for each group
- Group level parameters do not vary independently, but are constrained by a distribution – often a normal with a variance that we model

Example hierarchical regression

- 30 young rats, weights measured weekly for five weeks
- Dependent variable (Y_{ij}) is weight for rat “i” at week “j”
- Hierarchical: weights (observations) within rats (groups)
- Data:

	Weights Y_{ij} of rat i on day x_j				
	$x_j = 8$	15	22	29	36
Rat 1	151	199	246	283	320
Rat 2	145	199	249	293	354
.....					
Rat 30	153	200	244	286	324

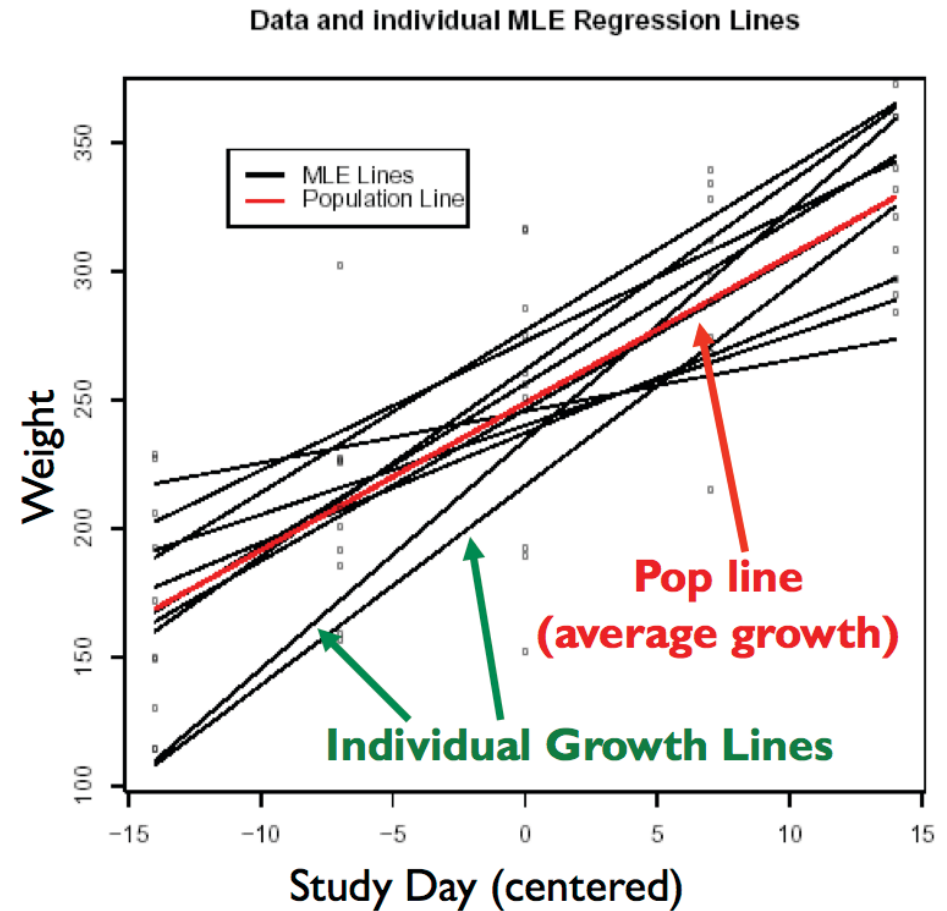
Options



- Possible analyses
 - Each rat (cluster) has its own line:
 - Intercept= b_{i0} , slope= b_{i1}
 - All rats follow the same line:
 - $b_{i0} = \beta_0$, $b_{i1} = \beta_1$
 - A compromise between these two:
 - Each rat has its own line, BUT...
 - The lines come from a common assumed distribution (a slope and intercept are estimated from each rat)

Rats!

- NON-hierarchical options
- Rat “i” has its own expected growth line:
- $E(Y_{ij}) = b_{0i} + b_{1i}X_j$
- There is also an overall, average population growth line:
- $E(Y_{ij}) = \square_0 + \square_1 X_j$



The hierarchical option

- A compromise between pooling and individual estimates:

