Introduction to hierarchical models

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Online workshop, but would have been in beautiful Montpellier
☹

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Outline of talk

- Variability, "random things"

- How to describe random "things"   --- random variables

- Hierarchical models (HMs) ? --- Why are they useful/beautiful ?

- Components of HMs: GLM; what are they ?

- Heart of a GLM: linear model; how do we describe it ?

- What are random effects ? --- Why/when do we specify parameters as random variables ?

- Modeling measurement error

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Variability

- Law of Life/Biology: EVERYTHING varies !

- e.g., the number of individuals at a site/at a time (population size), the number of species ...., whether an individual survives or dies, whether it reproduces or not, ...

- Variability causes uncertainty or (partial) unpredictability

- Unpredictable or chance element in ANYTHING that we might want to study or observe in the world

- Hence, great importance of understanding of statistical principles in science and also in everyday life

Variability

- e.g. the number of asp vipers (*Vipera aspis*) seen at 6 sites:
    5, 1, 3, 0, 0, 2

Photo: MK, Doubs, 2017

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Variability

- e.g. the number of asp vipers (*Vipera aspis*) seen at 6 sites:
    5, 1, 3, 0, 0, 2

- want to describe (explain) these numbers, both in terms of mean/systematic patterns, but also in terms of variation/noise

Photo: MK, NE Doubs, 2017

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Description of variability: random variable (r.v.)

- in statistics, use probability to describe random variation

- random variable (r.v.): stochastic (or chance) process that produces some data (usually as *observed* outcome, though may sometimes be *hidden*)

- description of a r.v.: continuous: probability density function (pdf) --- discrete: probability mass function (pmf)

- pdf/pmf: "rule" that gives probability ("relative frequency") of observing any among an exhaustive set of all possible observations (i.e., sums/integrates to 1)

- pdf/pmf have key descriptors that govern specific form = parameters

- best known rv's/pdfs/pmfs: Normal distribution, Poisson distribution, Binomial/Bernoulli distribution

A Poisson random variable

- e.g., the number of asp vipers observed at a site

- pmf:
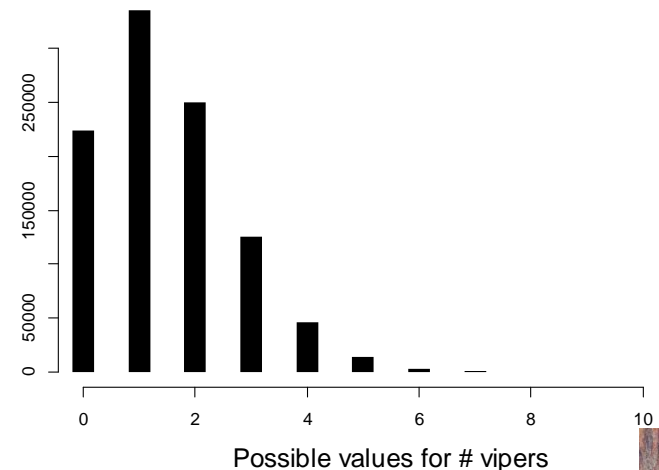$$p(\text{y} \mid \lambda) = \frac{e^{-\lambda}\lambda^{y}}{y!}$$

- "key descriptor": parameter λ

- two shorthands:

    y ~ Poisson(λ)

    glm(y ~ 1, family = 'poisson')

- one possible picture (with λ = 1.5):

Possible values for # vipers

Parametric statistical models

- parametric statistical model: description of one or more random variables

- Distribution of the data as a function of params: $[y \mid \theta]$

- hence, can say: statistical model = pmf/pdf

- statistical inference: use observed data from some putative random process (= pdf) to estimate parameters of the process that produced these data

- best known statistical models: generalized linear models (GLMs): pdf's for certain (very broad) class of random variables; see later

