

# ZIKA VIRUS DISEASE

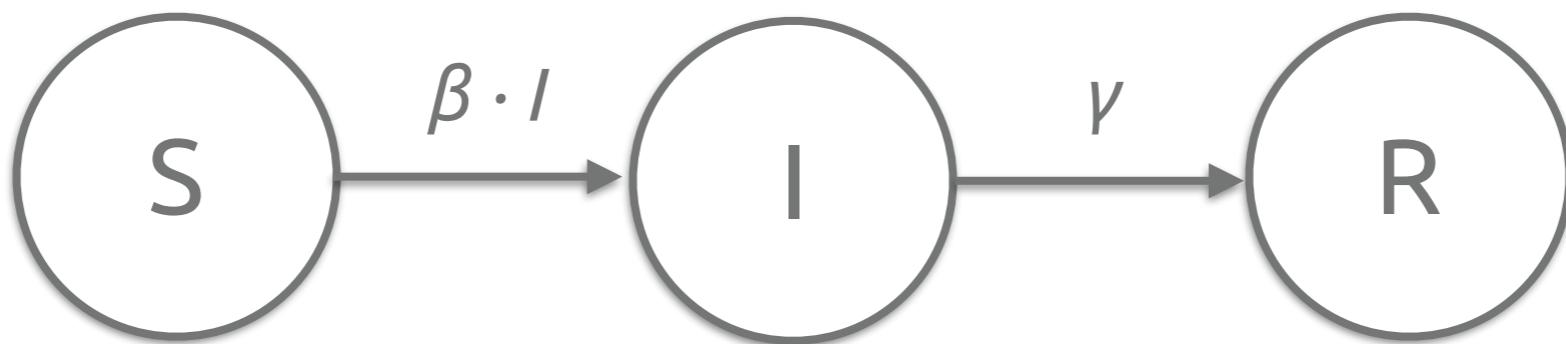
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*Variation in the Basic Reproduction Number  
for the 2015/2016 Colombia Outbreak*

*William Rittasse, S. M. Z. Rizvi, & Stephen Thomas*

# MODELING DISEASE OUTBREAKS

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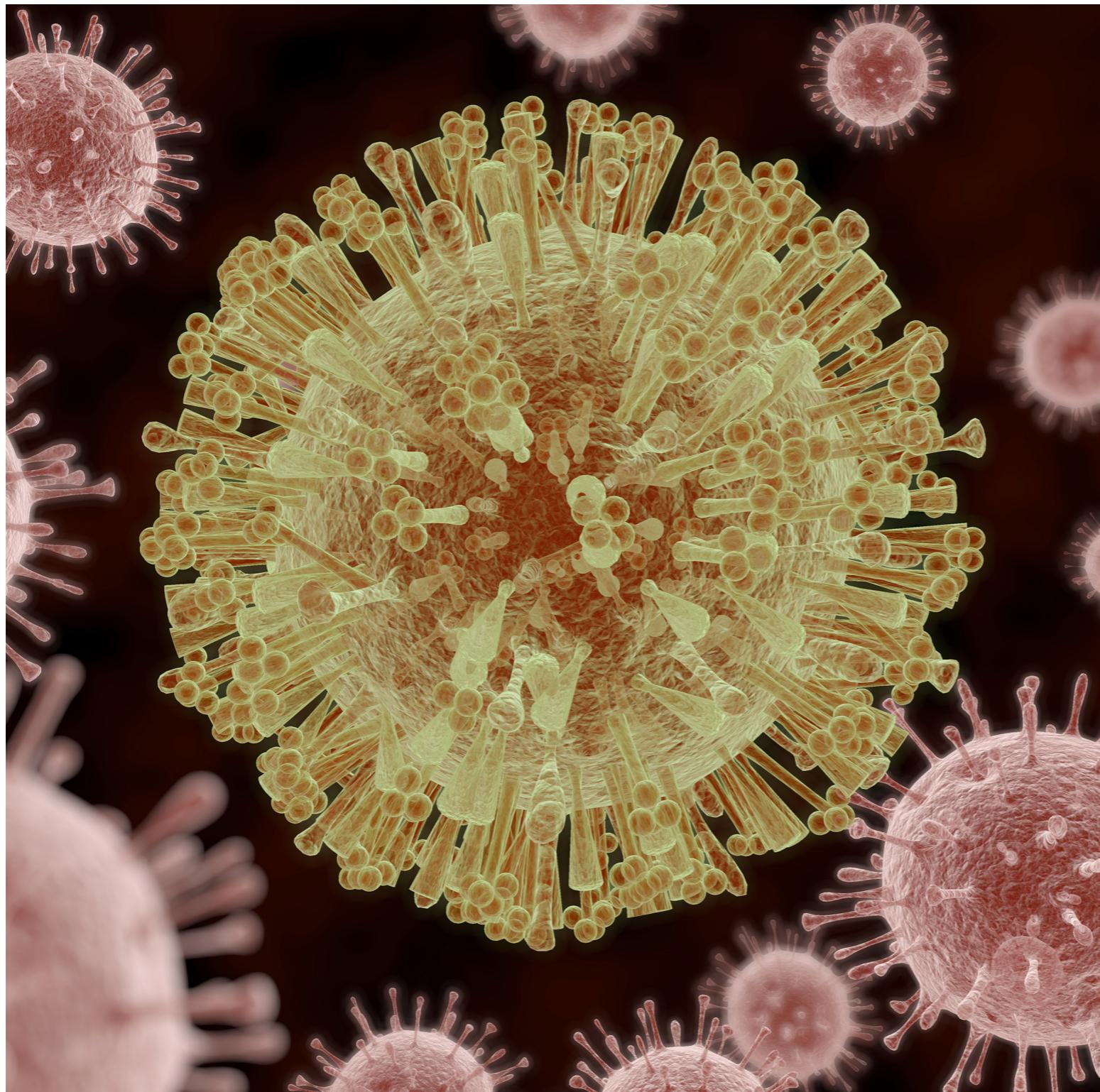


$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Kermack, W. O.; McKendrick, A. G. (1927). "A Contribution to the Mathematical Theory of Epidemics". *Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences* **115** (772): 700

