https://nataliaciria.com/mcmodule/
Available on CRAN!

mcmodule::

An R Package for Multi-Pathway Monte Carlo Risk Assessment

R!sk conference 2026 – 19th February

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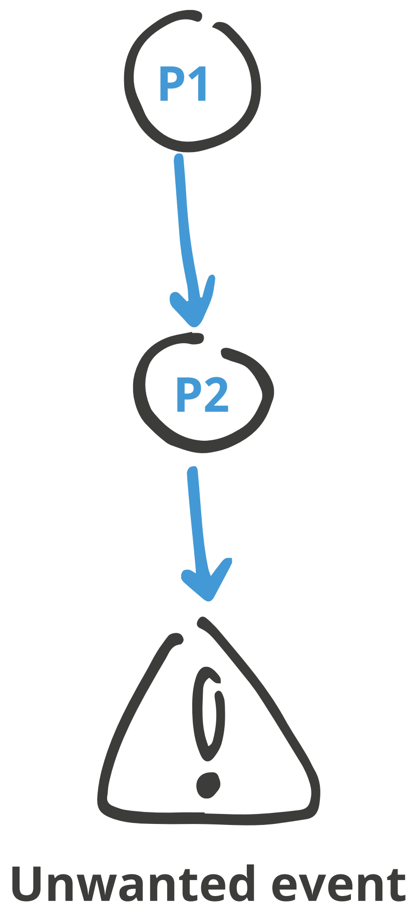
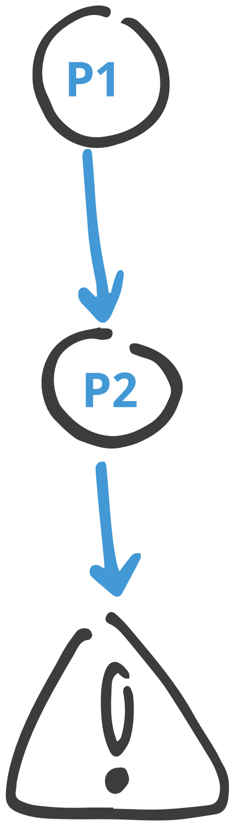
Quantifying risk through probability steps is **neat**



With mc2d
Quantifying risk through **stochastic** probability steps is **neat**



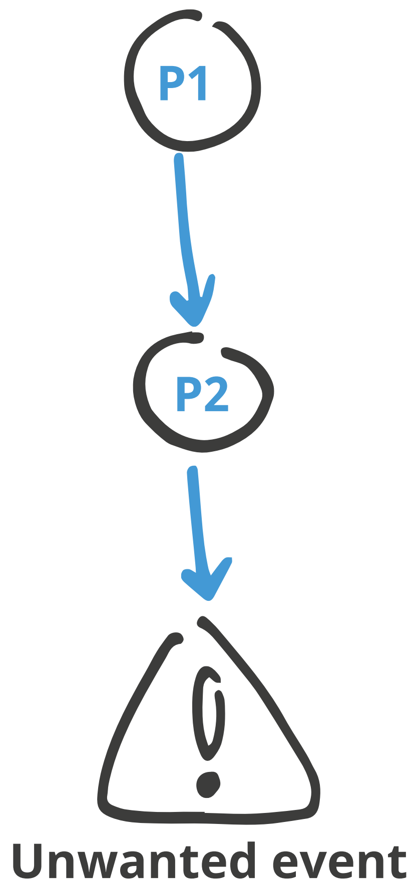
Unwanted event

```r
library(mc2d)
# Probability an animal is infected
inf_animal <- mcstoc(runif, min = 0.002, max = 0.08)


# Probability an infected animal is tested
test_animal <- mcstoc(rpert, min = 0.4, mode = 0.5, max = 0,6)
test_inf_animal <- inf_animal * test_animal


# Probability an animal infected animal is not detected
test_se <- mcstoc(runif, min = 0.8, max = 0.95)
not_detected <- test_inf_animal * (1 - test_se)
```

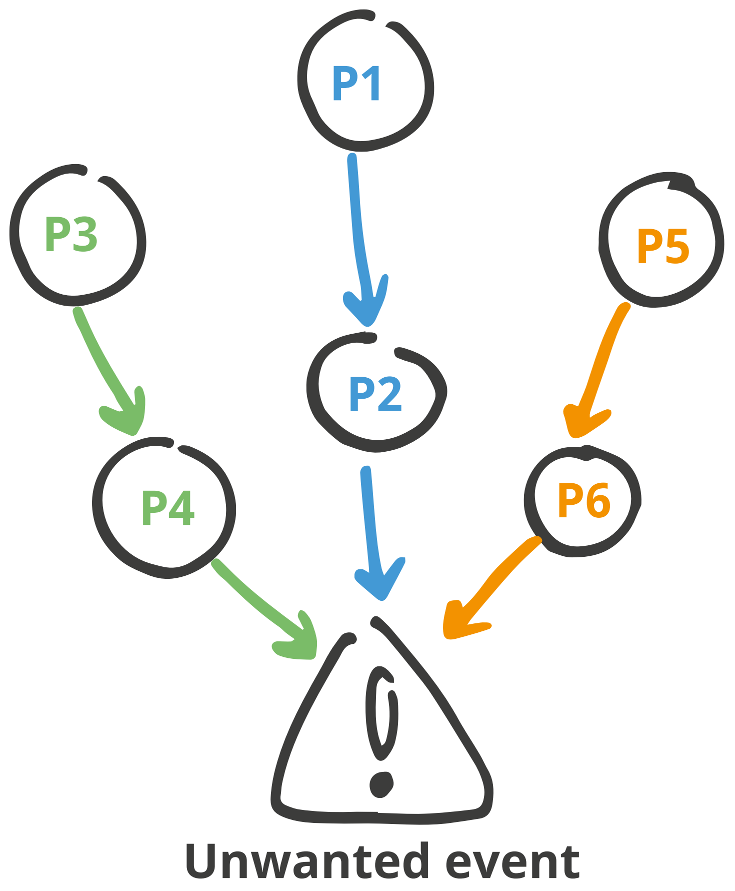
With `mc2d`
Quantifying risk through **stochastic** probability steps is **neat**