Hierarchical model: sequence of random variables

- Hierarchical model (HM): sequence of random variables (rv's), observed (y) or unobserved (x)

$$x \sim f(\omega)$$
$$y \sim g(x, \theta)$$

- Factorization of joint distribution [x,y] into marginal ([x]) and conditional distribution, [y|x]:

$$[x,y] = [x]\ [y|x]$$

- Estimands: parameters ω and θ; latent variables x

- **x: latent variables = unobserved rv's = random effects**

- Large class of models can be described as HMs

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Hierarchical model: sequence of random variables

- HMs powerful manner of building statistical models

- **Typically reflect our thinking about mechanistic structure of process studied: science-based statistical modeling**

- Describe stochastic processes with multiple layers/levels of variability and sources of uncertainty

- (Note: variability *vs.* uncertainty)

- HMs can be fit using classical (i.e., likelihood) methods (e.g., R packages **lme4**, **unmarked**, **secr**, …)

- Bayesian analysis often more straightforward

- BUGS language ideal for fitting HMs: indeed, BUGS software developed especially for HMs !

- Models naturally described hierarchically in BUGS language

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Why hierarchical models ?

- HMs make the fitting of complex models easier (especially bayesianly)

- … foster mechanistic, cleaner thinking about a problem

- … lead to mechanistic modeling

- … can often be called **science-based statistical models**

- … foster synthetic understanding of large array of models

- … enable honest accounting for all components of variability and uncertainty in a system

- … ideal for rigorous modeling of measurement-error processes in ecological field data

- great for combining information ('integrated models', meta-analyses)

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HMs foster mechanistic thinking about system and synthetic understanding of large class of models

- e.g., state-space model for time-series of observations (y)

  Ecological process

  $[y] =$ initial system state z_0 *

        system state z_{t+1} given system state z_t *

        observation y given system state z

  Measurement-error process, observation process

- y counts at 1 site:
  state-space model (BPA chap. 5)

- y individual detection histories, multiple individuals:
  JS model (BPA chap. 10)

- y site-detection histories, multiple sites:
  dynamic occupancy model (BPA chap. 13)

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HMs foster synthetic understanding of models

- **moreover ...**

  [y] =   initial system state z_0 *

  system state z_{t+1} given system state z_t *

  observation y given system state z

- y counts, no dynamics:
  random-effects models, GLMMs (BPA chap. 4)

- y counts, multiple sites:
  Dail-Madsen Nmix model (BPA chap. 12, AHM2 chap. 2)

- y individual detection histories, no dynamics:
  closed-population model (BPA chap. 6)

- y individual detection histories, initial state not modelled:
  CJS model (BPA chap. 7, AHM2 chap. 3), multi-state models (BPA chap. 8, AHM2 chap. 6)

- y site-detection histories or counts, multiple sites, but no dynamics: static occupancy model (BPA chap. 13, AHM1 chap. 10),
  static N-mixture model (BPA chap. 12, AHM1 chap. 6)

Components of HMs: Generalized linear models (GLMs)

- HMs represent description of two or more linked random variables

- And how do we describe structure in random variables ?
        --- > typically via a GLM

- **Hence, can say that HMs consist of a sequence of 2 or more GLMs !**

- **GLMs represent the modules with which we typically 'assemble' an HM**

- Therefore, have a quick look at GLMs

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Generalized linear models (GLMs)

- Outcome of a random variable y (response); explanatory variable(s) x

- Explain variability in mean response as a linear model:

    -> weighted sum of explanatory variables

- Linear model in terms of x applied to transformation g of mean response E(y),
    i.e., g(E(y)) = some linear model in x

- Three components of GLM:

    (1)   random part of response: statistical distr. ("expo. family")

    (2)   link function g

    (3)   systematic part of response (linear predictor): some linear function of x

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Three most frequent GLMs

- Normal response:

    Random part: $y \sim Normal(\mu, \sigma^2)$

    (typical) Link function: none ("identity")

    Systematic part: SLM (some linear model)

- Poisson response:

    Random part: $y \sim Poisson(\lambda)$

    (typical) Link function: log

    Systematic part: SLM

- Binomial response:

    Random part: $y \sim Binomial(p, N) = N*Bernoulli(p)$

    (typical) Link function: logit = log(p / (1-p))