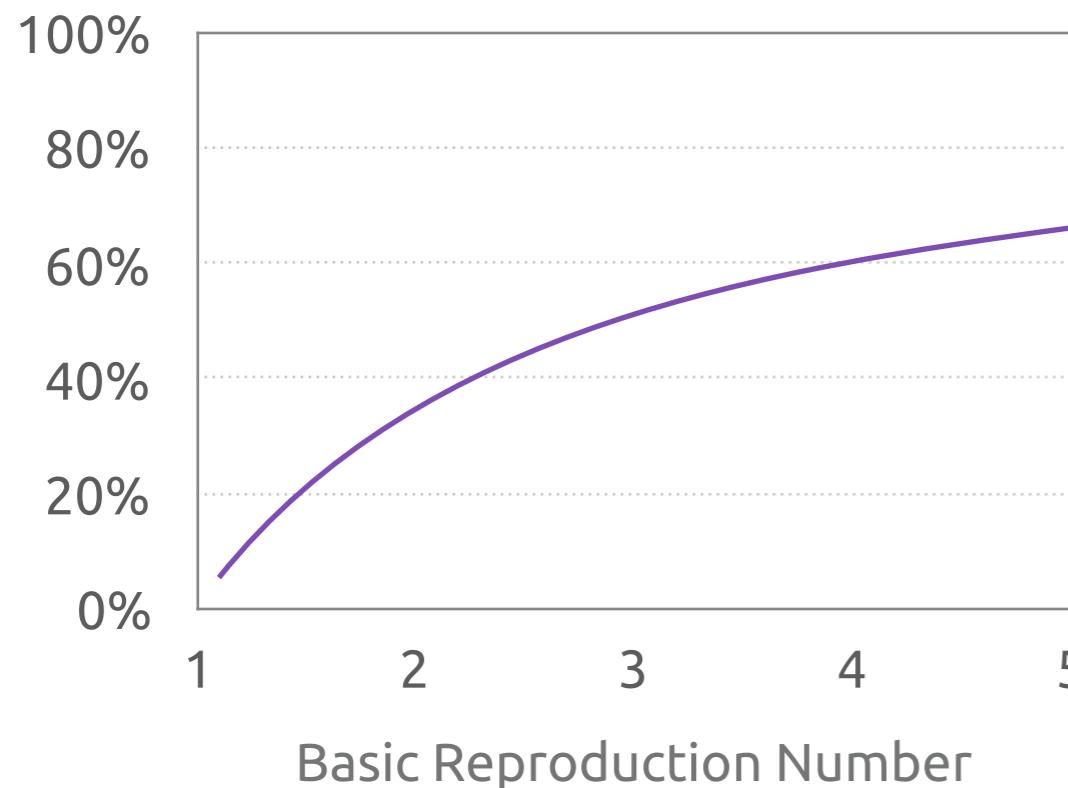


BASIC REPRODUCTION NUMBER: e.g.  $R_0 = \beta/\gamma$

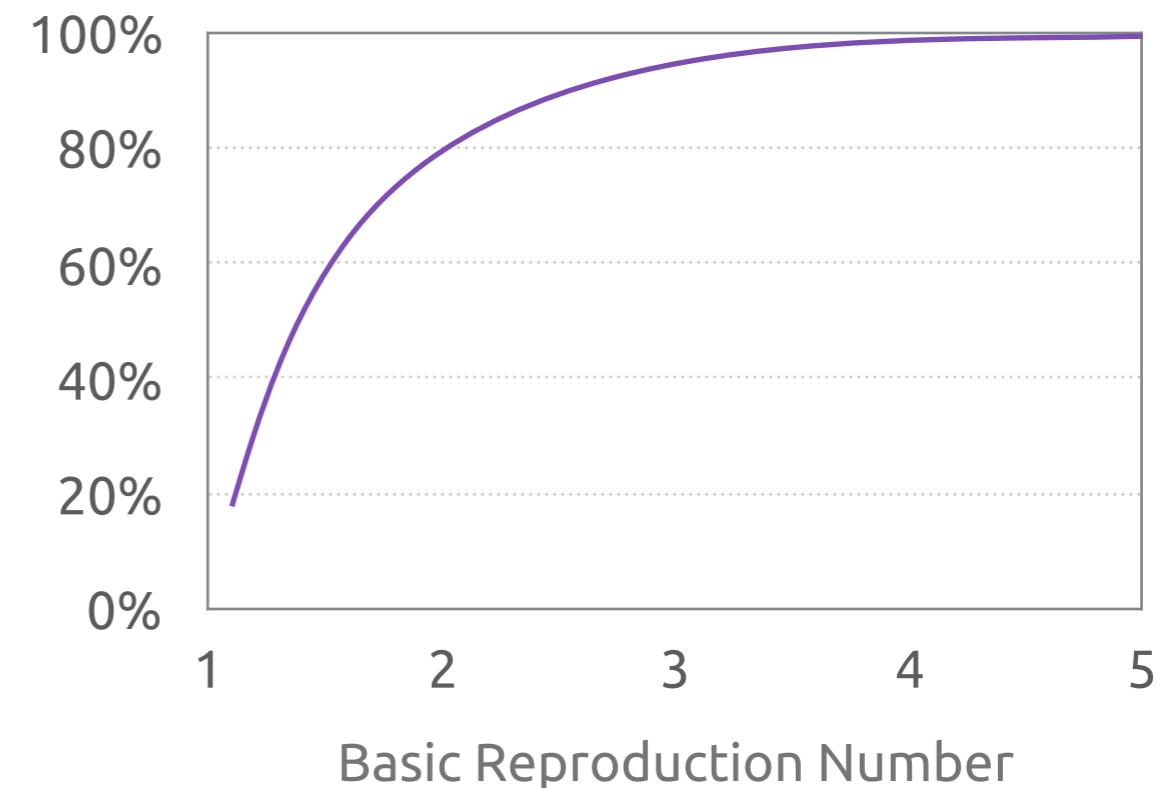
# $R_0$ DESCRIBES KEY CHARACTERISTICS OF AN EPIDEMIC

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Peak Infection Rate



Final Size of Epidemic



Critical Vaccination Threshold:

$$P_c = \frac{1}{\varepsilon} \left( 1 - \frac{1}{R_0} \right)$$

# DATA: COLOMBIA NATIONAL INSTITUTE OF HEALTH

**BES**  
BOLETÍN EPIDEMIOLÓGICO SEMANAL

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Dirección de Vigilancia y Análisis del Riesgo en Salud Pública  
INSTITUTO NACIONAL DE SALUD  
TODOS POR UN NUEVO PAÍS  
PAZ EQUIDAD EDUCACIÓN

Semana epidemiológica número 01 de 2016 (03 ene. al 09 ene.)

