

# Simulation data and comparison of simulation with approximation

## Simulation data with four clusters

Distances between clusters based on centers of gravity of clusters

```
In[81]:= distance = {{0, 97.8631780678727, 156.182654236229, 126.383383714482},  
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  {156.182654236229, 166.54935834812, 0, 94.4550453288847},  
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```

Individual reproduction numbers exceeding 1 with cluster identifier

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```

---

## Reproduction numbers per cluster

```
In[83]:= Print["number of clusters : ", nclusters = Length[distance], "\n"];
number of clusters : 4

In[84]:= Do[cluster[i] = Select[allreproductionnumbers, #[[2]] == i &][[All, 1]],
  {i, 1, nclusters}];
Do[Print["mean, variance, shape and scale of individual reproduction
  numbers for cluster ", i, " : ", mean[i] = Mean[cluster[i]], "\t",
  var[i] = Variance[cluster[i]], "\t", shape[i] = mean[i]^2/var[i],
  "\t", scale[i] = var[i]/mean[i]], {i, 1, nclusters}];
reproductionnumbers = Table[mean[i], {i, 1, nclusters}];

mean, variance, shape and scale of individual reproduction numbers for cluster
1 : 3.82292    1.6639    8.78341    0.435244

mean, variance, shape and scale of individual reproduction numbers for cluster
2 : 2.57817    0.698602    9.51467    0.270968

mean, variance, shape and scale of individual reproduction numbers for cluster
3 : 2.08025    0.324342    13.3422    0.155915

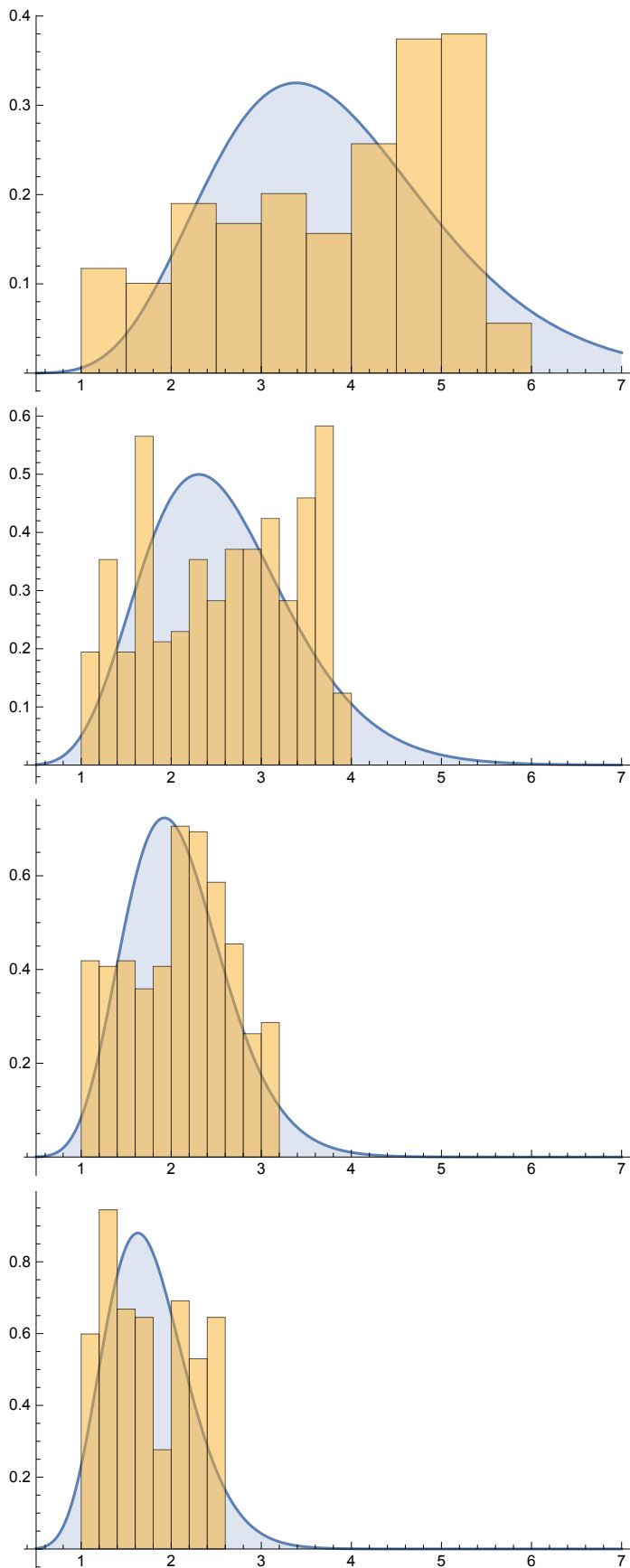
mean, variance, shape and scale of individual reproduction numbers for cluster
4 : 1.75429    0.218452    14.0879    0.124524