Thanks to `mc2d`

Quantifying risk through stochastic probability steps is **neat**

But real-life risk pathways are **messy**

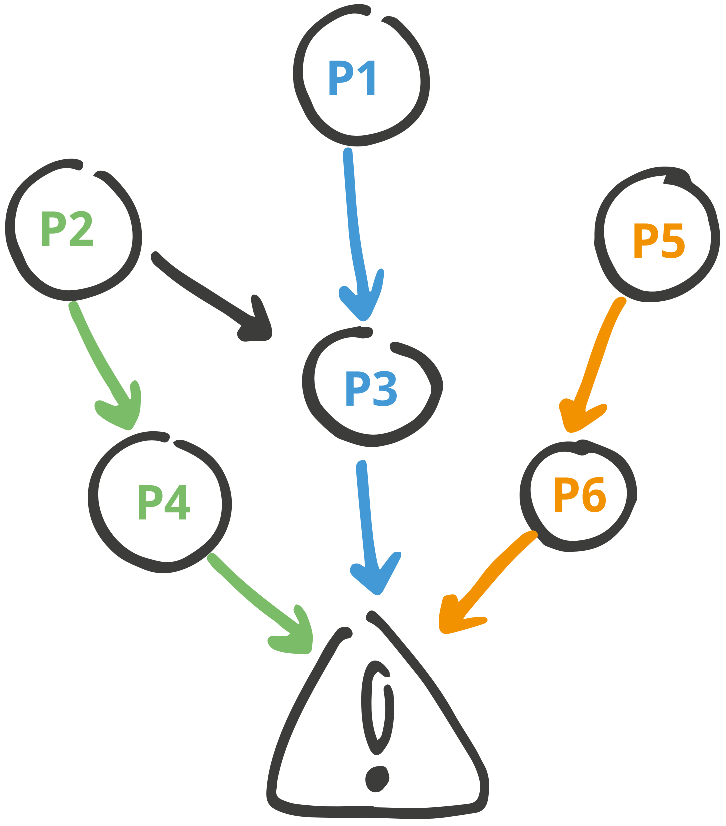


Thanks to `mc2d`

Quantifying risk through stochastic probability steps is **neat**

But real-life risk pathways are **messy**

interconnected



Unwanted event

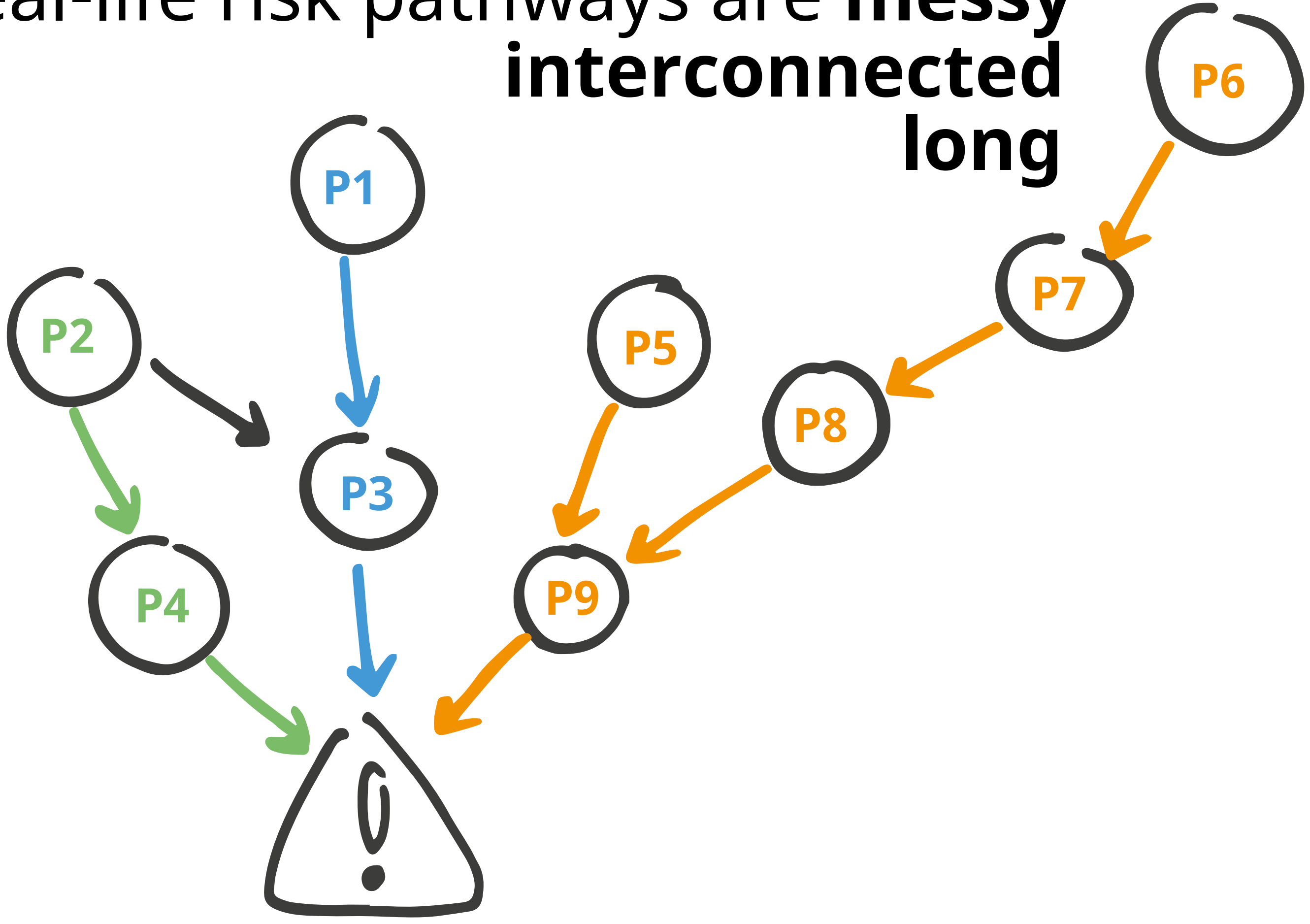
Thanks to `mc2d`

Quantifying risk through stochastic probability steps is **neat**

But real-life risk pathways are **messy**

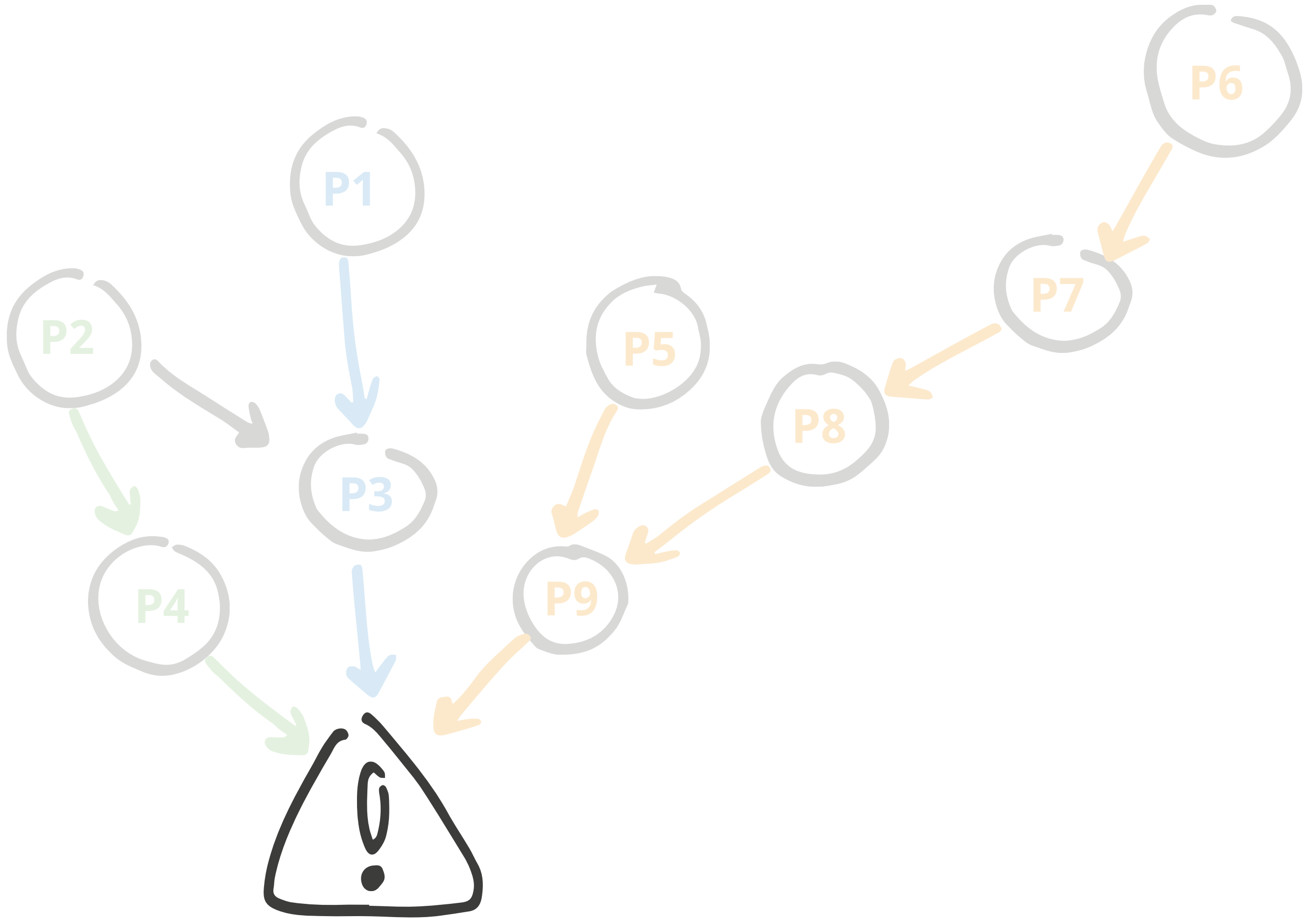
interconnected

long



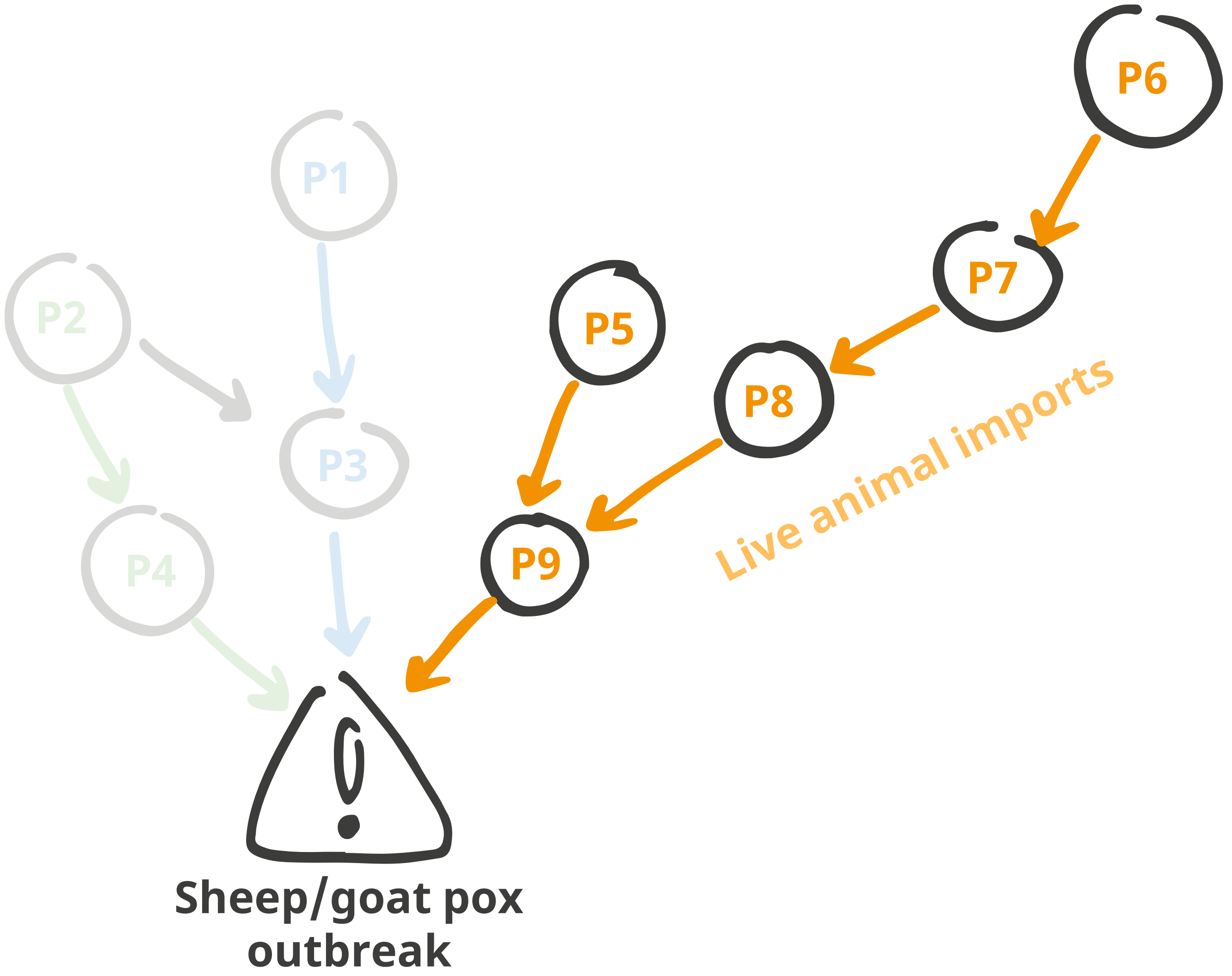
Unwanted event

For example