**"FIN DEL BROTE MÁS RECENTE DE ÉBOLA EN LIBERIA, PERO NO PUEDEN DESCARTARSE NUEVOS BROTES".**

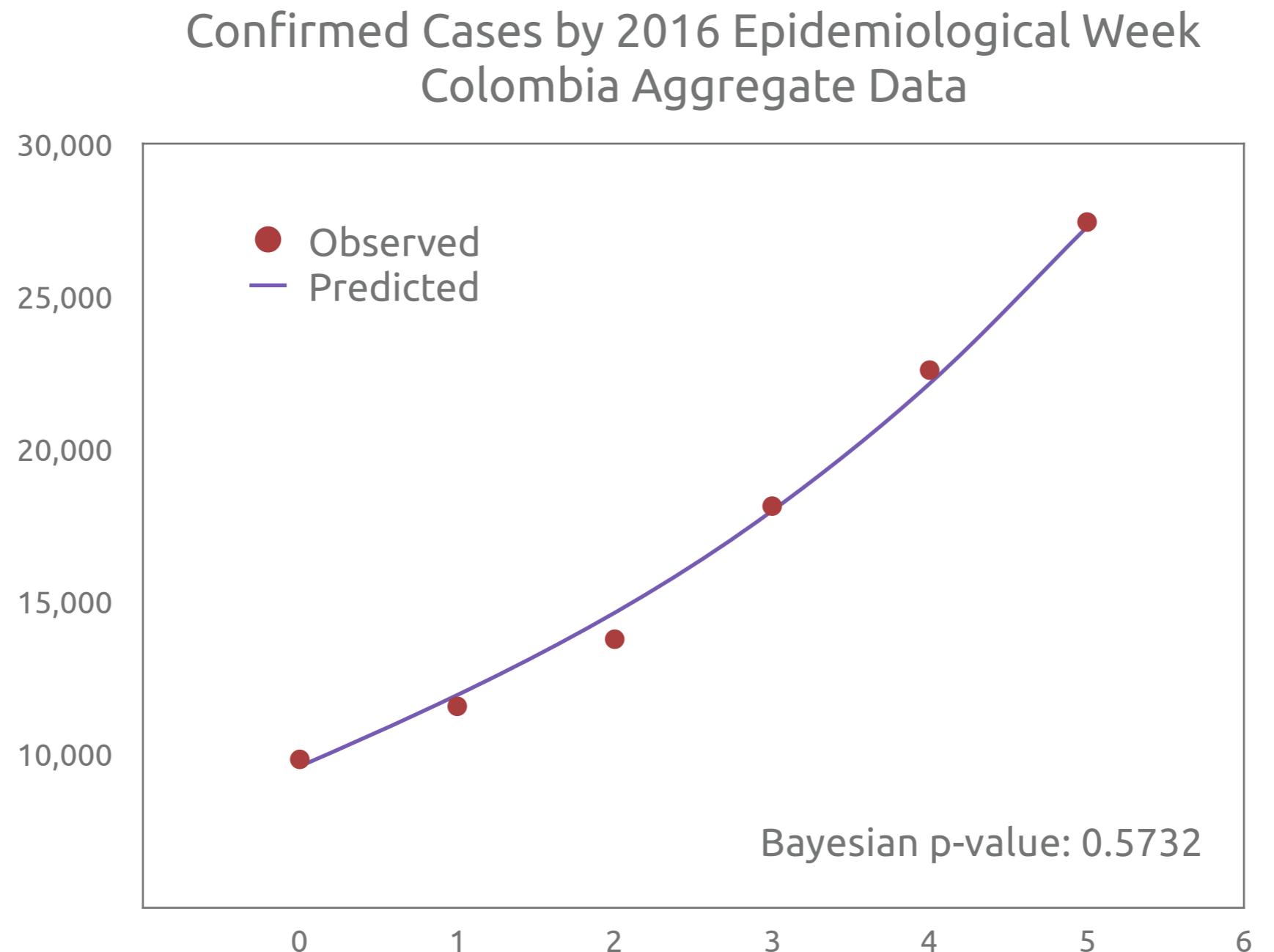
14 de enero de 2016 -- La OMS declara hoy el fin del brote más reciente de enfermedad por el virus del Ébola en Liberia. No obstante, la Organización advierte de que la tarea no se ha

<http://www.ins.gov.co/Noticias/ZIKA/Forms/AllItems.aspx>

<https://github.com/cdcepi/zika>

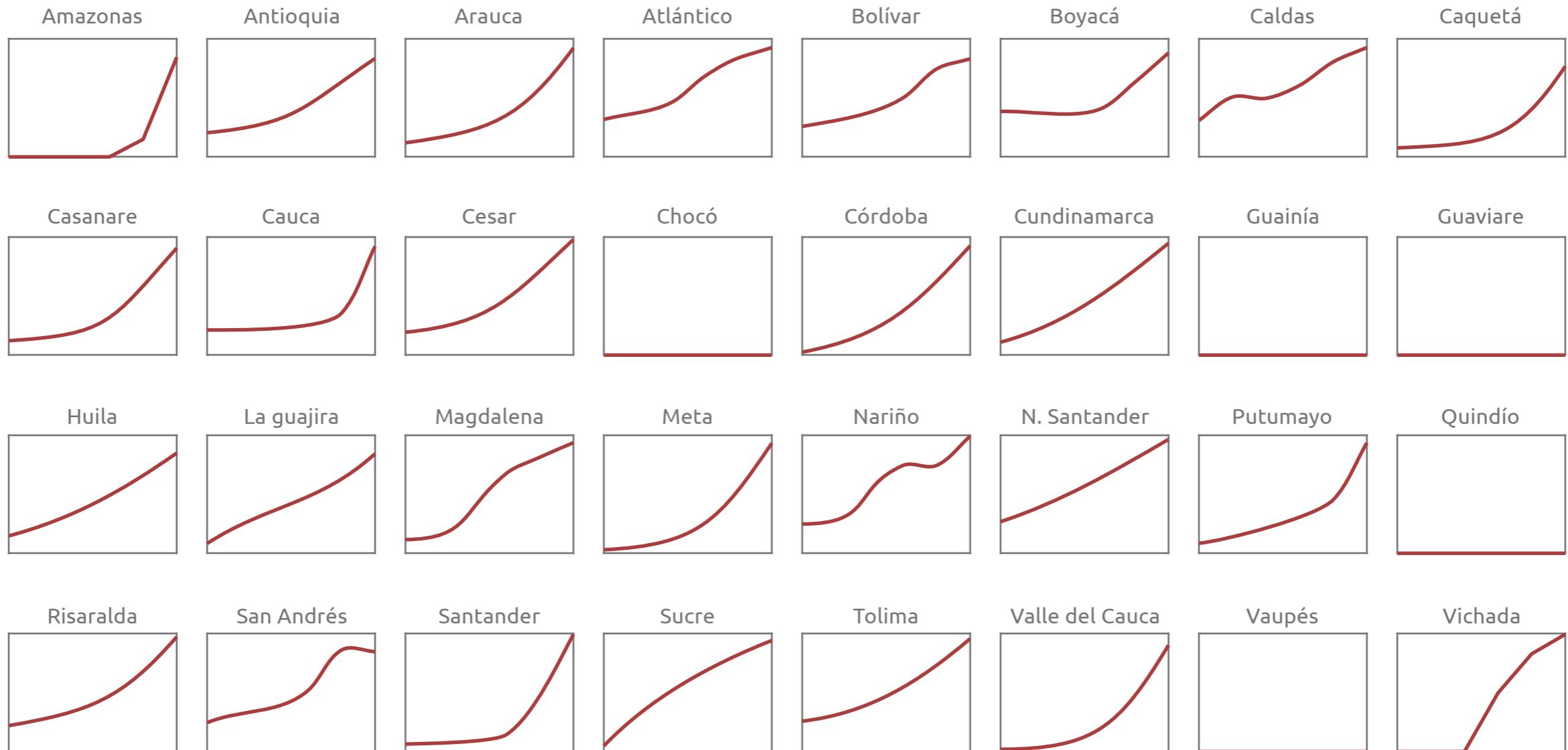
# VALIDATING THE DATA USING AGGREGATE CASES