In[87]:= Print["number of hosts per cluster : ",
  n = Table[Length[cluster[i]], {i, nclusters}], "\n"];
number of hosts per cluster : {358, 283, 418, 217}
```

---

## Plot of reproduction numbers

```
In[88]:= Do[Print[
  Show[Plot[PDF[GammaDistribution[shape[i], scale[i]], x], {x, 0.5, 7}, Filling → Axis],
  Histogram[{cluster[i]}, 10, "PDF"], PlotRange → All]], {i, 1, nclusters}]
```



---

Probabilities of a large outbreak



Probability generating function of Z

```
In[89]:= g[s_, i_] := (1 + (mean[i] / shape[i]) (1 - s)) ^ (-shape[i])
In[90]:= Do[pl[i] = FindRoot[g[1 - q, i] == 1 - q, {q, 0.6}][[1, 2]], {i, 1, nclusters}];
In[91]:= Do[Print["cluster ", i, " : probability of a large outbreak : ", pl[i]],
  {i, 1, nclusters}]
cluster 1 : probability of a large outbreak : 0.952461
cluster 2 : probability of a large outbreak : 0.865201
cluster 3 : probability of a large outbreak : 0.786216
cluster 4 : probability of a large outbreak : 0.683707
```

## Final size in clusters

Standard final size using means of individual reproduction numbers

```
In[92]:= Do[zstandard[i] = NSolve[z == 1 - Exp[-reproductionnumbers[[i]] z], z][[2, 1, 2]],
  {i, 1, nclusters}] // Quiet
```

Final size based on individual reproduction numbers (and assumption that hosts are independent and topology unimportant). See Miller JC (2012) Bull Math Biol 74, 2125-2141

```
In[93]:= Do[zmillier[i] =
  FindRoot[z == 1 - (1 / Length[cluster[i]]) Sum[Exp[-z cluster[i][[j]]], {j,
    1, Length[cluster[i]]}], {z, 0.6}][[1, 2]], {i, 1, nclusters}]
```

Final size based on assumption of gamma distribution of reproduction numbers (and independence assumption). See Katriel (2012) J Math Biol 65, 237-262

```
In[94]:= Do[zkatriel[i] =
  FindRoot[z == 1 - (1 + (mean[i] z) / shape[i]) ^ (-shape[i]), {z, 0.6}][[1, 2]], {i,
    1, nclusters}]
```

Print calculations

```
In[95]:= Do[Print["cluster ", i, " : standard final size (fraction): ",
  zstandard[i], "\tfinal size (Miller) : ", zmillier[i],
  "\tfinal size (Katriel): ", zkatriel[i]], {i, 1, nclusters}]
cluster 1 : standard final size (fraction): 0.976039
          final size (Miller) : 0.940922    final size (Katriel): 0.952461
cluster 2 : standard final size (fraction): 0.902356
          final size (Miller) : 0.859401    final size (Katriel): 0.865201
cluster 3 : standard final size (fraction): 0.817382
          final size (Miller) : 0.783579    final size (Katriel): 0.786216
cluster 4 : standard final size (fraction): 0.714458
          final size (Miller) : 0.683046    final size (Katriel): 0.683707
```

```
In[96]:= Do[Print["cluster ", i, " : standard final size (numbers): ",
  zstandard[i] n[[i]], "\tfinal size (Miller) : ", zmillier[i] n[[i]],
  "\tfinal size (Katriel): ", zkatriel[i] n[[i]]], {i, 1, nclusters}]

cluster 1 : standard final size (numbers): 349.422
          final size (Miller) : 336.85    final size (Katriel): 340.981
cluster 2 : standard final size (numbers): 255.367
          final size (Miller) : 243.21    final size (Katriel): 244.852
cluster 3 : standard final size (numbers): 341.666
          final size (Miller) : 327.536    final size (Katriel): 328.638
cluster 4 : standard final size (numbers): 155.037
          final size (Miller) : 148.221    final size (Katriel): 148.364
```

---

## Spatial transmission kernel