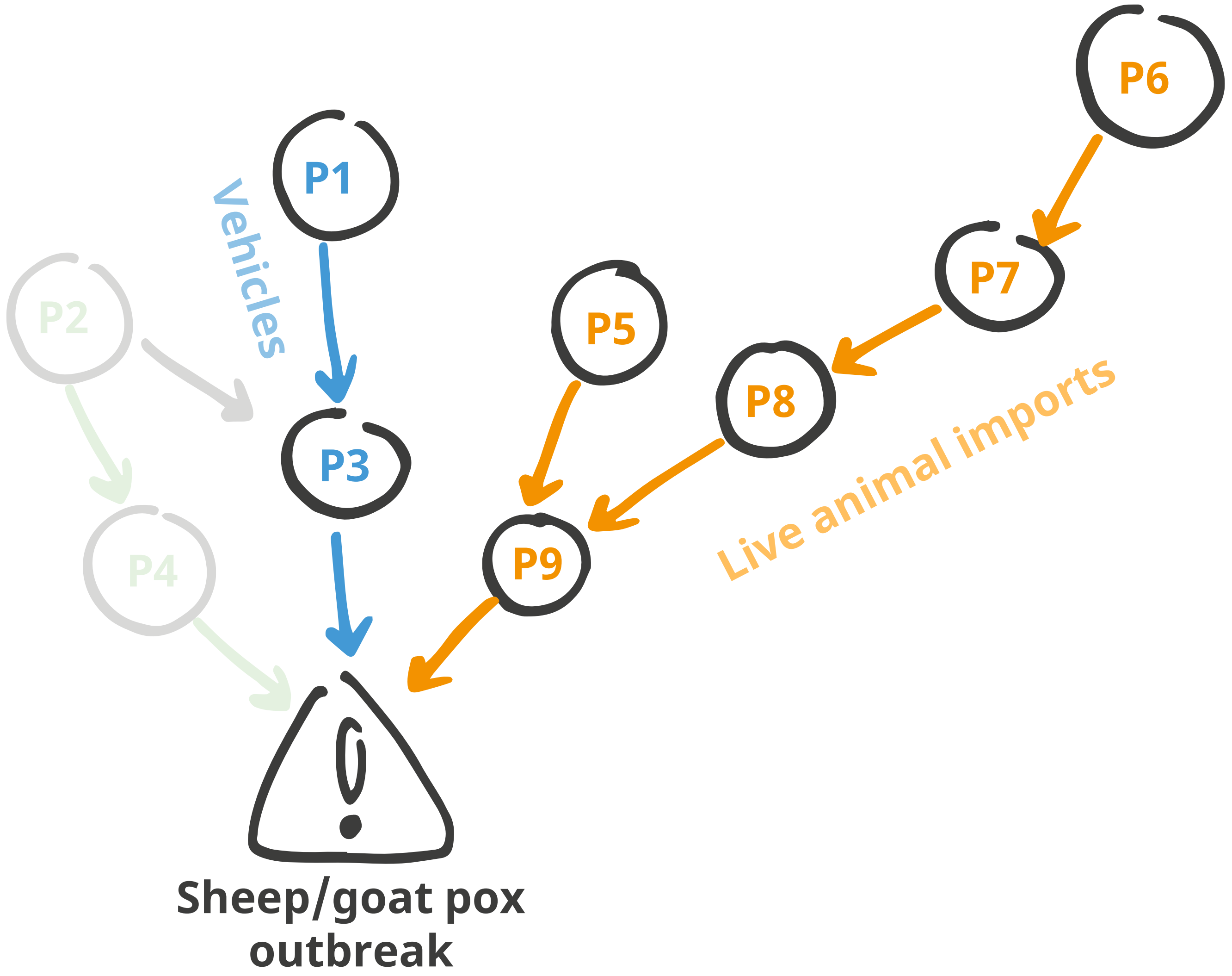


Sheep/goat pox outbreak

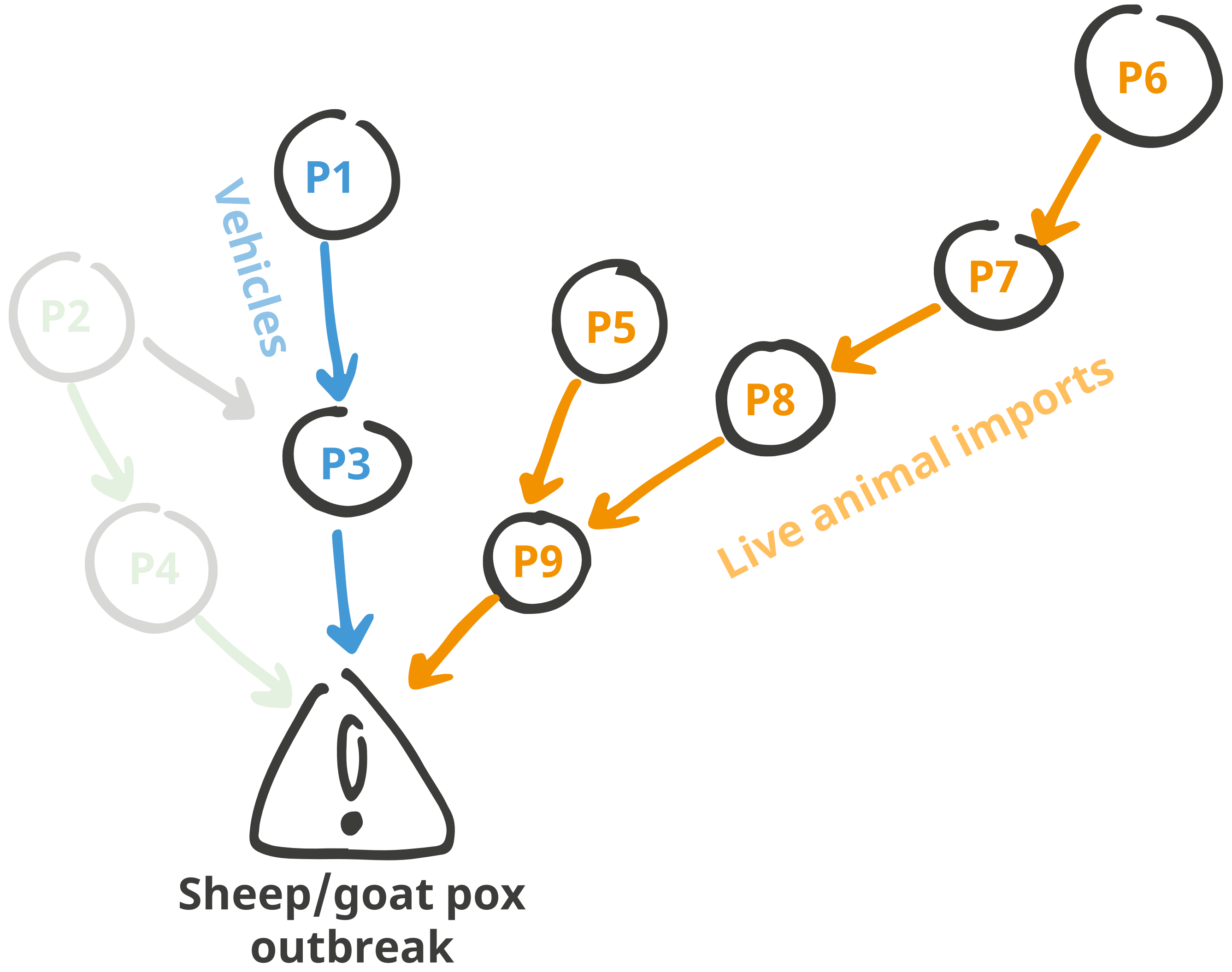
For example


P6
P1
P7
P5
P2
P8
P3
Live animal imports
P9
P4
Sheep/goat pox outbreak

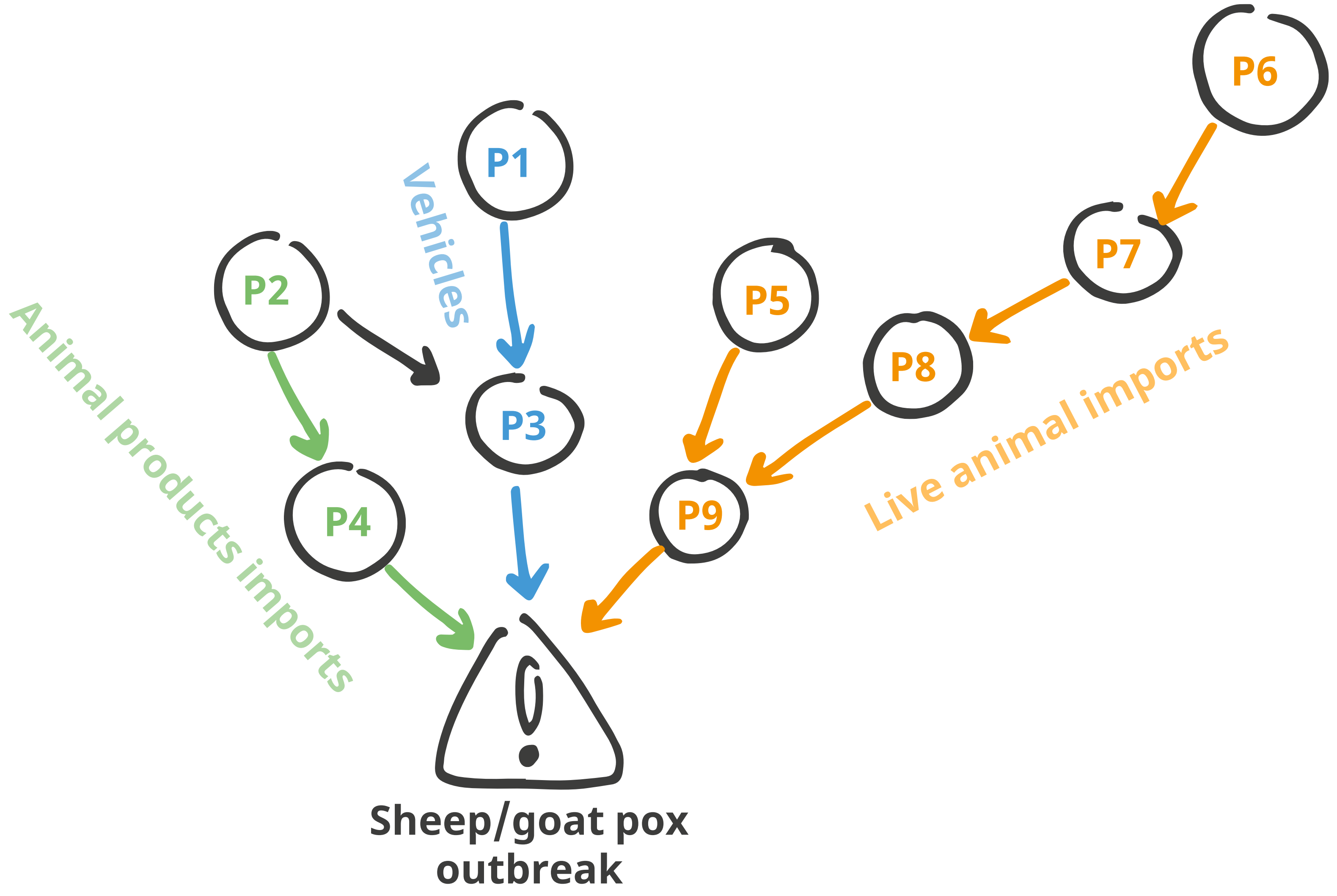
For example


P1
P2
P3
P4
P5
P6
P7
P8
P9
Vehicles
Live animal imports
Sheep/goat pox outbreak

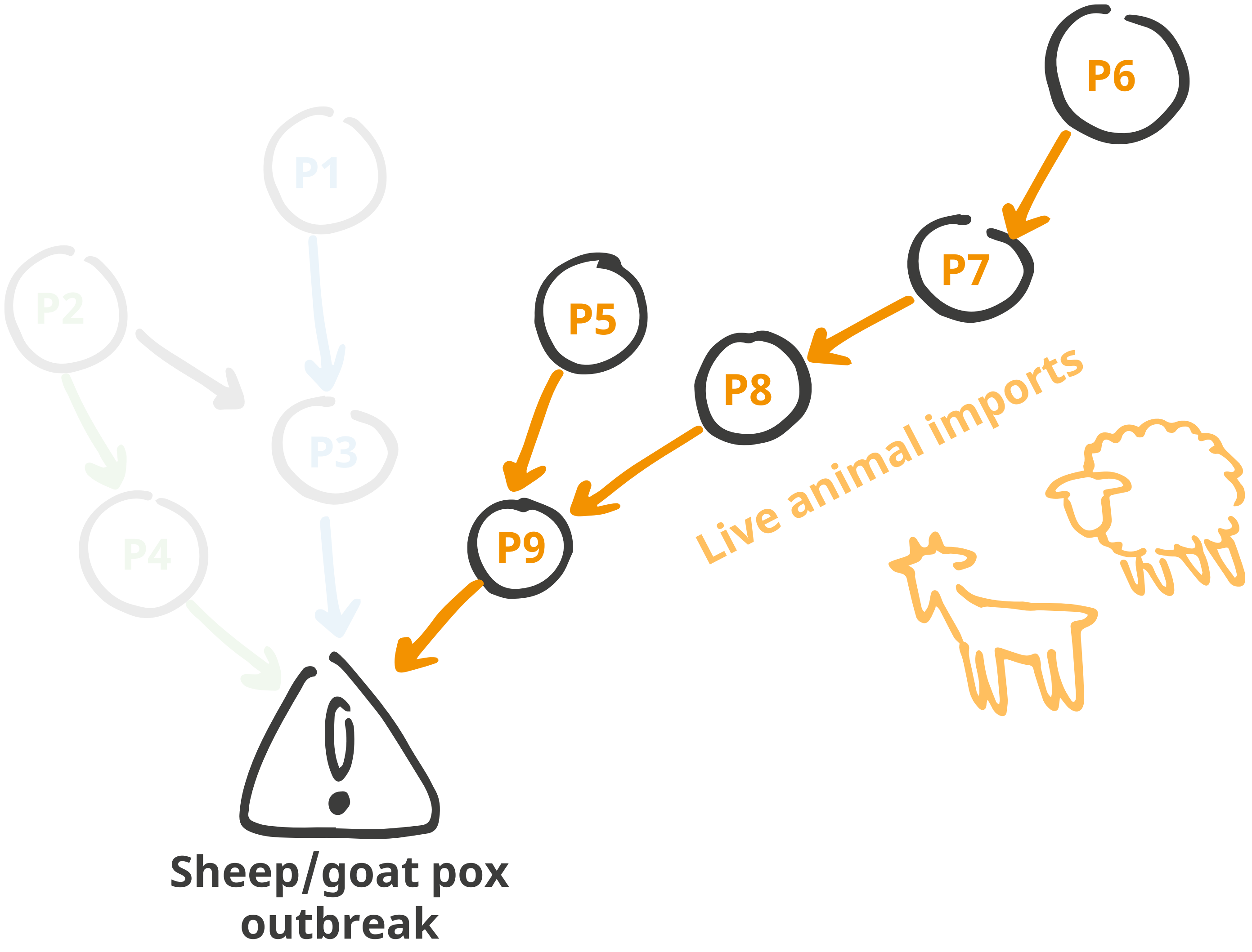
For example


P1
Vehicles
P2
P3
P4
P5
P6
P7
P8
P9
Live animal imports
Sheep/goat pox outbreak

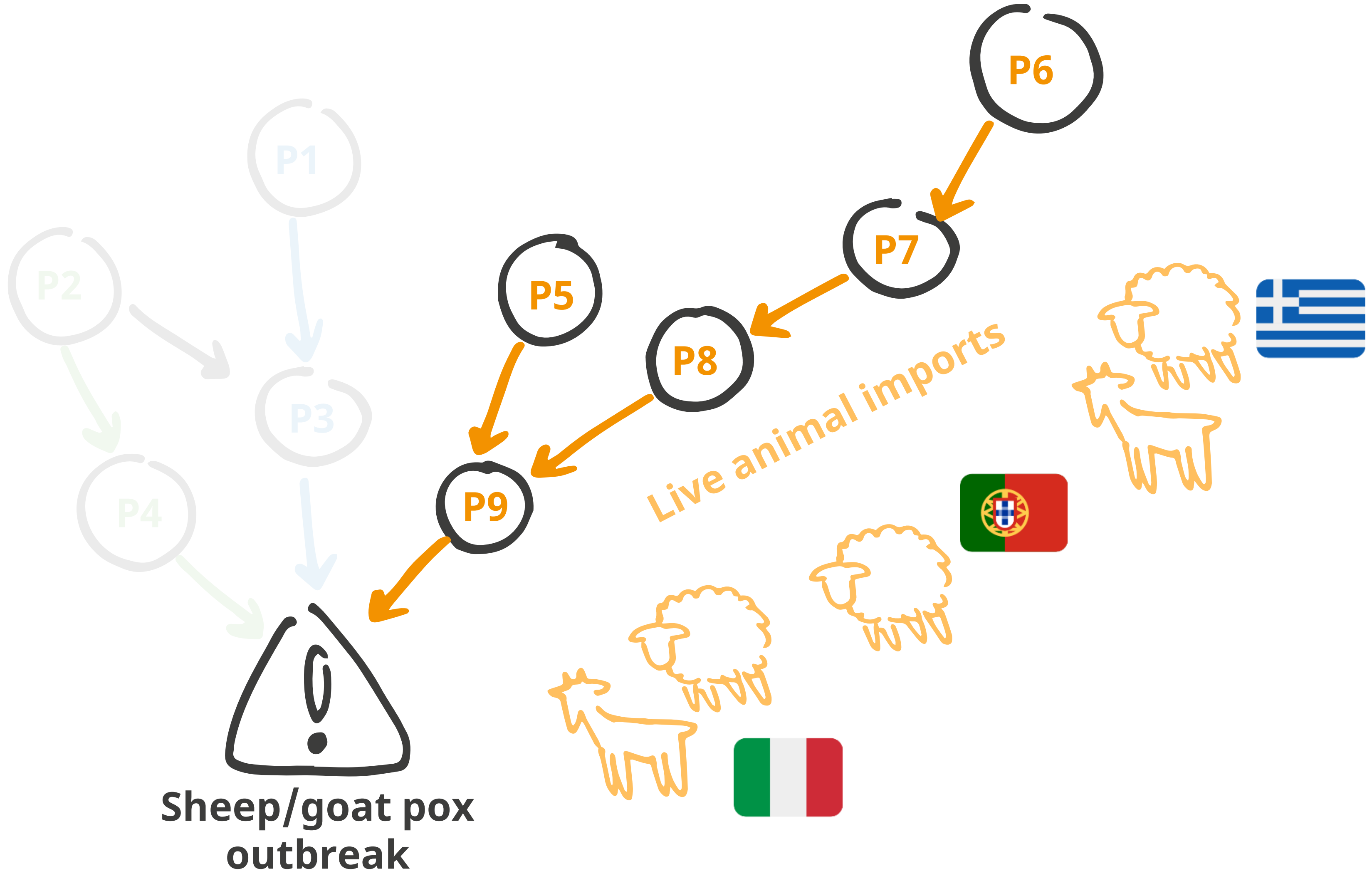
For example


P1
P2
P3
P4
P5
P6
P7
P8
P9
Vehicles
Animal products imports
Live animal imports
Sheep/goat pox outbreak

For example


P1
P2
