Meta analysis – weighting schemes

1. Unweighted
2. Cluster weight – define cluster as unique study+geog (w\_1)
   1. Equal weight (1) given to the observation within cluster.

=number of observation within cluster

= Total number of clusters

1. Cluster+natural log of sample size (w\_2)

= is elasticity that adjusted with cluster weight

A graph of different colored lines

Description automatically generated

**First approach to calculate mean elasticity:**

Determine a distance point where we pre-assume that the point can stand as the center point for waterfront homes and non-waterfront homes.

By looking at the graph, if we assume that elasticity at a distance of 160 meters will represent the average elasticity at waterfront homes, and similarly, 500 meters for non-waterfront. Then the results using frequentist approaches:

A screenshot of a data

Description automatically generated

Waterfront – elasticity estimations at 150 meter

Non-waterfront – elasticity estimations 500 meters

A screenshot of a graph

Description automatically generated

**Second approach to calculate mean elasticity:**

Use Bayesian model to estimate the distribution within elasticity 300-meter distance buffer:

* We do not need to define the distance point which we use later for benefit transfer. (i.e waterfront = 150 and non-waterfont 500)
* Instead, we use all elasticity estimations across 0-300meters to estimate the Bayesian distribution – for waterfront and 300-500 meters elasticities for non-waterfront
  + We extract all potential elasticities within a study with a varying distance up to 300 or 300 to 500
* This make more sense for benefit transfer as we take building count we take all the building foot print within 300 meters not the building on the circle of specific distance. 🡪 so this estimate represent the average elasticity across 0-300 (or 300-500) distance bin. Please take advice pros and cons from Dr. Patrick

**Waterfront:**

Family: gaussian

Links: mu = identity; sigma = identity

Formula: elast | se(vi\_log) ~ 1 + (1 | study\_name)

Data: df\_wf (Number of observations: 6812)

Draws: 4 chains, each with iter = 1e+05; warmup = 50000; thin = 1;

total post-warmup draws = 2e+05

Group-Level Effects:

~study\_name (Number of levels: 30)

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

sd(Intercept) 0.19 0.03 0.14 0.24 1.00 19633 35664

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

Intercept 0.16 0.03 0.09 0.23 1.00 12871 20400

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

sigma 0.00 0.00 0.00 0.00 NA NA NA

Draws were sampled using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

A graph with blue and black lines

Description automatically generated

**Non-waterfront**

Family: gaussian

Links: mu = identity; sigma = identity

Formula: elast | se(vi\_log) ~ 1 + (1 | study\_name)

Data: df\_wf (Number of observations: 2138)

Draws: 4 chains, each with iter = 1e+05; warmup = 50000; thin = 1;

total post-warmup draws = 2e+05

Group-Level Effects:

~study\_name (Number of levels: 9)

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

sd(Intercept) 0.09 0.03 0.05 0.16 1.00 29062 41983

Population-Level Effects:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

Intercept 0.08 0.03 0.01 0.14 1.00 30007 40247

Family Specific Parameters:

Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS

sigma 0.00 0.00 0.00 0.00 NA NA NA

Draws were sampled using sampling(NUTS). For each parameter, Bulk\_ESS

and Tail\_ESS are effective sample size measures, and Rhat is the potential

scale reduction factor on split chains (at convergence, Rhat = 1).

A graph with blue lines

Description automatically generated