```
In[97]:= h[x_] := h0 / (1 + (x / r0)^α);
rule = {h0 → 0.005, r0 → 1.9, α → 2.1, T → 7, c → 10};
```

---

## Cluster to cluster transmission

Probability of a large outbreak in  $i$  given an introduction in  $j$

```
In[99]:= p[i_, j_] :=
  If[i == j, 0, 1 - Exp[-p1[i] n[[i]] (1 - Exp[-(1 - (c / (c + T h[distance[[i, j]])) ^ c])])
    zmillier[j] n[[j]] p1[j]]] /. rule
```

Probability of a large outbreak in  $i$  given an introduction in  $j$ , conditioned on large outbreak in  $j$

```
In[100]:= pc[i_, j_] :=
  If[i == j, 0, 1 - Exp[-p1[i] n[[i]] (1 - Exp[-(1 - (c / (c + T h[distance[[i, j]])) ^ c])])
    zmillier[j] n[[j]]]] /. rule
```

(Modelled) direct and one-step cluster-to-cluster infection probabilities - notice: for 4 clusters, can be generalised. number of routes from  $j$  to  $i$  while visiting every intermediate at most once can be very large. for instance, if all hosts are visited, the number of combinations is  $\prod_{k=0}^{n-1} n-2-k$ . if  $l$  hosts are visited, the number of combination is  $\prod_{k=0}^{l-1} n-2-k$  (with appropriate range for  $l$ )

```
In[101]:= allclusters = Table[i, {i, nclusters}];
r[i_, j_] := Block[{comp = Complement[allclusters, {i, j}]},
  1 - (1 - p[i, j]) Product[(1 - pc[i, k] * p[k, j]), {k, comp}]
  (1 - pc[i, comp[[1]]] * pc[comp[[1]], comp[[2]]] * p[comp[[2]], j])
  (1 - pc[i, comp[[2]]] * pc[comp[[2]], comp[[1]]] * p[comp[[1]], j])]
```

## Overall result

```
In[103]:= Do[If[i ≠ j, Print["probability of large outbreak in ", i, " given introduction in ",
    j, " : r(", i, ", ", j, ") = ", r[i, j]]], {i, 1, nclusters}, {j, 1, nclusters}]
probability of large outbreak in 1 given introduction in 2 : r(1, 2) = 0.563281
probability of large outbreak in 1 given introduction in 3 : r(1, 3) = 0.412684
probability of large outbreak in 1 given introduction in 4 : r(1, 4) = 0.372733
probability of large outbreak in 2 given introduction in 1 : r(2, 1) = 0.595186
probability of large outbreak in 2 given introduction in 3 : r(2, 3) = 0.395299
probability of large outbreak in 2 given introduction in 4 : r(2, 4) = 0.402723
probability of large outbreak in 3 given introduction in 1 : r(3, 1) = 0.469786
probability of large outbreak in 3 given introduction in 2 : r(3, 2) = 0.424235
probability of large outbreak in 3 given introduction in 4 : r(3, 4) = 0.387547
probability of large outbreak in 4 given introduction in 1 : r(4, 1) = 0.466901
probability of large outbreak in 4 given introduction in 2 : r(4, 2) = 0.475569
probability of large outbreak in 4 given introduction in 3 : r(4, 3) = 0.427852
```

## Comparison with simulations

Observed probabilities of large outbreak in  $i$  given introduction in  $j$  (with operational threshold of 10 infected hosts)

```
In[104]:= q[i_, j_] := Which[i == 1 && j == 2, 0.551,
    i == 1 && j == 3, 0.44,
    i == 1 && j == 4, 0.359,
    i == 2 && j == 1, 0.601,
    i == 2 && j == 3, 0.395,
    i == 2 && j == 4, 0.35,
    i == 3 && j == 1, 0.556,
    i == 3 && j == 2, 0.491,
    i == 3 && j == 4, 0.387,
    i == 4 && j == 1, 0.539,
    i == 4 && j == 2, 0.544,
    i == 4 && j == 3, 0.447]
```

Absolute error (approximation - simulation) and relative error

