# NGA East Median GMMs

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# Part I

# **Continuous Distribution**

Capture *center*, *body* and *range* of median ground motion predictions.

#### Approach

- Select (adjusted) seed GMMs.
- Estimate continuous distribution of median ground motion predictions.
- Discretize continuous distribution to get a manageable number of GMMs.
- Evaluate/Weigh selected GMMs.

- For illustration, assume a one-dimensional distribution.
- Only one *M*/*R*-scenario is relevant.
  - Estimate continuous distribution.
  - Discretize space.
  - Select representative models.
  - Assign weights.

- Predictions of seed GMMs at M = 6,  $R_{RUP} = 100$
- Estimated continuous normal distribution  $P(Y) = N(\mu, \sigma)$



- Partitioning of 1D-normal distribution into cells to get representative models (for P(Y)).
- Each "model" is just a single number.



- Sample 5000 "models" from P(Y)
- Select samples inside each cell, calculate mean ⇒ selected/representative model.



- Assume there is data available,  $D = \{y_1^*, \dots, y_{N_d}^*\}$ .
- The data points are distributed according to a normal distribution  $Y^* \sim N(\mu^*, \sigma^*)$ , where  $\sigma^*$  corresponds to aleatory variability.
- P(Y) describes epistemic uncertainty about  $\mu^*$ .



• For each sampled model y<sub>i</sub>, calculate residual and likelihood to D



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#### Weights can be calculated proportional to

- number of samples per cell
- integral of density P(Y) over cell
- 1/mean residual per cell
- mean likelihood per cell



- In the example, only one *M*/*R*-scenario was considered: one ground-motion value *Y*, distribution *P*(*Y*)
- Go to various M/R-scenarios: multiple ground-motio values  $Y = \{Y_1, \dots, Y_N\}$ , joint distribution P(Y)
- Basic approach stays the same.

## **Ground-Motion Distribution**



Assumption:

• function values *f* are distributed according to a (multivariate) normal distribution  $\mathcal{N}_N(\mu, \Sigma)$ 

$$\begin{bmatrix} Y_1 \\ \vdots \\ Y_N \end{bmatrix} \sim \mathcal{N} \begin{bmatrix} \mu_1 \\ \vdots \\ \mu_N \end{bmatrix}, \begin{pmatrix} \Sigma_{1,1} & \dots & \Sigma_{1,N} \\ \vdots & \ddots & \vdots \\ \Sigma_{N,1} & \dots & \Sigma_{N,N} \end{pmatrix}$$

where  $\Sigma_{i,j} = \rho_{i,j}\sigma_i\sigma_j$ .

A full description of the distribution  $P(\mathbf{Y})$  requires specification of  $\mu$ ,  $\sigma$  and  $\rho$  for all M/R-scenarios. This is done by estimating these terms as functions of M, R.

$$\sigma_i = f_{\sigma}(M_i, R_i)$$
$$\rho_{i,j} = k(\{M_i, R_i\}, \{M_j, R_j\})$$

# Variance Model

- $f_{\sigma}$  is a smooth function
- $\sigma$  is larger than in the West
- $\sigma$  is large for large *R* and large *M*



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The correlation model is a sum of a rational-quadratic term and a dot-product term. The second term models a linear relationship, the first one models nonlinearities.

$$egin{aligned} k(oldsymbol{x},oldsymbol{x}') &= heta_1 (1 + (oldsymbol{x} - oldsymbol{x}')^T igg( egin{aligned} heta_2 & 0 \ 0 & heta_3 \end{array} igg) (oldsymbol{x} - oldsymbol{x}')/(2 heta_4))^{- heta_4} \ &+ oldsymbol{x}^T igg( egin{aligned} heta_5 & 0 \ 0 & heta_6 \end{array} igg) oldsymbol{x}' \end{aligned}$$

$$\begin{split} k(\boldsymbol{x}, \boldsymbol{x}') &= \theta_1 (1 + (\boldsymbol{x} - \boldsymbol{x}')^T \begin{pmatrix} \theta_2 & 0 \\ 0 & \theta_3 \end{pmatrix} (\boldsymbol{x} - \boldsymbol{x}') / (2\theta_4))^{-\theta_4} \\ &+ \boldsymbol{x}^T \begin{pmatrix} \theta_5 & 0 \\ 0 & \theta_6 \end{pmatrix} \boldsymbol{x}' \end{split}$$

The parameters  $\boldsymbol{\theta}$  are estimated by maximizing the marginal likelihood, given mean GMM predictions.