P3
P4
P5
P6
P7
P8
P9
Live animal imports
Sheep/goat pox outbreak

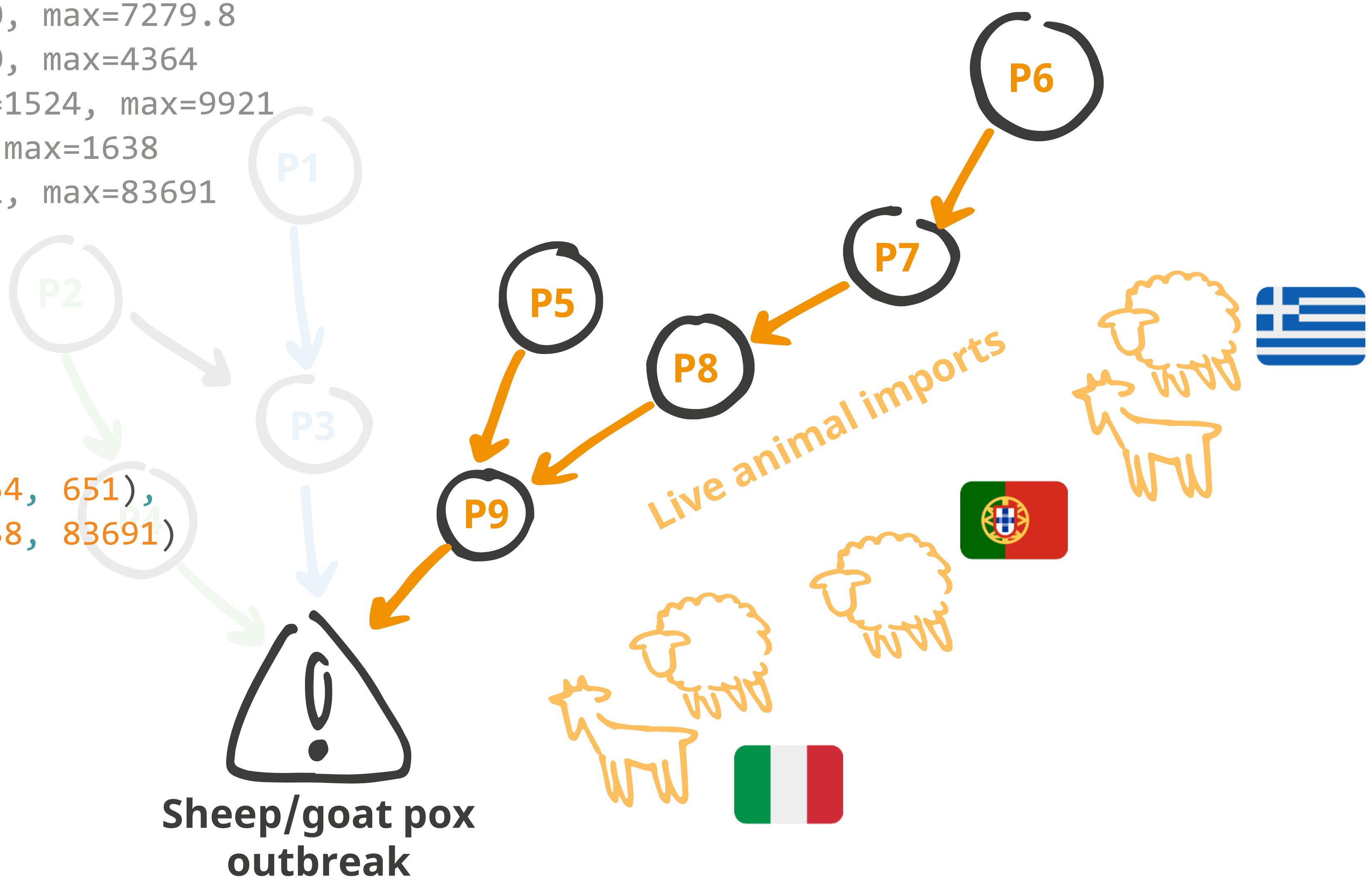
For example


P1
P2
P3
P4
P5
P6
P7
P8
P9
Live animal imports
Sheep/goat pox outbreak

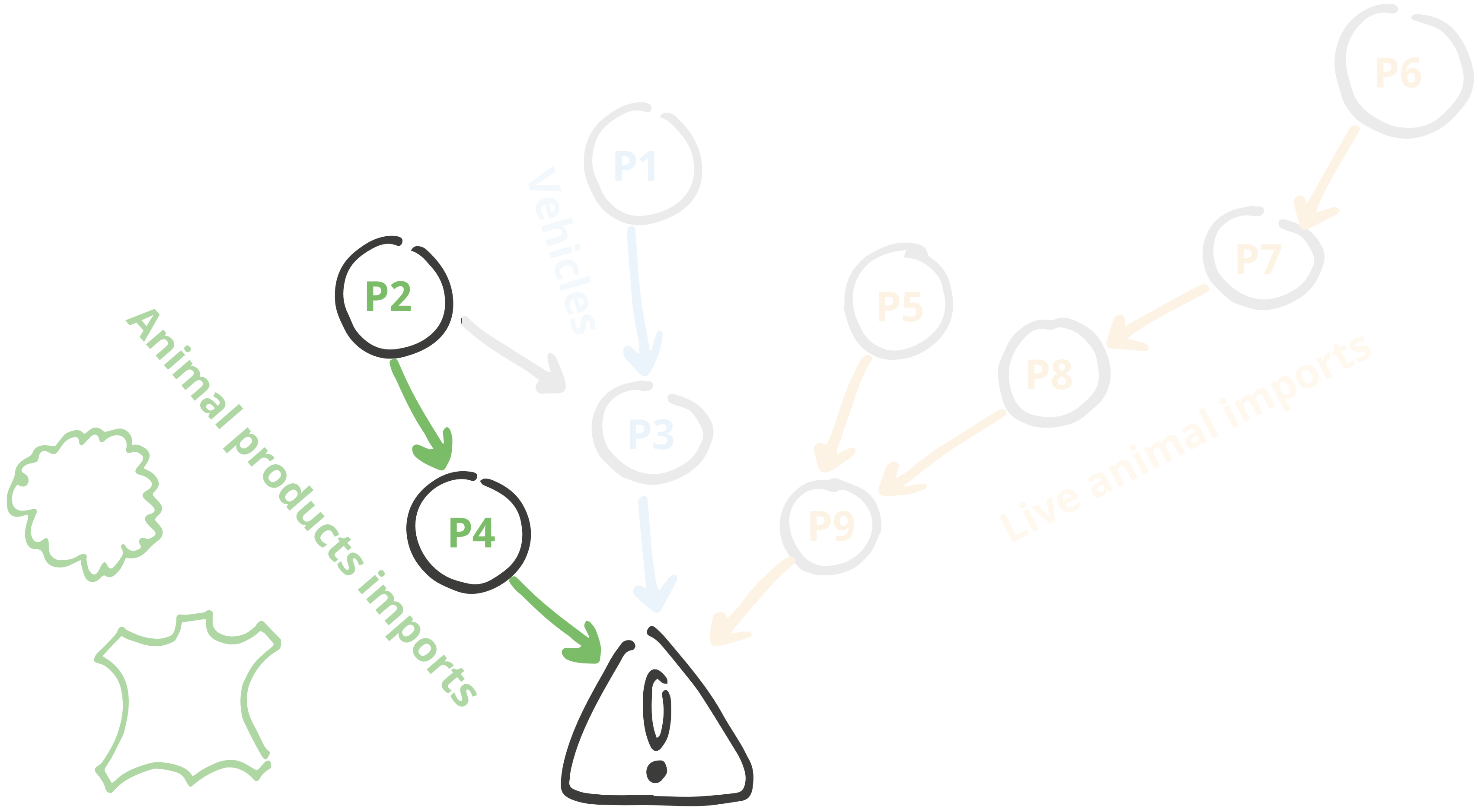
For example

```
# GRC - sheep: min=1, mode=1250, max=7279.8
# GRC - goat: min=74, mode=1650, max=4364
# ITA - sheep: min=10.38, mode=1524, max=9921
# ITA - goat: min=6, mode=154, max=1638
# PRT - sheep: min=49, mode=651, max=83691


animal_import_qty <- mcstoc(
  rpert,
  nvariates = 5,
  min = c(1, 74, 10.38, 6, 49),
  mode = c(1250, 1650, 1524, 154, 651),
  max = c(7279, 4364, 9921, 1638, 83691)
)
```