```
In[105]:= abserror[i_, j_] := Evaluate[If[i == j, 0, (r[i, j] - q[i, j])]]
Print["mean absolute error : ",
    Sum[Abs[abserror[i, j]], {i, 1, nclusters}, {j, 1, nclusters}] /
    (nclusters * (nclusters - 1))]
relerror[i_, j_] := Evaluate[If[i == j, 0, (r[i, j] - q[i, j]) / q[i, j]]]
Print["mean relative error : ",
    Sum[Abs[relerror[i, j]], {i, 1, nclusters}, {j, 1, nclusters}] /
    (nclusters * (nclusters - 1))]
mean absolute error : 0.0354474
mean relative error : 0.0732112
```

# Simulation and approximation for avian influenza in poultry in the Netherlands

## Poultry farms in high-density areas in the Netherlands

```
In[109]:= distance = {{0, 88.62}, {88.62, 0}};
```

```
In[110]:= allreproductionnumbers = {{2.519411724, 1}, {1.675181836, 1},
  {1.674327066, 1}, {1.591636301, 1}, {1.506983895, 1}, {2.103285498, 1},
  {1.253559036, 1}, {1.808613619, 1}, {1.481922273, 1}, {1.754203231, 1},
  {1.840495073, 1}, {1.71648653, 1}, {1.442648714, 1}, {1.7727936, 1},
  {2.421988834, 1}, {1.851934033, 1}, {2.014545951, 1}, {2.016369511, 1},
  {1.878728439, 1}, {1.331577808, 1}, {1.127154927, 1}, {1.889064475, 1},
  {1.10832657, 1}, {1.130090969, 1}, {1.135872145, 1}, {2.513951694, 1},
  {1.152233232, 1}, {2.292004411, 1}, {1.754905083, 1}, {2.426070523, 1},
  {2.294835701, 1}, {1.227115273, 1}, {1.271006612, 1}, {2.115576647, 1},
  {2.289731681, 1}, {1.56088241, 1}, {1.773125927, 1}, {1.488160538, 1},
  {2.471904049, 1}, {1.846155388, 1}, {1.896504511, 1}, {1.457424252, 1},
  {1.034373883, 1}, {1.032441243, 1}, {1.367251413, 1}, {1.215054825, 1},
  {1.090543274, 1}, {1.001257086, 1}, {2.205100765, 1}, {1.70345806, 1},
  {1.540820911, 1}, {1.442600465, 1}, {1.59808322, 1}, {1.881590328, 1},
  {2.104295593, 1}, {1.016221006, 1}, {1.821122108, 1}, {1.307592545, 1},
  {1.338955842, 1}, {1.944157555, 1}, {1.032819487, 1}, {1.621657008, 1},
  {1.519776531, 1}, {1.082059271, 1}, {1.982845234, 1}, {1.074664155, 1},
  {1.590420474, 1}, {1.114941276, 1}, {2.113556158, 1}, {1.629205755, 1},
  {1.050110517, 1}, {2.058425754, 1}, {2.468162092, 1}, {2.379806973, 1},
  {1.657674379, 1}, {1.315435048, 1}, {1.414996745, 1}, {2.149427677, 1},
  {1.574324239, 1}, {1.77480352, 1}, {2.420875677, 1}, {2.463819696, 1},
  {1.438949981, 1}, {1.44597268, 1}, {1.201348742, 1}, {1.054389102, 1},
  {2.066336389, 1}, {1.056213798, 1}, {1.030095341, 1}, {1.650892658, 1},
  {2.0297726, 1}, {1.694016687, 1}, {2.418375787, 1}, {1.595920521, 1},
  {1.5279701, 1}, {2.111373315, 1}, {2.457543105, 1}, {1.39964175, 1},
  {1.118917522, 1}, {2.425847104, 1}, {1.302873469, 1}, {1.63594634, 1},
  {1.667845129, 1}, {1.686330256, 1}, {1.154978276, 1}, {1.315073759, 1},
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  {1.671987381, 1}, {1.643594199, 1}, {2.108805597, 1}, {1.552265949, 1},
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  {2.132579441, 1}, {2.004168765, 1}, {2.011134596, 1}, {1.936805203, 1},
  {2.115199528, 1}, {1.578727638, 1}, {1.945325533, 1}, {2.446566711, 1},
```