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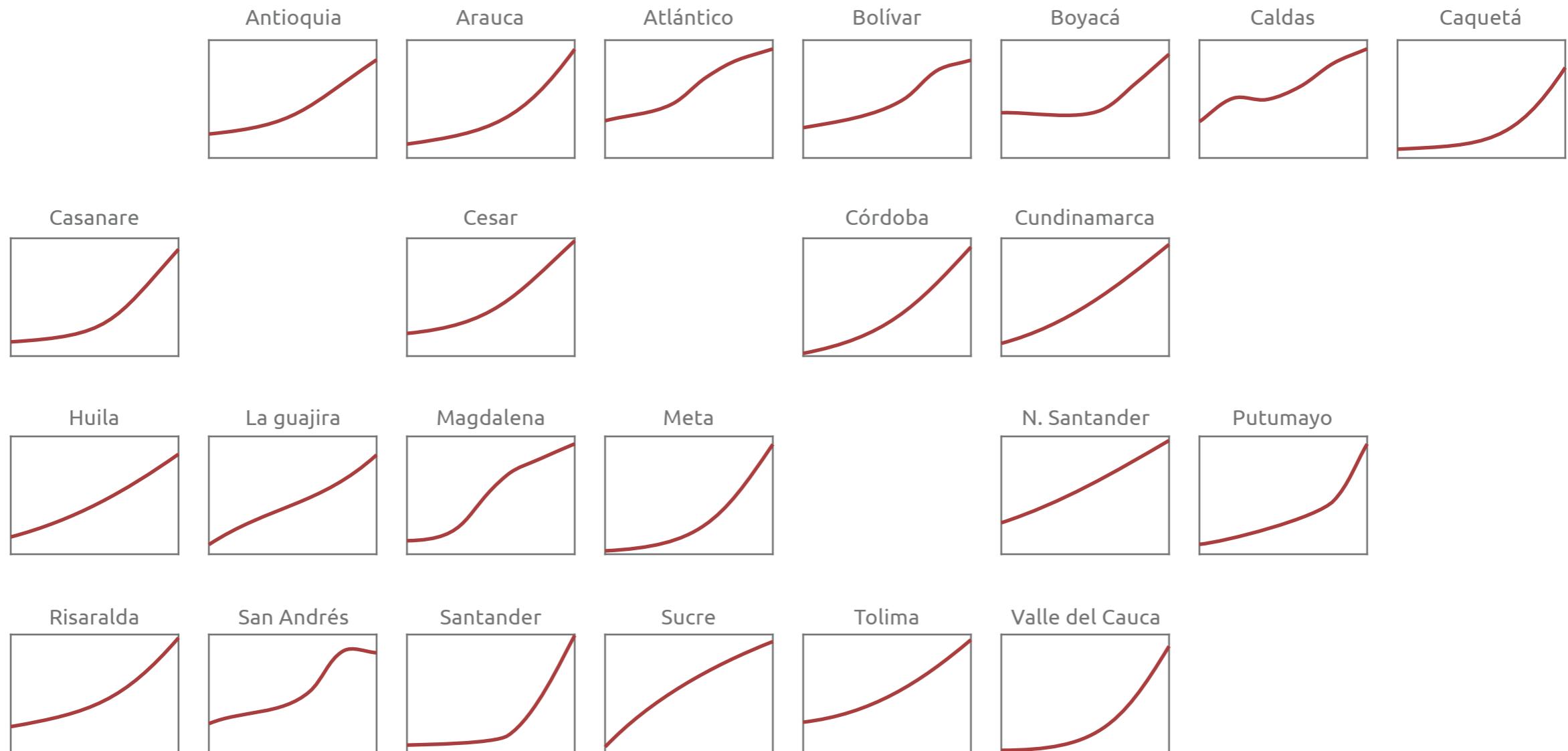
# CONFIRMED CASES BY DEPARTMENT

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# CONFIRMED CASES BY DEPARTMENT (> 50 CASES)