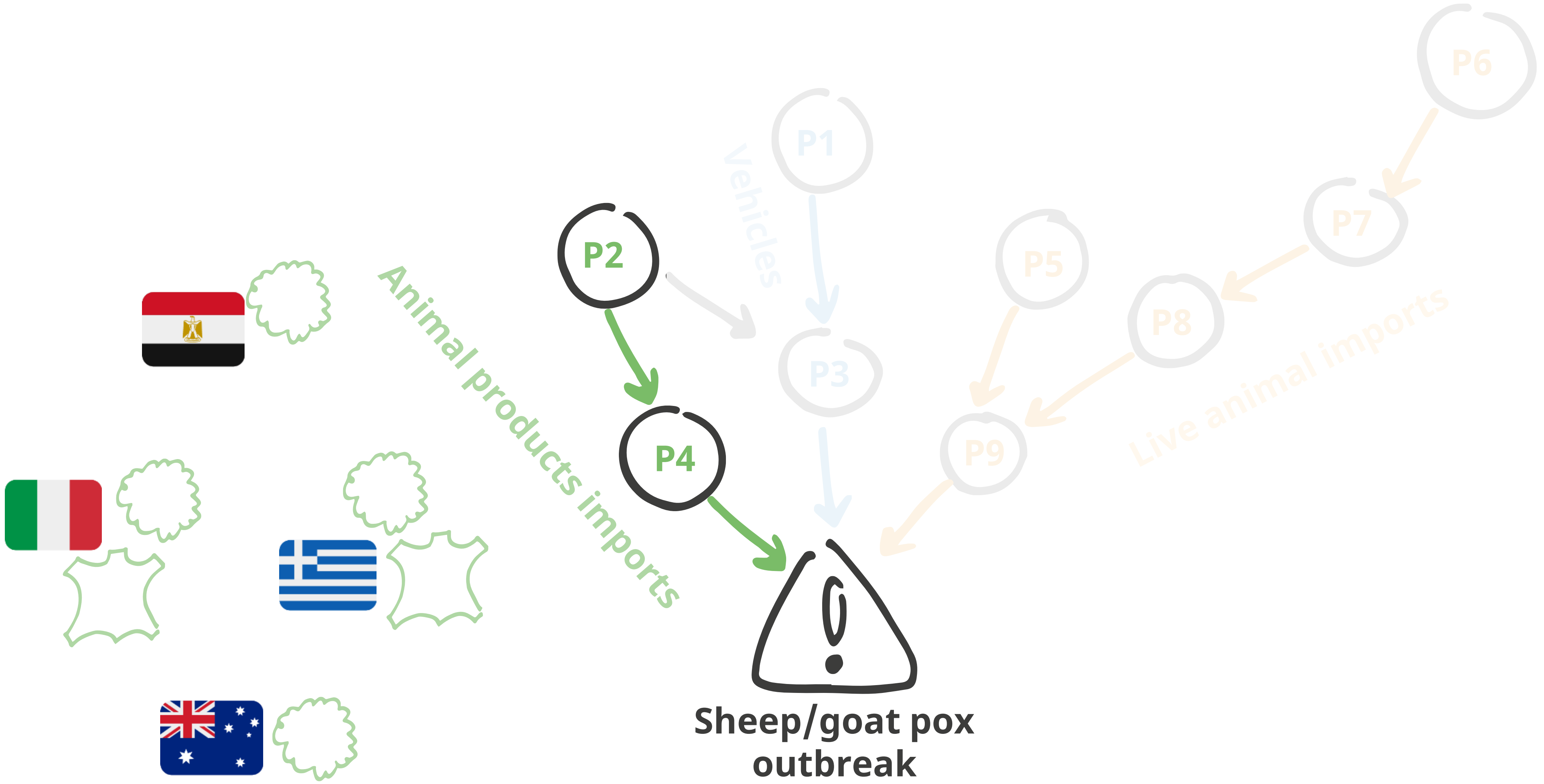


For example



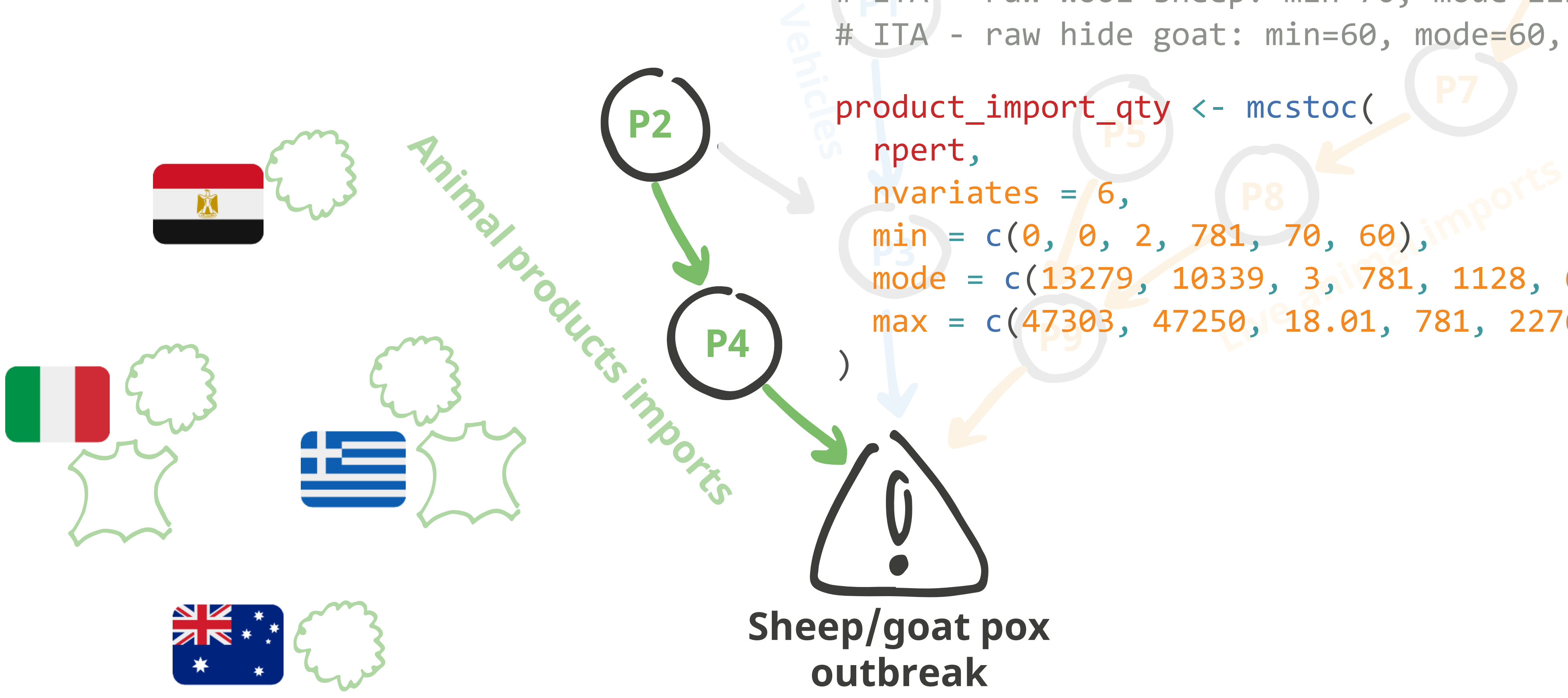
Sheep/goat pox outbreak

For example



P1
P2
P3
P4
P5
P6
P7
P8
P9
Vehicles
Animal products imports
Live animal imports
Sheep/goat pox outbreak

For example



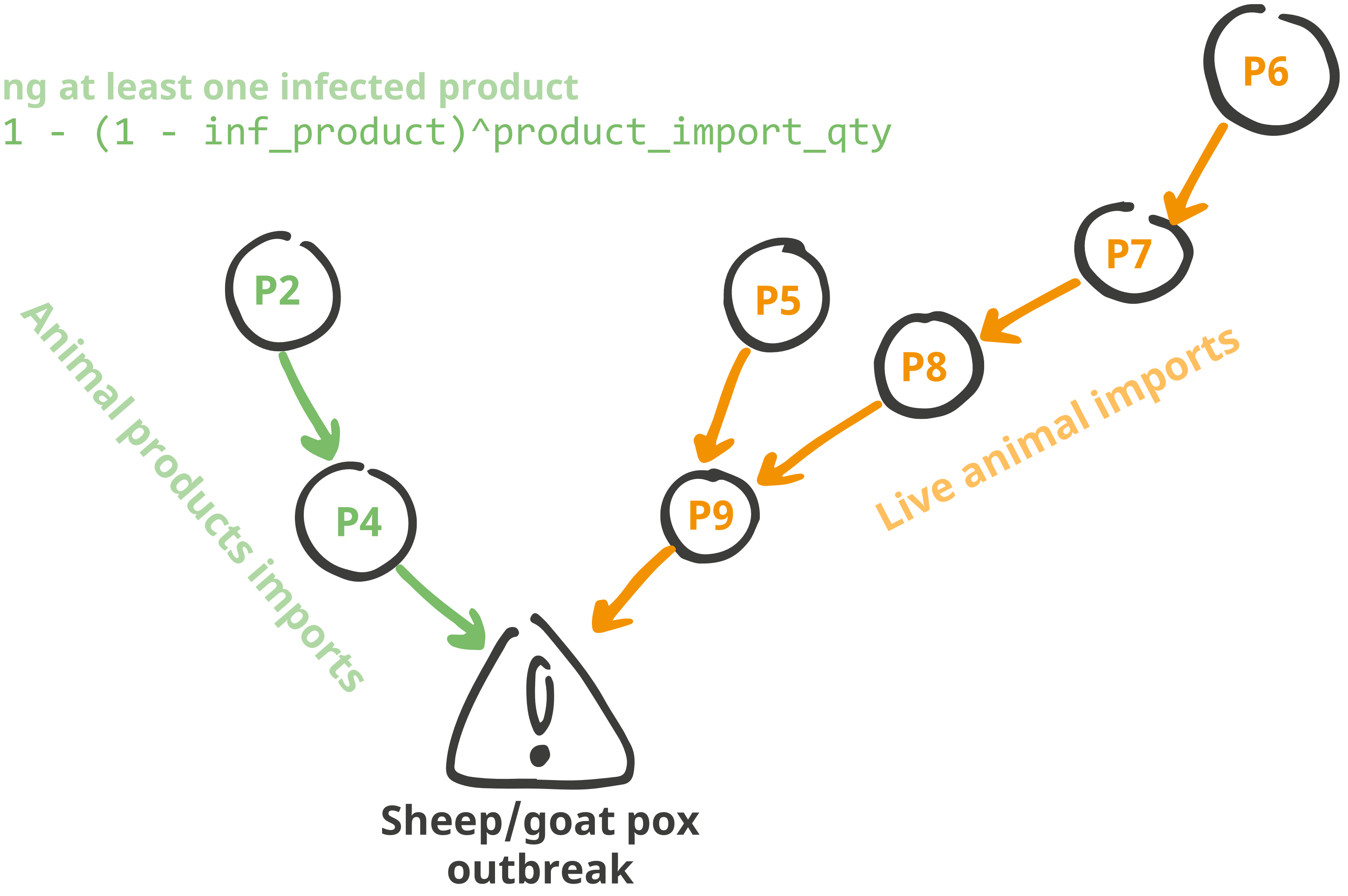
```
# AUS - raw wool sheep: min=0.5, mode=13279, max=47303
# BGR - raw wool sheep: min=0, mode=10339.59, max=47250
# GRC - raw wool sheep: min=1.46, mode=3, max=18.01
# GRC - raw hide goat: min=781.8, mode=781.8, max=781.8
# ITA - raw wool sheep: min=70, mode=1128, max=22768
# ITA - raw hide goat: min=60, mode=60, max=60

product_import_qty <- mcstoc(
  rpert,
  nvariates = 6,
  min = c(0, 0, 2, 781, 70, 60),
  mode = c(13279, 10339, 3, 781, 1128, 60),
  max = c(47303, 47250, 18.01, 781, 22768, 60)
)
```