```

{1.570158358`, 1}, {1.497815854`, 1}, {1.746089775`, 1}, {1.810521638`, 1},
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{1.111298572`, 2}, {1.063122447`, 2}, {1.394757139`, 2}, {1.541741457`, 2},
{1.326702197`, 2}, {1.076426839`, 2}, {1.554843899`, 2}, {1.221516995`, 2},
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{1.042219655`, 2}, {1.164329828`, 2}, {1.251269703`, 2}, {1.467563142`, 2},
{1.128746631`, 2}, {1.185256673`, 2}, {1.099793878`, 2}, {1.094082012`, 2},
{1.44873016`, 2}, {1.092917605`, 2}, {1.237594335`, 2}, {1.239611188`, 2}};

```

## Reproduction numbers in high-density areas

```

In[111]:= Print["number of clusters : ", nclusters = Length[distance], "\n"];
          number of clusters : 2

In[112]:= Do[cluster[i] = Select[allreproductionnumbers, #[[2]] == i &][[All, 1]],
             {i, 1, nclusters}];
Do[Print["mean, variance, shape and scale of individual reproduction
        numbers for cluster ", i, " : ", mean[i] = Mean[cluster[i]], "\t",
        var[i] = Variance[cluster[i]], "\t", shape[i] = mean[i]^2/var[i],
        "\t", scale[i] = var[i]/mean[i]], {i, 1, nclusters}];
reproductionnumbers = Table[mean[i], {i, 1, nclusters}];

mean, variance, shape and scale of individual reproduction numbers for cluster
1 : 1.71207    0.174687    16.7797    0.102033

mean, variance, shape and scale of individual reproduction numbers for cluster
2 : 1.24531    0.0273038    56.7983    0.0219252

In[115]:= Print["number of hosts per cluster : ",
               n = Table[Length[cluster[i]], {i, nclusters}], "\n"];
          number of hosts per cluster : {303, 67}

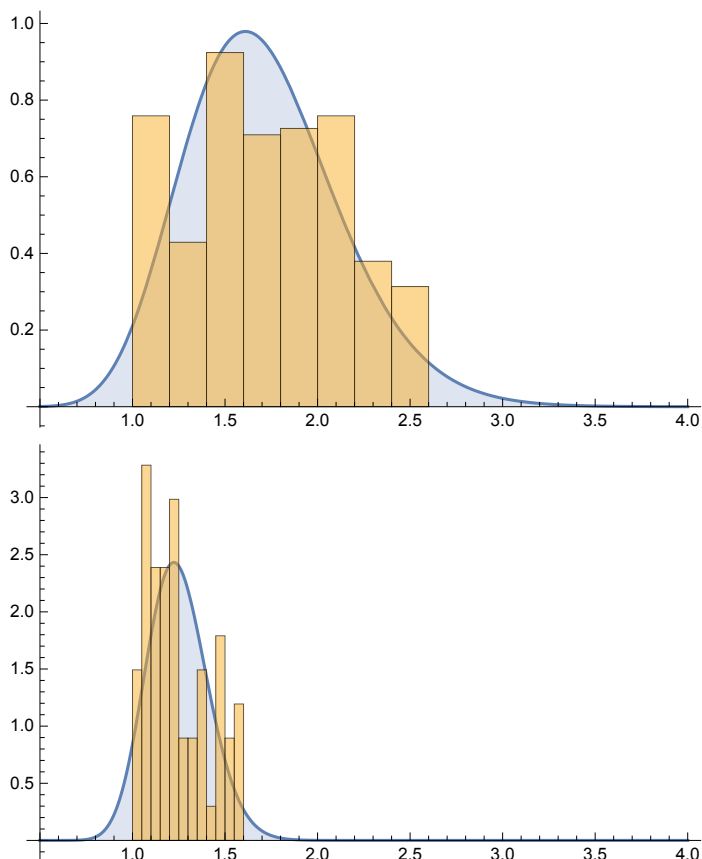
```

## Plot of reproduction numbers

```

In[116]:= Do[Print[Show[Plot[PDF[GammaDistribution[shape[i], scale[i]], x],
                             {x, 0.5, 4}, Filling -> Axis, PlotRange -> All],
                Histogram[{cluster[i]}, 10, "PDF", PlotRange -> All], {i, 1, nclusters}]]

```



## Probabilities of a large outbreak in high-density areas

```
In[117]:= g[s_, i_] := (1 + (mean[i] / shape[i]) (1 - s)) ^ (-shape[i]) (* PGF of Z *)
Do[pl[i] = FindRoot[g[1 - q, i] == 1 - q, {q, 0.6}][[1, 2]], {i, 1, nclusters}];
Do[Print["cluster ", i, " : probability of a large outbreak : ", pl[i]],
  {i, 1, nclusters}]

cluster 1 : probability of a large outbreak : 0.670642
cluster 2 : probability of a large outbreak : 0.360811
```

## Final size in high-density areas

Standard final size using means of individual reproduction numbers