- Calculate mean of seed GMMs  $y_{\mu}$  at different M/R-scenarios ( $M = 4., 4.5, \dots, 8., 8.2, R_{RUP} = 10. 1200$  km)
- Maximize marginal likelihood of mean predictions  $y_{\mu}$  at M/R-values X with respect to parameters  $\theta$

$$\ln p(\boldsymbol{y}_{\mu}|\boldsymbol{X},\boldsymbol{\theta}) = -\frac{1}{2}\boldsymbol{y}^{T}K_{Y}^{-1}\boldsymbol{y} - \frac{1}{2}\log|K_{Y}| - \frac{n}{2}\ln 2\pi$$

where  $K_y = K_f + \sigma^2 I$  and I is the identity matrix. The matrix  $K_f = k(\mathbf{x}_i, \mathbf{x}_j)$  is the covariance evaluated at the predictor variables (the different M/R-scenarios).

### **Covariance Model**

- Combine the variance model and correlation model
- $\rho_{ij} = k(\mathbf{x}_i, \mathbf{x}_j)$

• 
$$\Sigma_{ij} = \sigma_i \sigma_j \rho_{ij}$$

The covariance matrix can be evaluated for any *M*/*R*-value. Hence, samples can be drawn for any number of *M*/*R*-values. The distribution specified by  $\Sigma$  (and  $\mu$ ) is a distribution over functions. For further calculations, the following *M*/*R*-scenarios are used:

- M = 4., 4.5, 5., 5.5, 6., 6.5, 7., 7.5, 7.8, 8., 8.2
- R = 0., 1., 5., 10., 15., 20., 25., 30., 40., 50., 60., 70., 80., 90., 100., 110., 120., 130., 140., 150., 175., 200., 250., 300., 350., 400., 450., 500., 600., 700., 800., 1000., 1200., 1500.
- 374 M/R-scenarios
- Each resulting GMM is a vector of ground-motion values at these M/R-scenarios.

Example



• 10 samples from continuous distribution with covariance model.

Example



• 10 samples from continuous distribution with no correlation.

Example



• 10 samples from continuous distribution with full correlation ( $\rho_{ij} = 1$ ).

The continuous distribution with the covariance model is a "compromise" between a distribution with full correlation (scaled backbone) and no correlation. The covariance model is closer to full correlation.

- The pointwise (marginal) distribution at each M/R-scenario P(Y) is the same for all three joint distributions P(Y).
- The pointwise quantiles are the same.
- The joint quantiles are different.

- The correlation between different M/R-scenarios is rather strong.
- This leads to small perturbations in scaling relative to the mean model.
- To retain the characteristics of the seed GMMs, these are used as means

 $\Rightarrow P(Y)$  is a mixture model, with covariance defined by the the covariance model and means defined by the seed GMMS.



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- The continuous distribution  $P(\mathbf{Y})$  needs to be discretized to have a small, manageable number of GMMs for hazard calculations.
- P(Y) is a high-dimensional distribution.
- Draw samples from *P*(*Y*), combine "similar" samples into one model.
- Similarity is defined by the average GM-distance between GMMs.
- Models are visualized in 2D such that GM-distances in 2D correspond to GM-distances in HD.

5000 samples are drawn from  $P(\mathbf{Y})$  according to:

- Randomly select one of the seed GMMs.
- Sample from a multivariate normal distribution with the seed GMM as mean and the covariance model.
- Oheck if sample passes criteria for physicality.
  - if yes, proceed
  - if no, go to step 1
- Add sample to list of sampled models.

Criteria for physicality:

- Y(M = 6, R) > Y(M = 5, R) for  $R \ge 10$
- Y(M = 7, R) > Y(M = 6, R) for  $R \ge 10$
- The distance slope between  $R_{RUP} = 10$  and  $R_{RUP} = 40$  must be larger than 0.4: sl(10,40) > 0.4
- Isl(40, 150) > −0.2
- sl(150,400) > min[0.45,0.9min(GMM)]



• Number of rejected samples.

### Sampling Physicality



• Number of samples per model in set of 5000 samples

- Joint continuous distribution over ground-motion vectors (functions)
  Y, P(Y).
- 5000 (physical) samples drawn from P(Y) at 374 M/R-scenarios for each frequency.
- Appreciation of samples/GM-space is done by visualization tools.