For example

Probability of introducing at least one infected product

```
inf_product_all <- 1 - (1 - inf_product)^product_import_qty
```



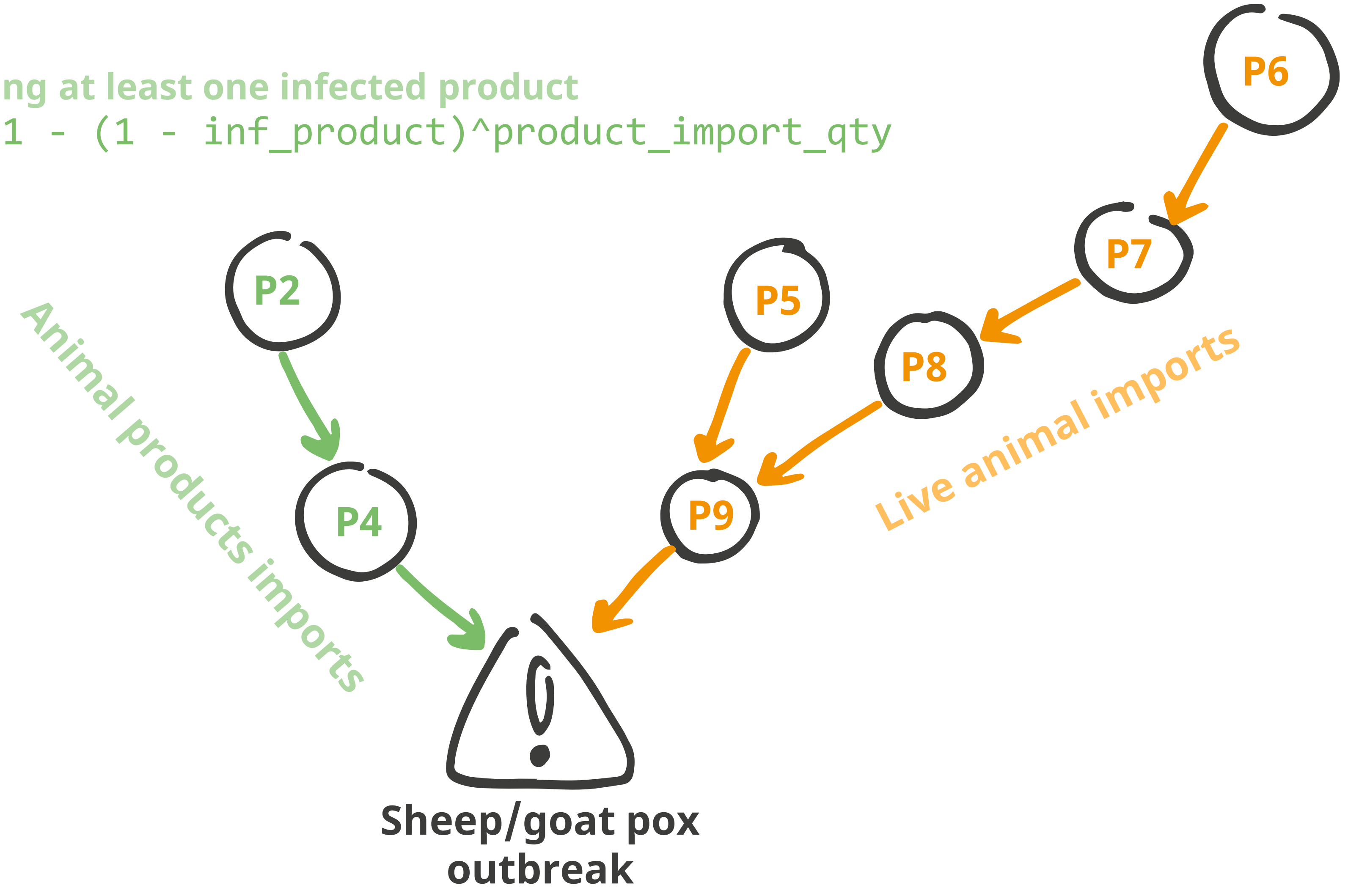
For example

Probability of introducing at least one infected animal

```
inf_animal_all <- 1 - (1 - inf_animal)^animal_import_qty
```

Probability of introducing at least one infected product

```
inf_product_all <- 1 - (1 - inf_product)^product_import_qty
```



For example

Probability of introducing at least one infected product

```
> inf_product_all
  node    mode  nsv nsu nva variate     min  mean median max Nas type outm
1    x numeric 1001   1   6       1 0.00441 0.708  0.996   1   0    V each
2    x numeric 1001   1   6       2 0.00483 0.705  0.996   1   0    V each
3    x numeric 1001   1   6       3 0.00337 0.705  0.995   1   0    V each
4    x numeric 1001   1   6       4 0.00568 0.706  0.997   1   0    V each
5    x numeric 1001   1   6       5 0.00445 0.704  0.996   1   0    V each
6    x numeric 1001   1   6       6 0.00337 0.706  0.997   1   0    V each
```

Probability of introducing at least one infected animal

```
> inf_animal_all
  node    mode  nsv nsu nva variate   min  mean median max Nas type outm
1    x numeric 1001   1   5       1 0.336 0.996      1   1   0    V each
2    x numeric 1001   1   5       2 0.505 0.997      1   1   0    V each
3    x numeric 1001   1   5       3 0.401 0.995      1   1   0    V each
4    x numeric 1001   1   5       4 0.483 0.996      1   1   0    V each
5    x numeric 1001   1   5       5 0.454 0.996      1   1   0    V each
```

Probability of introducing at least one infected import

```
> inf_all <- 1 - (1 - inf_animal_all) * (1 - inf_product_all)
```

For example

Probability of introducing at least one infected product

```
> inf_product_all
  node    mode  nsv nsu nva variate     min  mean median max Nas type outm
1    x numeric 1001   1   6       1 0.00441 0.708  0.996   1   0    V each
2    x numeric 1001   1   6       2 0.00483 0.705  0.996   1   0    V each
3    x numeric 1001   1   6       3 0.00337 0.705  0.995   1   0    V each
4    x numeric 1001   1   6       4 0.00568 0.706  0.997   1   0    V each
5    x numeric 1001   1   6       5 0.00445 0.704  0.996   1   0    V each
6    x numeric 1001   1   6       6 0.00337 0.706  0.997   1   0    V each
```

Probability of introducing at least one infected animal

```
> inf_animal_all
  node    mode  nsv nsu nva variate   min  mean median max Nas type outm
1    x numeric 1001   1   5       1 0.336 0.996      1   1   0    V each
2    x numeric 1001   1   5       2 0.505 0.997      1   1   0    V each
3    x numeric 1001   1   5       3 0.401 0.995      1   1   0    V each
4    x numeric 1001   1   5       4 0.483 0.996      1   1   0    V each
5    x numeric 1001   1   5       5 0.454 0.996      1   1   0    V each
```

Probability of introducing at least one infected import

```
> inf_all <- 1 - (1 - inf_animal_all) * (1 - inf_product_all)
Error in `Ops.mcnode()`:
! Incompatible mcnode dimensions
```

For example

Probability of introducing at least one infected product

```
> inf_product_all
  node     mode  nsv nsu nva variate     min  mean median max Nas type outm
1    x numeric 1001   1   6       1 0.00441 0.708  0.996   1   0    V each
2    x numeric 1001   1   6       2 0.00483 0.705  0.996   1   0    V each
3    x numeric 1001   1   6       3 0.00337 0.705  0.995   1   0    V each
4    x numeric 1001   1   6       4 0.00568 0.706  0.997   1   0    V each
5    x numeric 1001   1   6       5 0.00445 0.704  0.996   1   0    V each
6    x numeric 1001   1   6       6 0.00337 0.706  0.997   1   0    V each
```

Probability of introducing at least one infected animal

```
> inf_animal_all
  node     mode  nsv nsu nva variate   min  mean median max Nas type outm
1    x numeric 1001   1   5       1 0.336 0.996      1   1   0    V each
2    x numeric 1001   1   5       2 0.505 0.997      1   1   0    V each
3    x numeric 1001   1   5       3 0.401 0.995      1   1   0    V each
4    x numeric 1001   1   5       4 0.483 0.996      1   1   0    V each
5    x numeric 1001   1   5       5 0.454 0.996      1   1   0    V each
```

$$
\underset{\textbf{node\_x}}{\begin{array}{c|ccccc}
 & 1 & 2 & 3 & \dots & u \\ \hline
1 & 0.01 & 0.02 & 0.01 & \dots & 0.02 \\
2 & 0.02 & 0.02 & 0.01 & \dots & 0.01 \\
3 & 0.39 & 0.37 & 0.41 & \dots & 0.4 \\
4 & 0.42 & 0.38 & 0.4 & \dots & 0.37 \\
\dots & 0.25 & 0.56 & 0.32 & \dots & 0.69 \\
i & 0.61 & 0.42 & 0.28 & \dots & \boxed{0.33}
\end{array}}
\cdot
\underset{\textbf{node\_y}}{\begin{array}{c|ccccc}
 & 1 & 2 & 3 & \dots & u \\ \hline
1 & 0.005 & 0.001 & 0.002 & \dots & 0.003 \\
2 & 0.001 & 0.002 & 0.004 & \dots & 0.002 \\
3 & 0.55 & 0.53 & 0.58 & \dots & 0.54 \\
4 & 0.17 & 0.2 & 0.18 & \dots & 0.15 \\
\dots & 0.02 & 0.03 & 0.02 & \dots & 0.02 \\
i & 0.03 & 0.02 & 0.02 & \dots & \boxed{0.02}
\end{array}}
=
\underset{\textbf{node\_xy}}{\begin{array}{c|ccccc}
 & 1 & 2 & 3 & \dots & u \\ \hline
1 & 5E\text{-}05 & 2E\text{-}05 & 2E\text{-}05 & \dots & 6E\text{-}05 \\
2 & 2E\text{-}05 & 4E\text{-}05 & 4E\text{-}05 & \dots & 2E\text{-}05 \\
3 & 0.21 & 0.2 & 0.24 & \dots & 0.22 \\
4 & 0.07 & 0.08 & 0.07 & \dots & 0.06 \\
\dots & 0.01 & 0.02 & 0.01 & \dots & 0.01 \\
i & 0.02 & 0.01 & 0.01 & \dots & \boxed{0.01}
\end{array}}
$$

$$node\_x_{iu} \cdot node\_y_{iu} = node\_xy_{iu}$$

For example

Probability of introducing at least one infected product

```
> inf_product_all
 node     mode  nsv nsu nva variate     min  mean median max Nas type outm
1    x numeric 1001   1   6       1 0.00441 0.708  0.996   1   0    V each
2    x numeric 1001   1   6       2 0.00483 0.705  0.996   1   0    V each
3    x numeric 1001   1   6       3 0.00337 0.705  0.995   1   0    V each
4    x numeric 1001   1   6       4 0.00568 0.706  0.997   1   0    V each
5    x numeric 1001   1   6       5 0.00445 0.704  0.996   1   0    V each
6    x numeric 1001   1   6       6 0.00337 0.706  0.997   1   0    V each
```

Probability of introducing at least one infected animal

```
> inf_animal_all
 node     mode  nsv nsu nva variate   min  mean median max Nas type outm
1    x numeric 1001   1   5       1 0.336 0.996      1   1   0    V each
2    x numeric 1001   1   5       2 0.505 0.997      1   1   0    V each
3    x numeric 1001   1   5       3 0.401 0.995      1   1   0    V each
4    x numeric 1001   1   5       4 0.483 0.996      1   1   0    V each
5    x numeric 1001   1   5       5 0.454 0.996      1   1   0    V each
```

node_x

	1	2	3	…	u
1	0.01	0.02	0.01	…	0.02
2	0.02	0.02	0.01	…	0.01
3	0.39	0.37	0.41	…	0.4
4	0.42	0.38	0.4	…	0.37
…	0.25	0.56	0.32	…	0.69
i	0.61	0.42	0.28	…	0.33