    Systematic part: SLM

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Also a GLM …

The CJS model fitted to the m-array:

- Multinomial response: $\mathbf{y} = \{y_{12}, y_{13}, y_{14}, R_1, ...\}$

    Random part: $\mathbf{y} \sim \text{Multinomial}(\boldsymbol{\pi}, N)$

    Cell probs: $\boldsymbol{\pi} = \{\pi_1, \pi_2, \pi_3, 1-(\pi_1 + \pi_2 + \pi_3))$

    Relationship cell probs/natural params (survival, recap):

    $$\pi_1 = \phi_1 \, p_1$$

    etc…

    Link function: logit

    Systematic part: some linear models, e.g.
    $$\text{logit}(\phi_1) = \alpha + \beta * \text{ice-days}_t$$
    $$\text{logit}(p_1) = \alpha' + \beta' * \text{trap-days}_t$$

Importance of linear models in GLMs and HMs

- statistical model as a description of a random variable:

  response ~ deterministic part + stochastic part

  e.g. $y_i =$ $\alpha_i + \varepsilon_i$

  with $\varepsilon_i \sim Normal(0, \sigma^2)$

- stochastic/random part: statistical distribution for ε_i

- deterministic/systematic part: non-linear or linear function α_i

- non-linear may be more mechanistic and better for extrapolation, but (much) more difficult to fit

- linear model by far easiest for deterministic part of response

- For hierarchical modeling, must understand GLM

- For GLM and HMs, must understand linear modeling

- see Chapter 3 in BPA; chap 3 in AHM1, also Kéry (2010)

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Types of descriptions of linear model in GLM

- words: e.g., "A and x act additively ...."
- graphs: e.g., lines and bars
- specific labels: e.g., ANOVA, ANCOVA, t-test, regression
- algebra: e.g., $y_i \sim Normal(\alpha_j + \beta * x_i, \sigma^2)$
- matrix algebra: e.g, **y** = **Xb** + **e**
- system of equations
- R language: e.g.,

    ```
    lm(y ~ A + x)
    ```

- BUGS language: e.g.,

    ```
    y[i] ~ dnorm(mu[i], tau)
    mu[i] <- alpha[A[i]] + beta * x[i]
    ```

- alternative, equivalent descriptions: parameterisations

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Specification of linear models in BUGS language

- almost exactly as we do in algebra !

- one of the main stumbling blocks of becoming a BUGS modeler at first is to know how to specify your linear models

- **HOWEVER:** wonderful side effect that it finally *enforces* an understanding of linear models fit by issuing R commands such as `lm(y ~ A*x)`
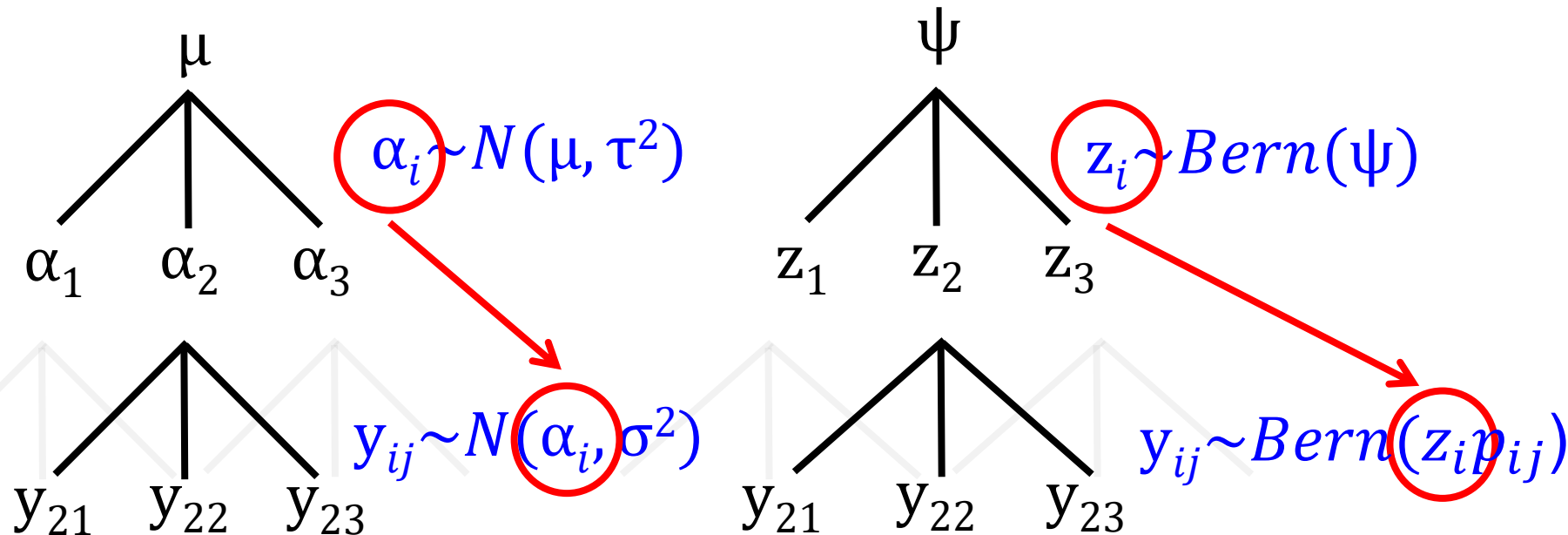
Some important linear models in glm/lm and BUGS