$$Y_{ij} \sim \text{Normal}(\alpha_i + \beta_i(x_j - \bar{x}), \tau_c)$$

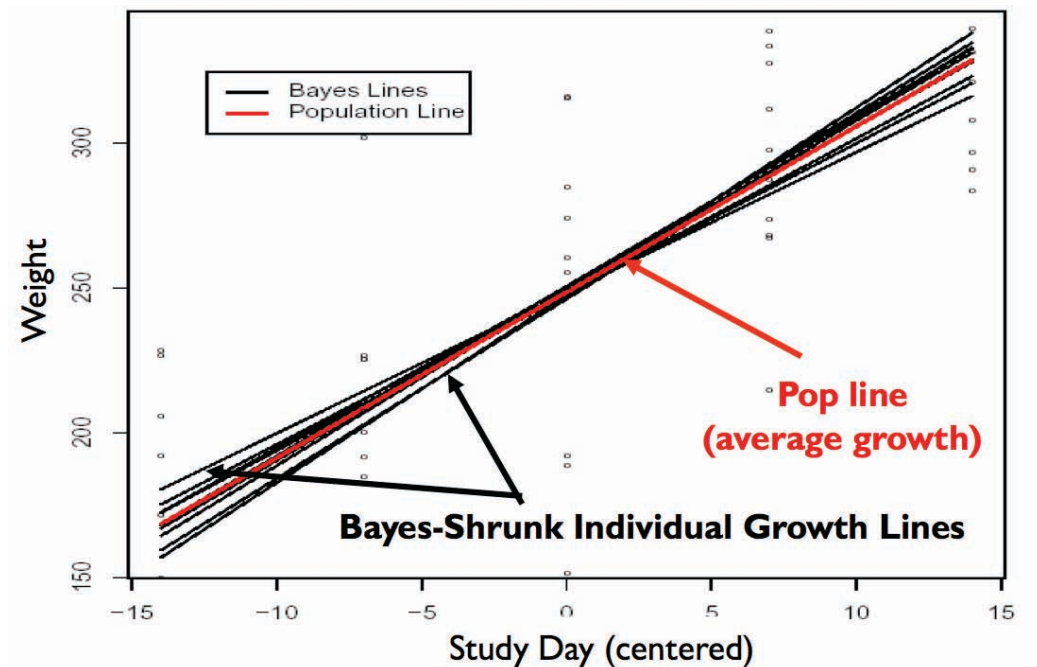
$$\alpha_i \sim \text{Normal}(\alpha_c, \tau_\alpha)$$

$$\beta_i \sim \text{Normal}(\beta_c, \tau_\beta)$$

- $\alpha_c, \tau_\alpha, \beta_c, \tau_\beta, \tau_c$ are given independent, uninformative priors

The hierarchical model

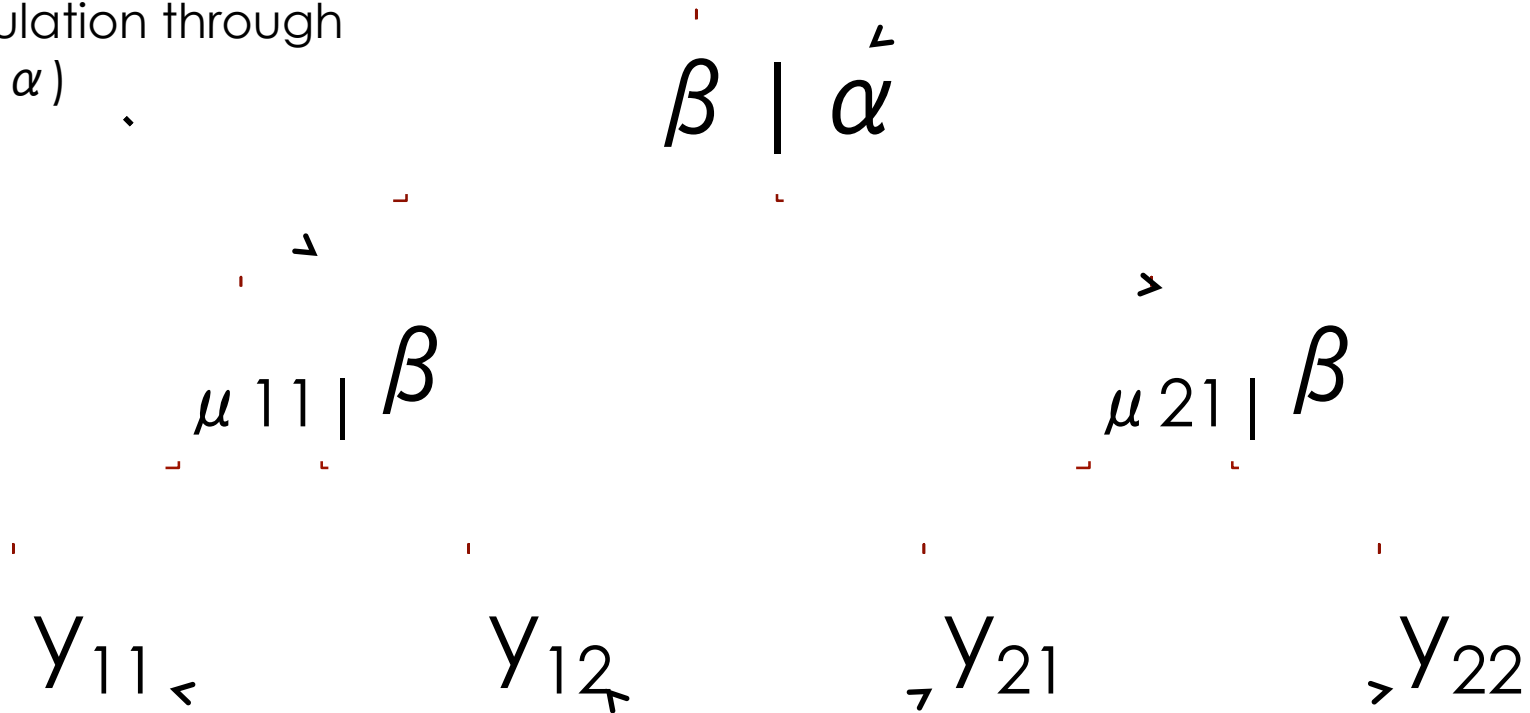
- A compromise: Each rat has its own line, but information is borrowed across rats to tell us about individual rat growth