·

node_y

	1	2	3	…	u
1	0.005	0.001	0.002	…	0.003
2	0.001	0.002	0.004	…	0.002
3	0.55	0.53	0.58	…	0.54
4	0.17	0.2	0.18	…	0.15
…	0.02	0.03	0.02	…	0.02
i	0.03	0.02	0.02	…	0.02

=

node_xy

	1	2	3	…	u
1	5E-05	2E-05	2E-05	…	6E-05
2	2E-05	4E-05	4E-05	…	2E-05
3	0.21	0.2	0.24	…	0.22
4	0.07	0.08	0.07	…	0.06
…	0.01	0.02	0.01	…	0.01
i	0.02	0.01	0.01	…	0.01

$$node\_x_{iu} \cdot node\_y_{iu} = node\_xy_{iu}$$

For example

Probability of introducing at least one infected product

```
  country_code species       commodity    min   mean median max Nas type outm
1          AUS   sheep raw_wool_sheep 0.00441 0.708  0.996   1   0    V each
2          BGR   sheep raw_wool_sheep 0.00483 0.705  0.996   1   0    V each
3          GRC   sheep raw_wool_sheep 0.00337 0.705  0.995   1   0    V each
4          GRC    goat   raw_hide_goat 0.00568 0.706  0.997   1   0    V each
5          ITA   sheep raw_wool_sheep 0.00445 0.704  0.996   1   0    V each
6          ITA    goat   raw_hide_goat 0.00337 0.706  0.997   1   0    V each
```

Probability of introducing at least one infected animal

```
  country_code species  commodity   min  mean median max Nas type outm
1          GRC   sheep live_sheep 0.336 0.996      1   1   0    V each
2          GRC    goat  live_goat 0.505 0.997      1   1   0    V each
3          ITA   sheep live_sheep 0.401 0.995      1   1   0    V each
4          ITA    goat  live_goat 0.483 0.996      1   1   0    V each
5          PRT   sheep live_sheep 0.454 0.996      1   1   0    V each
```

$$
\begin{array}{c}\textbf{node\_x}\\ \begin{array}{c|ccccc} & 1 & 2 & 3 & \dots & u \\ \hline 1 & 0.01 & 0.02 & 0.01 & \dots & 0.02 \\ 2 & 0.02 & 0.02 & 0.01 & \dots & 0.01 \\ 3 & 0.39 & 0.37 & 0.41 & \dots & 0.4 \\ 4 & 0.42 & 0.38 & 0.4 & \dots & 0.37 \\ \dots & 0.25 & 0.56 & 0.32 & \dots & 0.69 \\ i & 0.61 & 0.42 & 0.28 & \dots & \boxed{0.33} \end{array}\end{array}
\cdot
\begin{array}{c}\textbf{node\_y}\\ \begin{array}{c|ccccc} & 1 & 2 & 3 & \dots & u \\ \hline 1 & 0.005 & 0.001 & 0.002 & \dots & 0.003 \\ 2 & 0.001 & 0.002 & 0.004 & \dots & 0.002 \\ 3 & 0.55 & 0.53 & 0.58 & \dots & 0.54 \\ 4 & 0.17 & 0.2 & 0.18 & \dots & 0.15 \\ \dots & 0.02 & 0.03 & 0.02 & \dots & 0.02 \\ i & 0.03 & 0.02 & 0.02 & \dots & \boxed{0.02} \end{array}\end{array}
=
\begin{array}{c}\textbf{node\_xy}\\ \begin{array}{c|ccccc} & 1 & 2 & 3 & \dots & u \\ \hline 1 & 5E-05 & 2E-05 & 2E-05 & \dots & 6E-05 \\ 2 & 2E-05 & 4E-05 & 4E-05 & \dots & 2E-05 \\ 3 & 0.21 & 0.2 & 0.24 & \dots & 0.22 \\ 4 & 0.07 & 0.08 & 0.07 & \dots & 0.06 \\ \dots & 0.01 & 0.02 & 0.01 & \dots & 0.01 \\ i & 0.02 & 0.01 & 0.01 & \dots & \boxed{0.01} \end{array}\end{array}
$$

$$node\_x_{iu} \cdot node\_y_{iu} = node\_xy_{iu}$$

For example

Probability of introducing at least one infected product

```
> inf_product_all
  node     mode  nsv nsu nva variate     min  mean median max Nas type outm
1    x numeric 1001   1   6       1 0.00441 0.708  0.996   1   0    V each
2    x numeric 1001   1   6       2 0.00483 0.705  0.996   1   0    V each
3    x numeric 1001   1   6       3 0.00337 0.705  0.995   1   0    V each
4    x numeric 1001   1   6       4 0.00568 0.706  0.997   1   0    V each
5    x numeric 1001   1   6       5 0.00445 0.704  0.996   1   0    V each
6    x numeric 1001   1   6       6 0.00337 0.706  0.997   1   0    V each
```

Probability of introducing at least one infected animal

```
> inf_animal_all
  node     mode  nsv nsu nva variate   min  mean median max Nas type outm
1    x numeric 1001   1   5       1 0.336 0.996      1   1   0    V each
2    x numeric 1001   1   5       2 0.505 0.997      1   1   0    V each
3    x numeric 1001   1   5       3 0.401 0.995      1   1   0    V each
4    x numeric 1001   1   5       4 0.483 0.996      1   1   0    V each
5    x numeric 1001   1   5       5 0.454 0.996      1   1   0    V each
```

$$
\underset{\textbf{node\_x}}{\begin{array}{c|ccccc}
 & 1 & 2 & 3 & \dots & u \\ \hline
1 & 0.01 & 0.02 & 0.01 & \dots & 0.02 \\
2 & 0.02 & 0.02 & 0.01 & \dots & 0.01 \\
3 & 0.39 & 0.37 & 0.41 & \dots & 0.4 \\
4 & 0.42 & 0.38 & 0.4 & \dots & 0.37 \\
\dots & 0.25 & 0.56 & 0.32 & \dots & 0.69 \\
i & 0.61 & 0.42 & 0.28 & \dots & \boxed{0.33}
\end{array}}
\cdot
\underset{\textbf{node\_y}}{\begin{array}{c|ccccc}
 & 1 & 2 & 3 & \dots & u \\ \hline
1 & 0.005 & 0.001 & 0.002 & \dots & 0.003 \\
2 & 0.001 & 0.002 & 0.004 & \dots & 0.002 \\
3 & 0.55 & 0.53 & 0.58 & \dots & 0.54 \\
4 & 0.17 & 0.2 & 0.18 & \dots & 0.15 \\
\dots & 0.02 & 0.03 & 0.02 & \dots & 0.02 \\
i & 0.03 & 0.02 & 0.02 & \dots & \boxed{0.02}
\end{array}}
=
\underset{\textbf{node\_xy}}{\begin{array}{c|ccccc}
 & 1 & 2 & 3 & \dots & u \\ \hline
1 & 5E\text{-}05 & 2E\text{-}05 & 2E\text{-}05 & \dots & 6E\text{-}05 \\
2 & 2E\text{-}05 & 4E\text{-}05 & 4E\text{-}05 & \dots & 2E\text{-}05 \\
3 & 0.21 & 0.2 & 0.24 & \dots & 0.22 \\
4 & 0.07 & 0.08 & 0.07 & \dots & 0.06 \\
\dots & 0.01 & 0.02 & 0.01 & \dots & 0.01 \\
i & 0.02 & 0.01 & 0.01 & \dots & \boxed{0.01}
\end{array}}
$$