No.	Model in R	Model in algebra	Model in BUGS	Traditional name of technique based on that linear model	Number of coefficients	Meaning
1	1	α	alpha	"Model of the mean"	1	Constant term (intercept) only
2	pop	$\mu + \alpha_j$	mu + alpha[pop[i]] alpha[1] <- 0	One-way ANOVA	3	This is the default linear model parameterisation of a factor in R, which has an intercept (= the value for the first population) and two constants that are the differences between the values of population 2 and 1 and 3 and 1. In BUGS, the first level of the vector alpha must be manually set to zero to avoid overparameterisation. In R this is done automatically.
3	pop-1	α_j	alpha[pop[i]]	One-way ANOVA	3	This is a simple reparameterisation of model 2. There are three constants, one for each population (called the level of the factor). Called a t-test if factor has only two levels. In R this model is specified by "subtraction" of the intercept.
4	body	$\alpha + \beta * x_i$	alpha + beta * body[i]	Simple linear regression	2	An intercept plus a slope, common to all three populations (i.e., no effect of pop)
5	body-1	$\beta * x_i$	beta * body[i]	Simple linear regression through the origin	1	"Subtract the intercept": because body is a continuous covariate, this is NOT a mere reparameterisation of model 4. Regression through the origin; not usually a meaningful model.
6	pop+body	$\alpha_j + \beta * x_i$	alpha[pop[i]] + beta * body[i]	Main-effects ANCOVA	4	One separate intercept for each population and a common slope
7	pop*body	$\alpha_j + \beta_j * x_i$	alpha[pop[i]] + beta[pop[i]] * body[i]	Interaction-effects ANCOVA	6	Three separate intercepts and three separate slopes. That is, fully separate regression of wing on body for each population.

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(see AHM1 Chapter 3)

What are random effects ?

- **Hierarchical models: Linked sequence of random variables (observed & unobserved)**

- e.g., randomised block ANOVA, „hierarchical logistic regression"

$$\mu$$

$$\alpha_1 \quad \alpha_2 \quad \alpha_3$$

$$\alpha_i \sim N(\mu, \tau^2)$$

$$y_{ij} \sim N(\alpha_i, \sigma^2)$$

$$y_{21} \quad y_{22} \quad y_{23}$$

$$\psi$$

$$z_1 \quad z_2 \quad z_3$$

$$z_i \sim Bern(\psi)$$

$$y_{ij} \sim Bern(z_i p_{ij})$$

$$y_{21} \quad y_{22} \quad y_{23}$$

- Many other (similar) names: state-space, random-, mixed-effects, latent variables, unobserved components, **mixed models** …

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What are random effects ?