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# $R_0$ ESTIMATION MODEL

```
# This is a JAGS model for estimating the basic reproduction
# number ( $R_0$ ) for Colombia departments. It relies on a
# hierarchical linear regression with two levels of
# hierarchy. The input data consists of a set of
# observations where each observation includes an
# independent variable ( $x$ ) representing the week number, a
# dependent variable ( $y$ ) representing the cumulative
# confirmed cases, and an integer-valued department
# identification.
#
# The model assumes that the dependent variable  $y$  is
# exponentially related to the independent variable, and
# observations within a department are more closely related
# than observations between departments. In particular, it
# assumes that the slope parameters for individual groups
# are normally distributed around an overall slope.
# Intercept parameters, however, are assumed independent for
# each group and are derived from the data.
#
# The model reports goodness of fit using Bayesian p-value.
#
# Observation data is supplied in three vectors:
#   dept[] - department id
#   x[]    - week number
#   y[]    - cumulative confirmed cases
#
# In addition, a vector of observed intercepts for
# each department is supplied in the `intercept[]` vector.

data {
  # Transform Inputs
  #
  # Logarithmic transformation to allow linear regression
  ln_y <- log(y)
}

model {
  # Prior Probabilities
  #
  # Express all priors as reference (non-informative)
  # priors. The parameters for the model are:
  #
  #   beta_mu      - the mean for the aggregate slope
  #                   (all depts)
  #   beta_sigma   - the standard deviation for the
  #                   aggregate slope (all depts)
  #   sigma        - the standard deviation for the
  #                   residuals (assumed to be the same
  #                   for all depts)

  beta_mu ~ dnorm(0, 0.0001)
  beta_sigma ~ dunif(0.001, 1000)
  sigma ~ dunif(0.001, 1000)

  # The Likelihood
  #
  # Model the dependent variable `y` as Normal with mean
  # `mu` and standard deviation `sigma`. Model the mean
  # `mu` as a linear function of the independent variable
  # `x`. The parameters of that linear relationship vary
  # based on the department, and are:
  #
  #   alpha[dept[i]] - intercept for department
  #   beta[dept[i]]  - slope for the department
  #
  # The standard deviation `sigma` is assumed to be the
  # same for all observations, regardless of dept.
  #
  # Apply the model to all observations.
  for (i in 1:length(y)) {
    ln_y[i] ~ dnorm(mu[i], 1/(sigma^2))
    mu[i] <- alpha[dept[i]] + beta[dept[i]]*x[i]
  }

  # Model the slope for each dept as Normal with a mean
  # and standard deviation from hyper-priors. Apply the
  # model to all depts.
  for (j in 1:max(dept[])) {
    beta[j] ~ dnorm(beta_mu, 1/(beta_sigma^2))
  }

  # The intercept values for each dept are included in
  # the observations. Use the observed value as the
  # mean for a Normal distribution with a standard
  # deviation equal to the overall standard deviation.
  for (j in 1:max(dept[])) {
    alpha[j] ~ dnorm(intercept[j], 1/(sigma^2))
  }

  # Posterior Predictive Check
  #
  # Calculate the p-value using a sum-of-squares
  # test for fitness. To do that, first calculate
  # the sum of squares of the residuals. (The
  # residuals are the differences between the observed
  # y-values and the values that the current iteration's
  # parameters would predict.)
  for (i in 1:length(y)) {
    sq.res[i] <- pow((ln_y[i] - mu[i]), 2)
  }

  # Next, generate a new y-value given the current
  # iteration's parameters and compare that new
  # value with what the parameters would predict.

  for (i in 1:length(y)) {
    ln_y.new[i] ~ dnorm(mu.new[i], 1/(sigma^2))
    mu.new[i] <- alpha[dept[i]] + beta[dept[i]]*x[i]
    sq.new[i] <- pow((ln_y.new[i] - mu[i]), 2)
  }

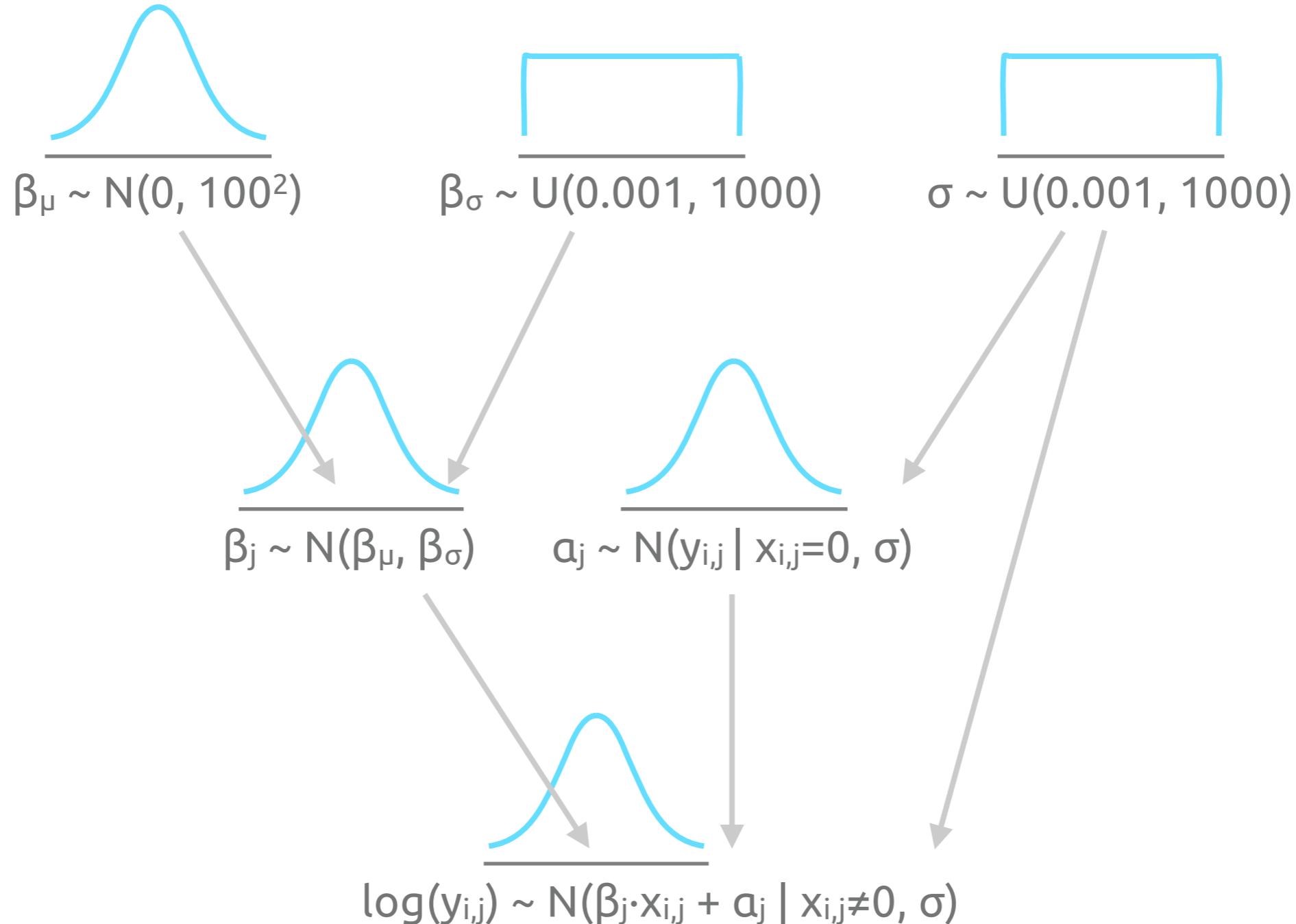
  # For the goodness of fit test, compare the sums
  # of the two squared values to see which is greater.
  # If the model is a good fit, neither sum is more
  # likely to be greater than the other. The
  # resulting p-value should, therefore, be close to
  # 0.5.
  test <- step(sum(sq.new[]) - sum(sq.res[]))
  pvalue <- mean(test)

  # Additional Processing
  #
  # Although not part of the regression itself, the
  # model can be used to estimate  $R_0$  from the
  # regression parameters. The following code relies
  # on the approach documented in
  #
  #   Heffernan, J M, Smith, R J, & Wahl, L M (2005).
  #   "Perspectives on the basic reproductive ratio."
  #   Journal of the Royal Society Interface, 2(4),
  #   281-293. http://doi.org/10.1098/rsif.2005.0042
  #
  # For the serial interval time, use data reported in
  #
  #   Majumder M S, Cohn E, Fish D & Brownstein J S.
  #   Estimating a feasible serial interval range for
  #   Zika fever [Submitted]. Bull World Health Organ,
  #   E-pub: 9 Feb 2016.
  #   http://dx.doi.org/10.2471/BLT.16.171009
  #
  # Majumder et al report only a range for their
  # estimates without a distribution, so the following
  # code assumes a uniform distribution within the
  # estimated range. (Note that Majumder et al's range
  # is specified in days. It must be converted to weeks
  # to correspond to the observations.)
  #
  # The initial growth rate ( $r$ ) in the calculation is
  # simply the estimated slope  $\beta$ .
  for (j in 1:max(dept[])) {
    si[j] ~ dunif(10, 23)
    R0[j] <- 1 + beta[j]*si[j]/7
  }

  # Also model an overall  $R_0$ 
  si_mean ~ dunif(10, 23)
  R0_mean <- 1 + beta_mu*si_mean/7
}
```