Summary: Visualizing a hierarchical model

Priors for each sub-population through $p(\beta | \alpha)$

Requires a hyperprior distribution $p(\alpha)$

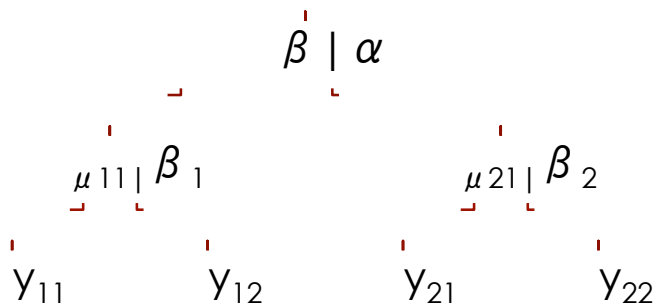


Data

From: Merow & Silander

What are the levels?

- Which ones are population-level parameters?
- Which ones are group-level parameters?



Bayesian inference of hierarchical model



- Non hierarchical model

$$p(\theta_1, \theta_2 \mid x, y) \propto p(y \mid \theta_1, \theta_2, x) \quad \text{Likelihood (data model)} \\ \times p(\theta_1) p(\theta_2) \quad \text{Prior (parameter model)}$$

- Hierarchical model

$$p(\theta_1, \theta_2, \theta_3 \mid x, y) \propto p(y \mid \theta_1, \theta_2, x) \quad \text{Likelihood} \\ \times p(\theta_1 \mid \theta_3) p(\theta_2) \quad \text{Prior} \\ \times p(\theta_3) \quad \text{Hyperprior}$$

Today's lecture

- Summarizing Bayesian results
- Linear models
 - Examples linear models
 - The Bayesian linear model
- Spatial linear models
 - The problem of space
 - How these work
- Hierarchical models
 - Why hierarchy
 - Pooling and not pooling
 - Group-level (sometimes called random) effects
 - Exercise

Exercise: Group means



- Data structure
 - J groups, with means θ_j , each with n_j observations
 - y_{ij} = i^{th} measurement from the j^{th} group variance of each group is σ_j^2 (assumed known)
- Model structure
 - Estimate θ_j for each of the J groups
 - Estimate μ , the group mean
 - Estimate τ , the variance of the θ_j

Model structure

- Data structure

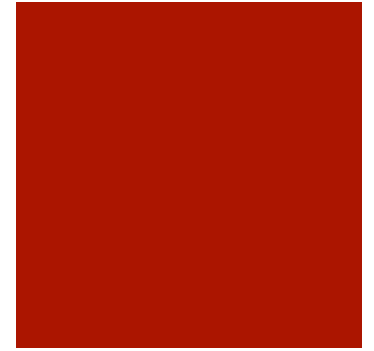
- J groups, with means θ_j , each with n_j observations
- y_{ij} = i^{th} measurement from the j^{th} group
- variance of each group is σ_j^2 (assumed known)
- ε_{ij} = error $\varepsilon_{ij} \sim N(0, \sigma^2)$

- Model structure

- Estimate θ_j for each of the J groups
- Estimate μ , the group mean
- Estimate τ , the variance of the θ_j

Model structure

- All groups the same
 - $y_{ij} = \mu + \varepsilon_{ij}$
- Each group unique
 - $y_{ij} = \theta_j + \varepsilon_{ij}$
- Compromise: Groups similar but different
 - $y_{ij} = \theta_j + \varepsilon_{ij}$, with: $\theta_j \sim N(\mu, \tau^2)$



Exercise: Hierarchical Normal Model



- Model from Gelman 2003
- Estimate the proportion of juveniles and dead individuals of *Aloe dichotoma* across their range for a matrix demographic model
- 35 populations, each with a subset of ~100 individuals measured 6 years apart
- Instructions in `hierarchical_exercise.R`



■ THE END