- **Random effects:
  Realized values of unobserved random variables in a HM !**

- two or more latent variables/parameters
  that are given a (prior) distribution; **that's all !**

- prior distribution assumed Normal in all classical GLMMs

- **BUT:** can be non-normal, e.g., Poisson (discrete) or even
  Bernoulli (discrete and binary): cf. Nmix and site-occ. models

- can estimate parameters of prior distribution (also called
  mixing distribution), e.g., τ^2 or ψ, **and** realized values α and z !

- parameter, prior/mixing distribution, hyperparameters,
  hyperpriors, …

$$\alpha_i \sim N(\mu, \tau^2)$$
$$y_{ij} \sim N(\alpha_i, \sigma^2)$$

$$z_i \sim Bern(\psi)$$
$$y_{ij} \sim Bern(z_i * p_{ij})$$

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What are random effects ?

- **Random effects:
  Realized values of unobserved random variables in a HM !**

- replication of study would (usually) yield different effects

- can estimate values of "new" draws from same prior distribution

- in analysis, treatment as fixed or random is your judgment; cannot be "tested"

- in Bayes, effects said exchangable: "similar but not identical", "no more recognizable internal structure"

  -> don't treat "dissimilar" effects as random (e.g., captive and wild populations)

- (also: bad estimates when few levels, e.g.only 3–5)
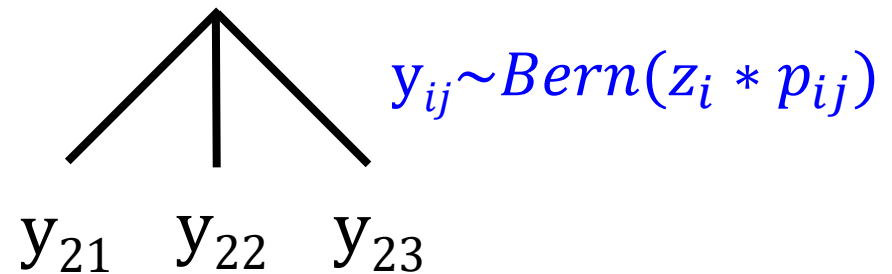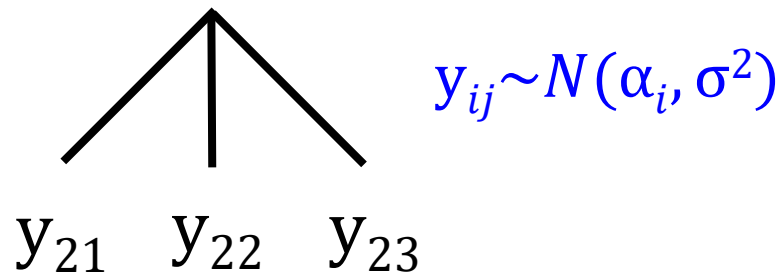
- (HMs computationally more expensive)

Motivations for treating as random a set of params

- extend scope of inference

- assess/partition system variability

- want to model variability among paramaters

- proper assessment of uncertainty

- model random effects, e.g., as a GLM, correlations

- spatial and temporal correlations

- avoid pseudo-replication

- borrow strength/improve individual random effects estimates/shrinkage

- combine information (meta-analysis)

- others

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Modeling of measurement errors in HMs

- Last level of HM before:
  measurement error = observation process

$$y_{ij} \sim N(\alpha_i, \sigma^2)$$

$$y_{ij} \sim Bern(z_i * p_{ij})$$

$$y_{21} \quad y_{22} \quad y_{23}$$

$$y_{21} \quad y_{22} \quad y_{23}$$

- <u>Qualitatively very different:</u>

(1) cancel out

$E(y_{i.}) = \alpha_i$

(2) do **NOT** cancel out

$E(y_{i.}) = z_i * p_{ij} \neq z_i$

=> Should care for measurement errors

Observation errors

Modeling of measurement errors in HMs

- What do you see ?

Importance of linear models and random effects

=> Your most common manner of interacting
with a HM/IPM will be to specify linear models and
making some factors random