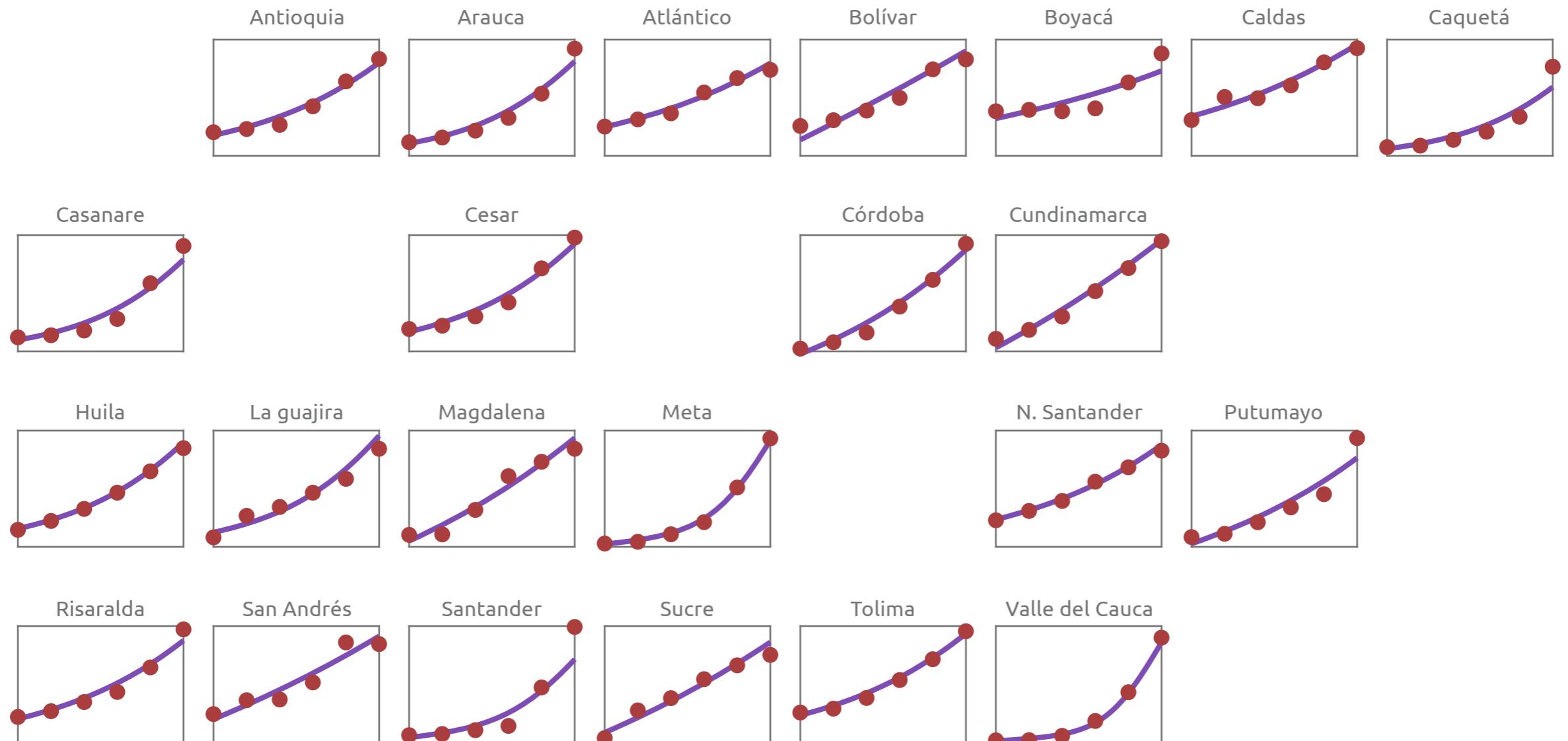
# HIERARCHICAL REGRESSION MODEL (LOG TRANSFORM)