```
In[120]:= Do[zstandard[i] = NSolve[z == 1 - Exp[-reproductionnumbers[[i]] z], z][[2, 1, 2]],
  {i, 1, nclusters}] // Quiet
```

Final size based on individual reproduction numbers (and assumption that hosts are independent).

See Miller JC (2012) Bull Math Biol 74, 2125-2141

```
In[121]:= Do[zmilller[i] =
  FindRoot[z == 1 - (1 / Length[cluster[i]]) Sum[Exp[-z cluster[i][[j]]], {j,
    1, Length[cluster[i]]}], {z, 0.6}][[1, 2]], {i, 1, nclusters}]
```

Final size based on assumption of gamma distribution of reproduction numbers (and independence assumption). See Katriel (2012) J Math Biol 65, 237-262

```
In[122]:= Do[zkatriel[i] =
  FindRoot[z == 1 - (1 + (mean[i] z) / shape[i]) ^ (-shape[i]), {z, 0.6}][[1, 2]], {i,
    1, nclusters}]
```

Print calculations

```
In[123]:= Do[Print["cluster ", i, " : standard final size : ",
  zstandard[i], "\tfinal size (Miller) : ", zmilller[i],
  "\tfinal size (Katriel): ", zkatriel[i]], {i, 1, nclusters}]

cluster 1 : standard final size : 0.696554
          final size (Miller) : 0.669838    final size (Katriel): 0.670642
cluster 2 : standard final size : 0.366237
          final size (Miller) : 0.360925    final size (Katriel): 0.360811
```

## Spatial transmission kernel

```
In[124]:= hh[x_] := h0 / (1 + (x / r0) ^ α);
rule = {h0 → 0.008, r0 → 1.9, α → 2.1, T → 7, c → 10};
(* notice increased height *)
```

## Transmission between high-density areas

Probability of a large outbreak in  $i$  given an introduction in  $j$

```

In[126]:= p[i_, j_] :=
  If[i == j, 0, 1 - Exp[-pl[i] n[[i]] (1 - Exp[-(1 - (c / (c + Th[distance[[i, j]])) ^ c])]]
    zmiller[j] n[[j]] pl[j]]] /. rule

Probability of a large outbreak in i given an introduction in j, conditioned on large outbreak in j

In[127]:= pc[i_, j_] :=
  If[i == j, 0, 1 - Exp[-pl[i] n[[i]] (1 - Exp[-(1 - (c / (c + Th[distance[[i, j]])) ^ c])]]
    zmiller[j] n[[j]]]] /. rule

In[128]:= allclusters = Table[i, {i, nclusters}];
r[i_, j_] :=
  1 - (1 - p[i, j]) Product[(1 - p[i, k] * p[k, j]), {k, Complement[allclusters, {i, j}]}]

```

---

## Overall result

```

In[130]:= Do[If[i != j, Print["probability of large outbreak in i given introduction in j : r(",
  i, ", ", j, ") = ", r[i, j]]], {i, 1, nclusters}, {j, 1, nclusters}]

probability of large outbreak in i given introduction in j : r(1, 2) = 0.0305904
probability of large outbreak in i given introduction in j : r(2, 1) = 0.0560282

```

---

## Comparison with simulations

Observed probabilities of large outbreak in i given introduction in j (with operational threshold of 10 infected hosts)

```

In[131]:= q[i_, j_] := Which[i == 1 && j == 2, 0.075,
  i == 2 && j == 1, 0.076]

Absolute error (approximation - simulation) and relative error

In[132]:= abserror[i_, j_] := Evaluate[If[i == j, 0, (r[i, j] - q[i, j])]]
Print["mean absolute error : ",
  Sum[Abs[abserror[i, j]], {i, 1, nclusters}, {j, 1, nclusters}] /
  (nclusters * (nclusters - 1))]
relerror[i_, j_] := Evaluate[If[i == j, 0, (r[i, j] - q[i, j]) / q[i, j]]]
Print["mean relative error : ",
  Sum[Abs[relerror[i, j]], {i, 1, nclusters}, {j, 1, nclusters}] /
  (nclusters * (nclusters - 1))]

mean absolute error : 0.0321907
mean relative error : 0.427457

```