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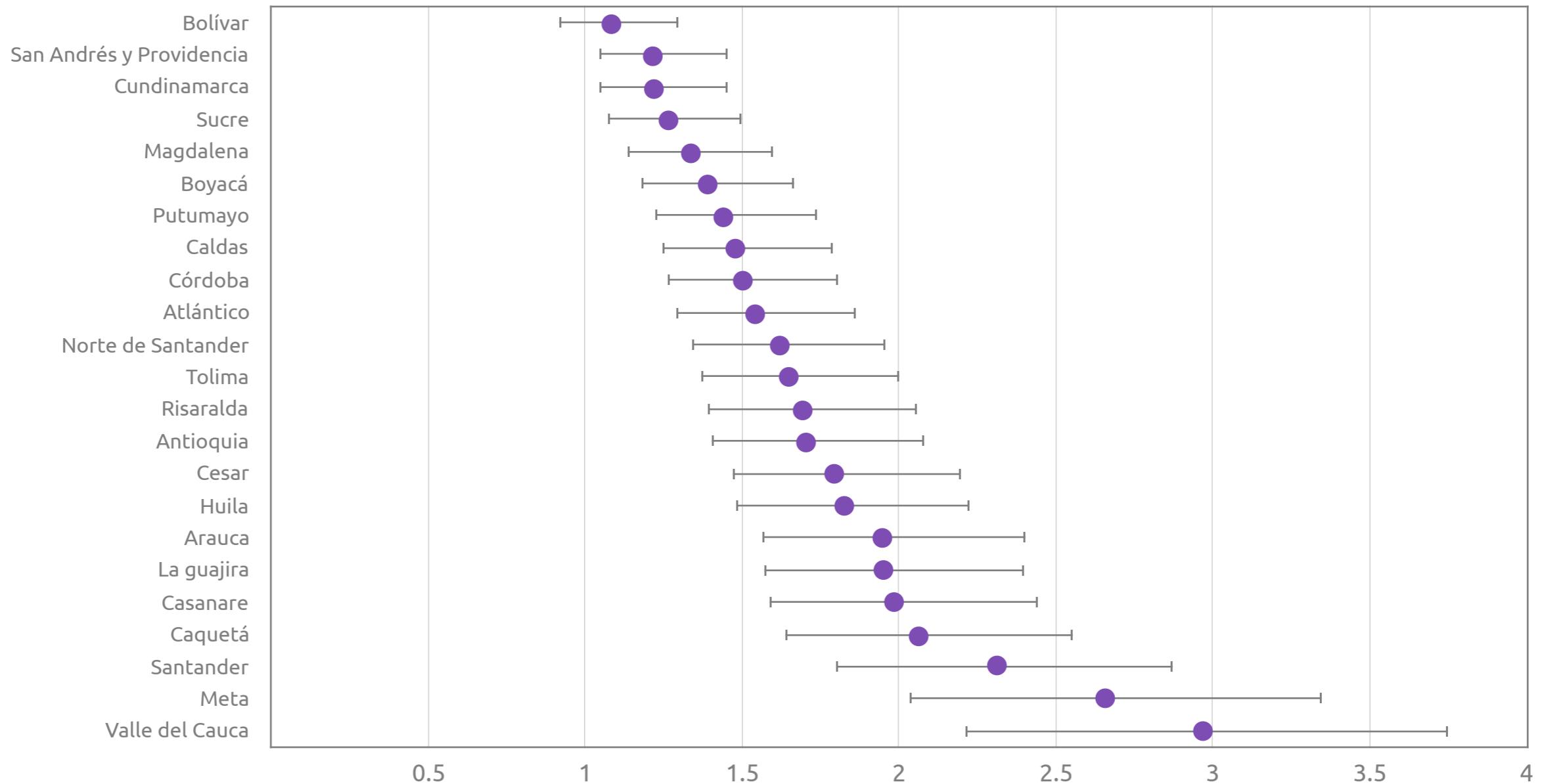
# REGRESSION RESULTS

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# 95% CREDIBLE INTERVALS FOR $R_0$ BY DEPARTMENT

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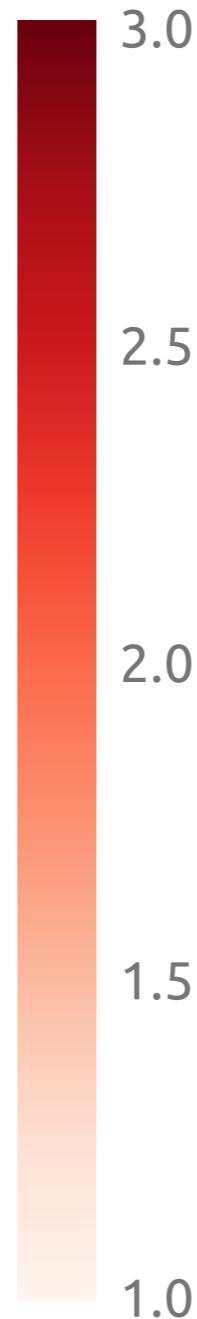
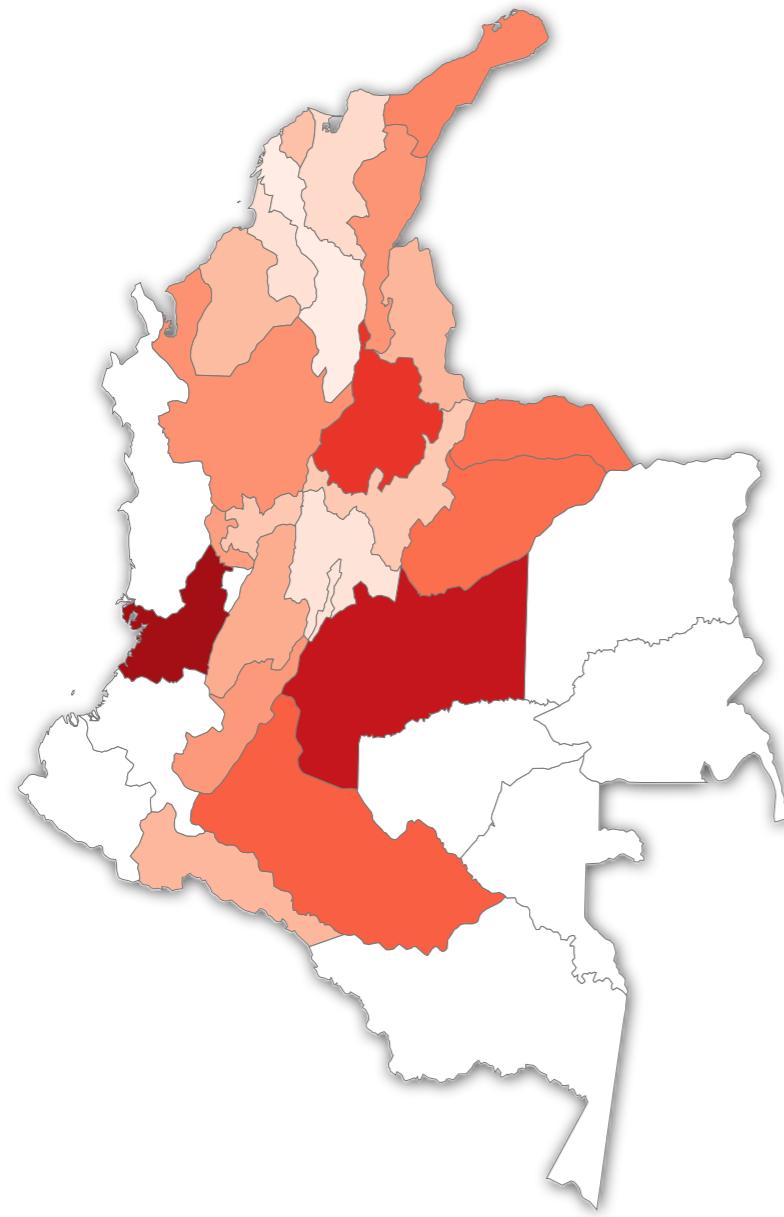


Compare with Nishiura, H., Kinoshita, R., Mizumoto, K., Yasuda, Y., & Nah, K. (2016). "Transmission potential of Zika virus infection in the South Pacific." *International Journal of Infectious Diseases*, 45, 95–97. <http://doi.org/10.1016/j.ijid.2016.02.017>

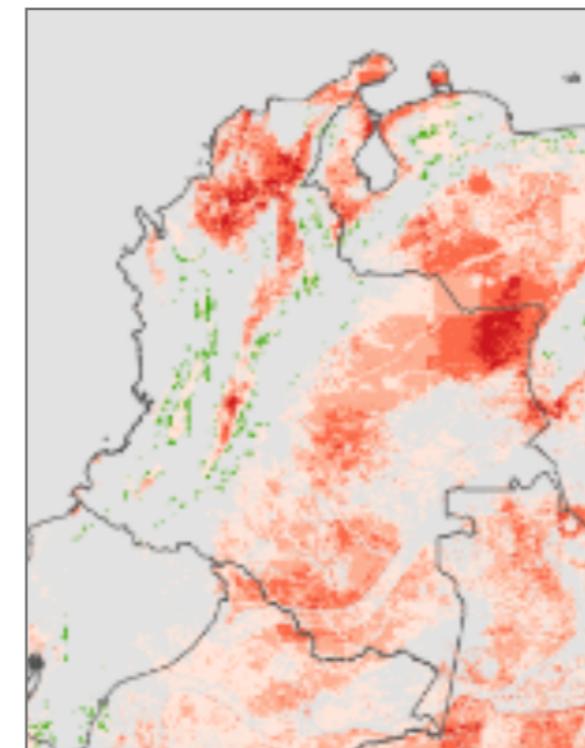
Yap Island: 2.7 - 5.0, French Polynesia: 1.8 - 2.0

# GEO-SPATIAL VARIATION IN $R_0$

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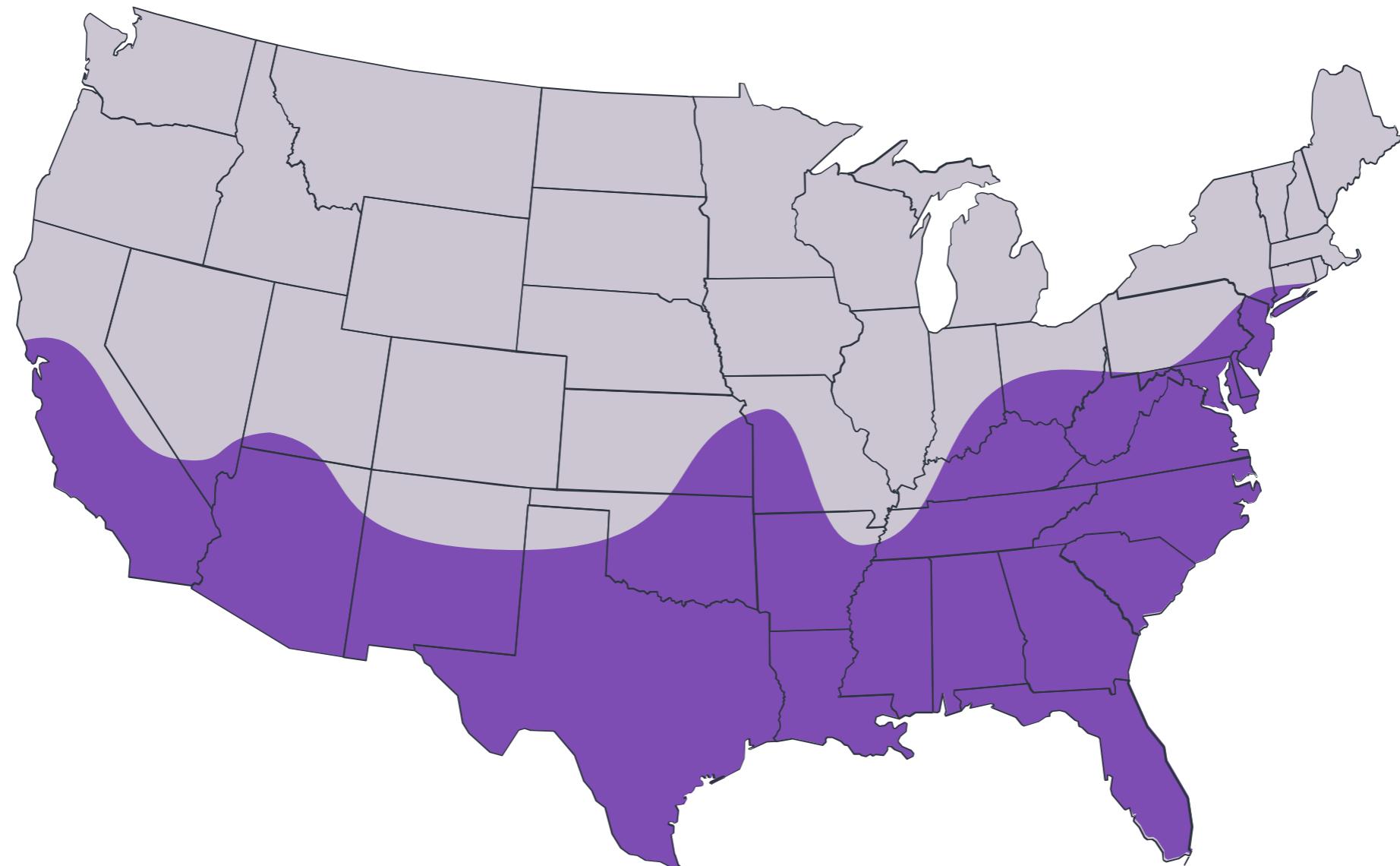
Compare with projected  $R_0$  from Perkins, et al, "Model-based projections of Zika virus infections in childbearing women in the Americas" based on discrete model parameters, e.g. daily temperature, mosquito mortality, transmission probabilities, mosquito biting rate, etc.



# DATA & MODELS:

<https://github.com/sathomas/zika-colombia-2016>

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Estimated range of *Aedes aegypti* in the United States, Summer 2016 (Source: [CDC](#))