$$node\_x_{iu} \cdot node\_y_{iu} = node\_xy_{iu}$$

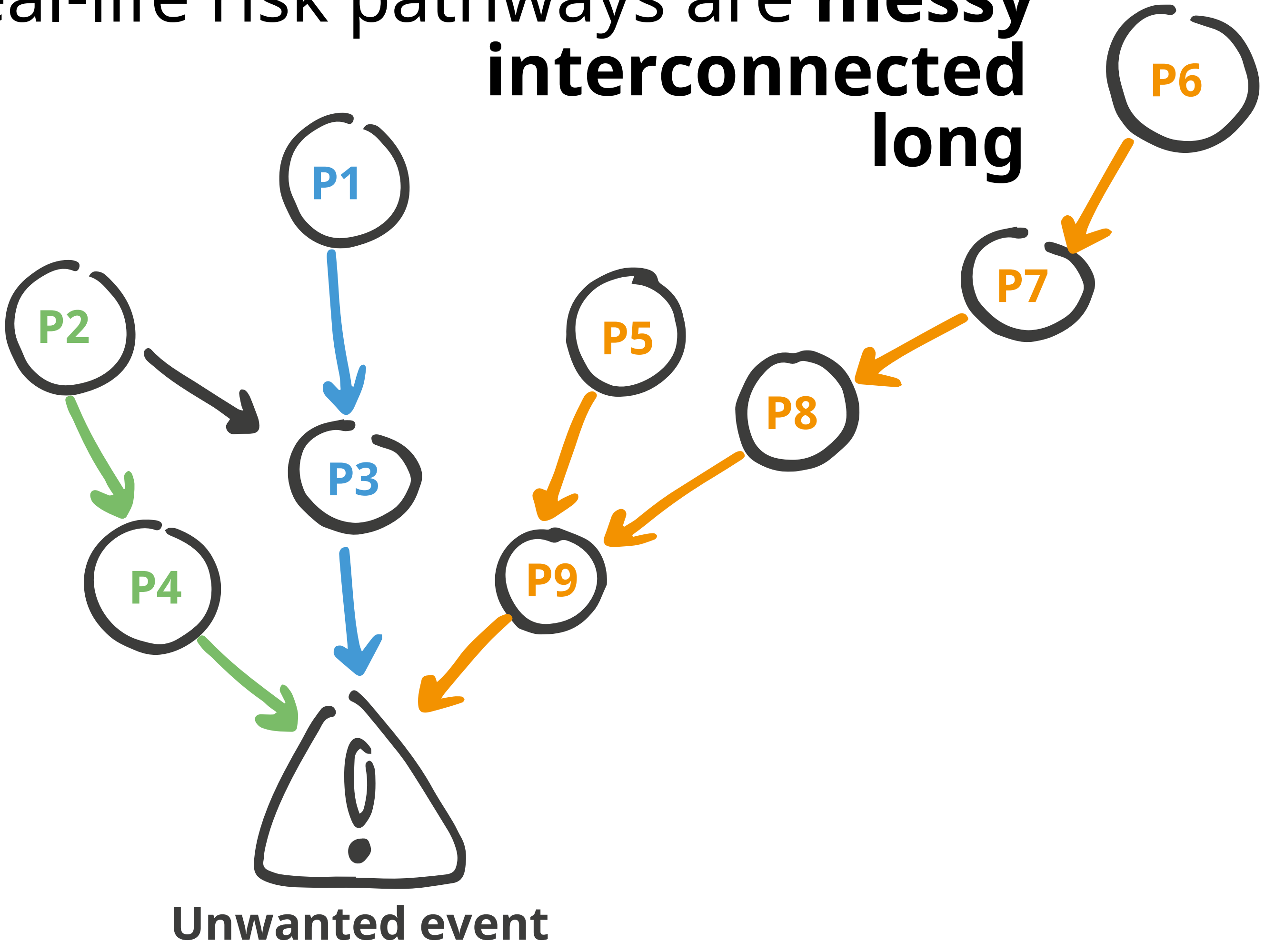
With `mc2d`

Quantifying risk through stochastic probability steps is **neat**

But real-life risk pathways are **messy**

interconnected

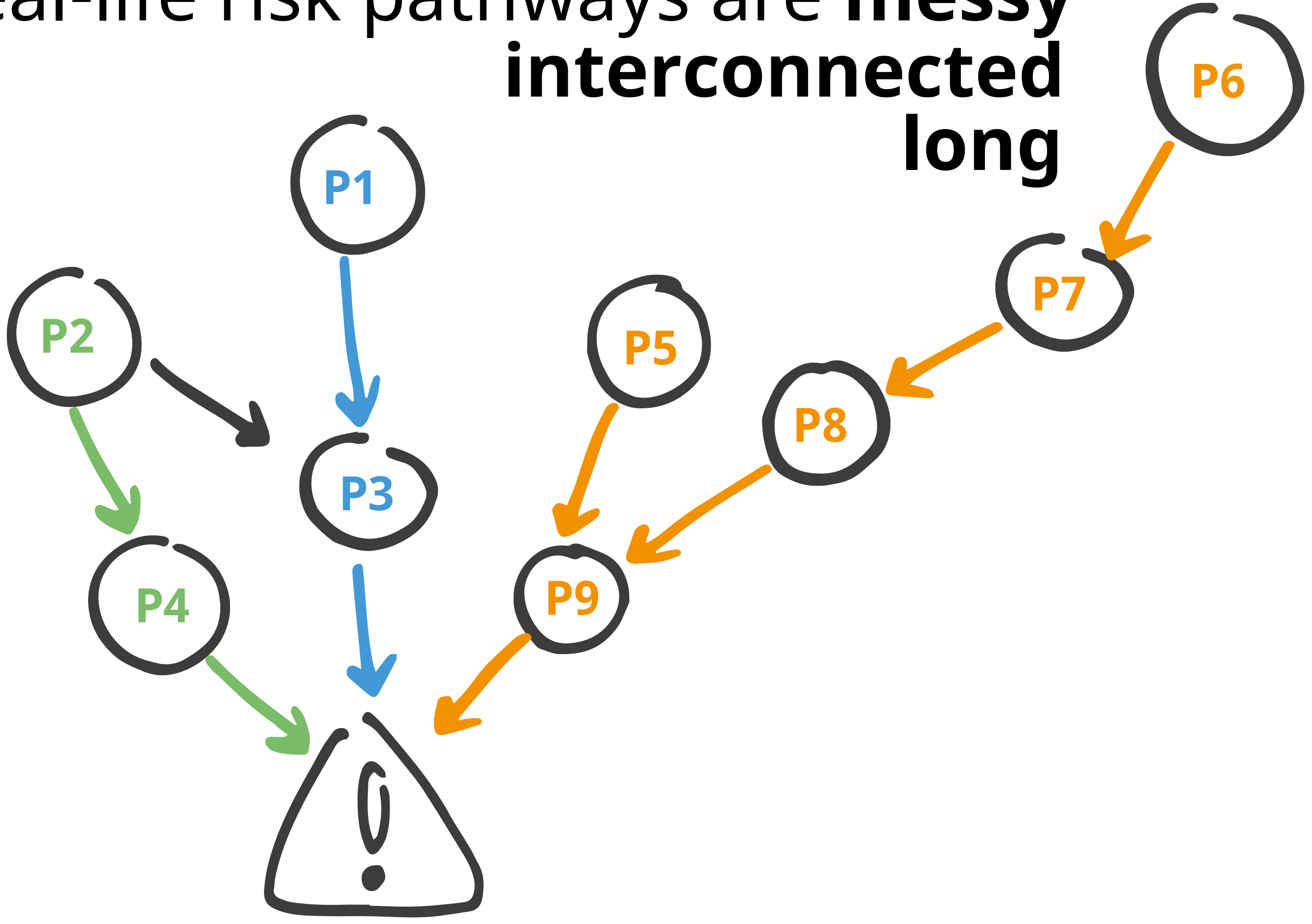
long



With `mc2d`
Quantifying risk through stochastic probability steps is **neat**

But real-life risk pathways are **messy**
interconnected
long

Multi-variate
(many rows)



Unwanted event

With `mc2d`

Quantifying risk through stochastic probability steps is **neat**

But real-life risk pathways are **messy**

interconnected

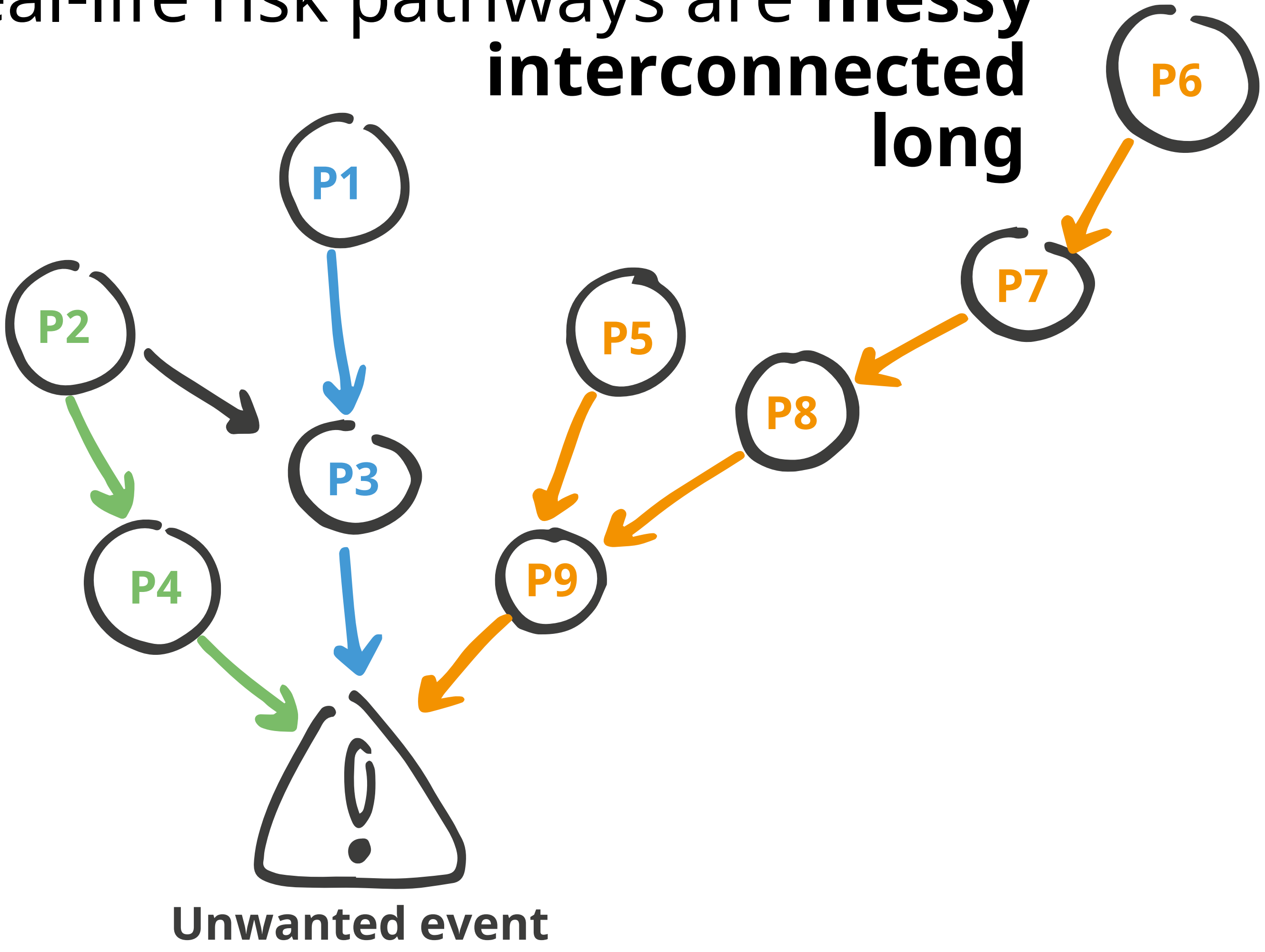
long

Multi-variate

(many rows)

Not-aligned pathway variates

(different rows)



With `mc2d`

Quantifying risk through stochastic probability steps is **neat**

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long

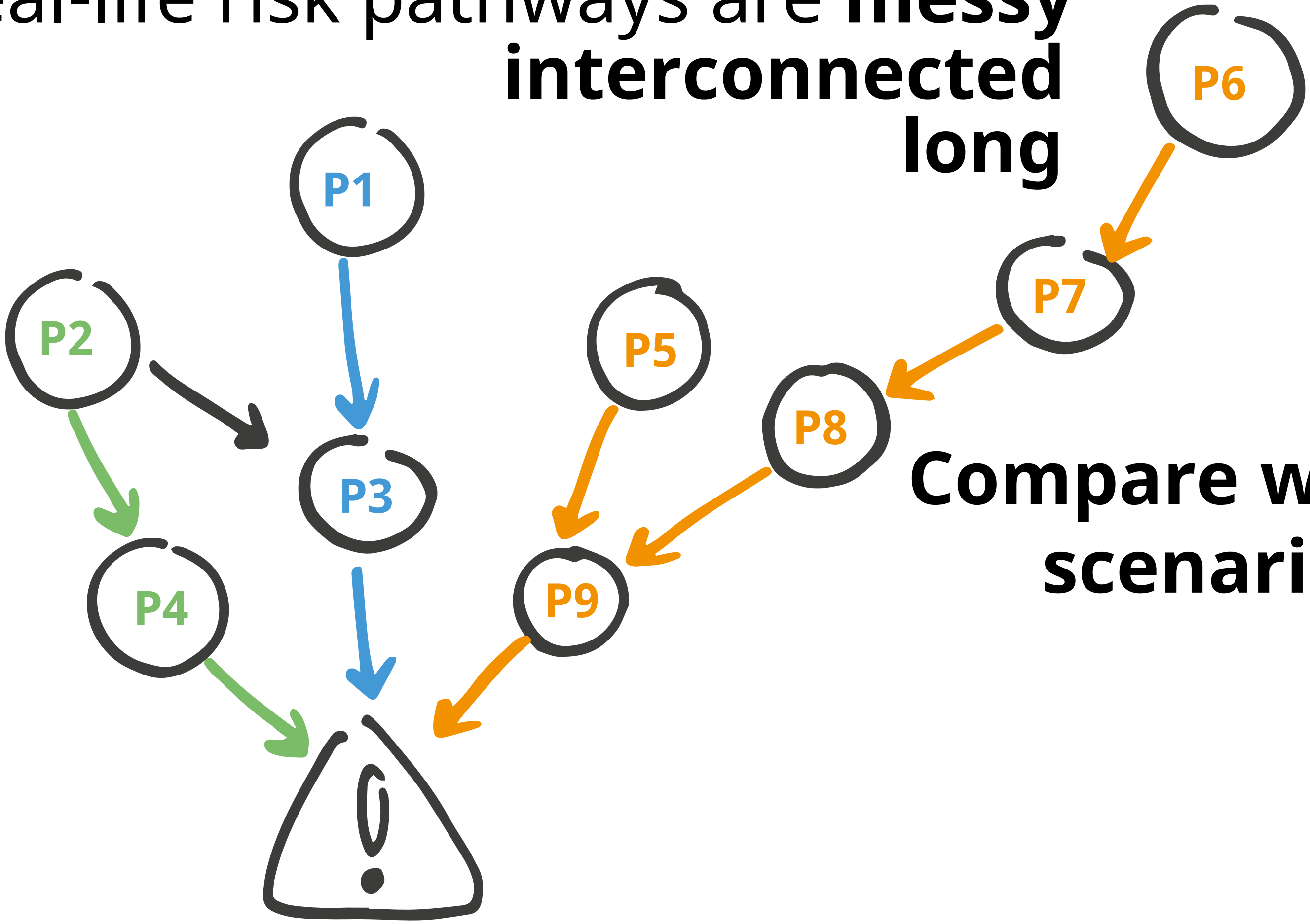
Multi-variate

(many rows)

Not-aligned pathway variates

(different rows)

Compare what-if scenarios



Unwanted event

With `mc2d`

Quantifying risk through stochastic probability steps is **neat**

But real-life risk pathways are **messy**

interconnected

long

Multi-variate

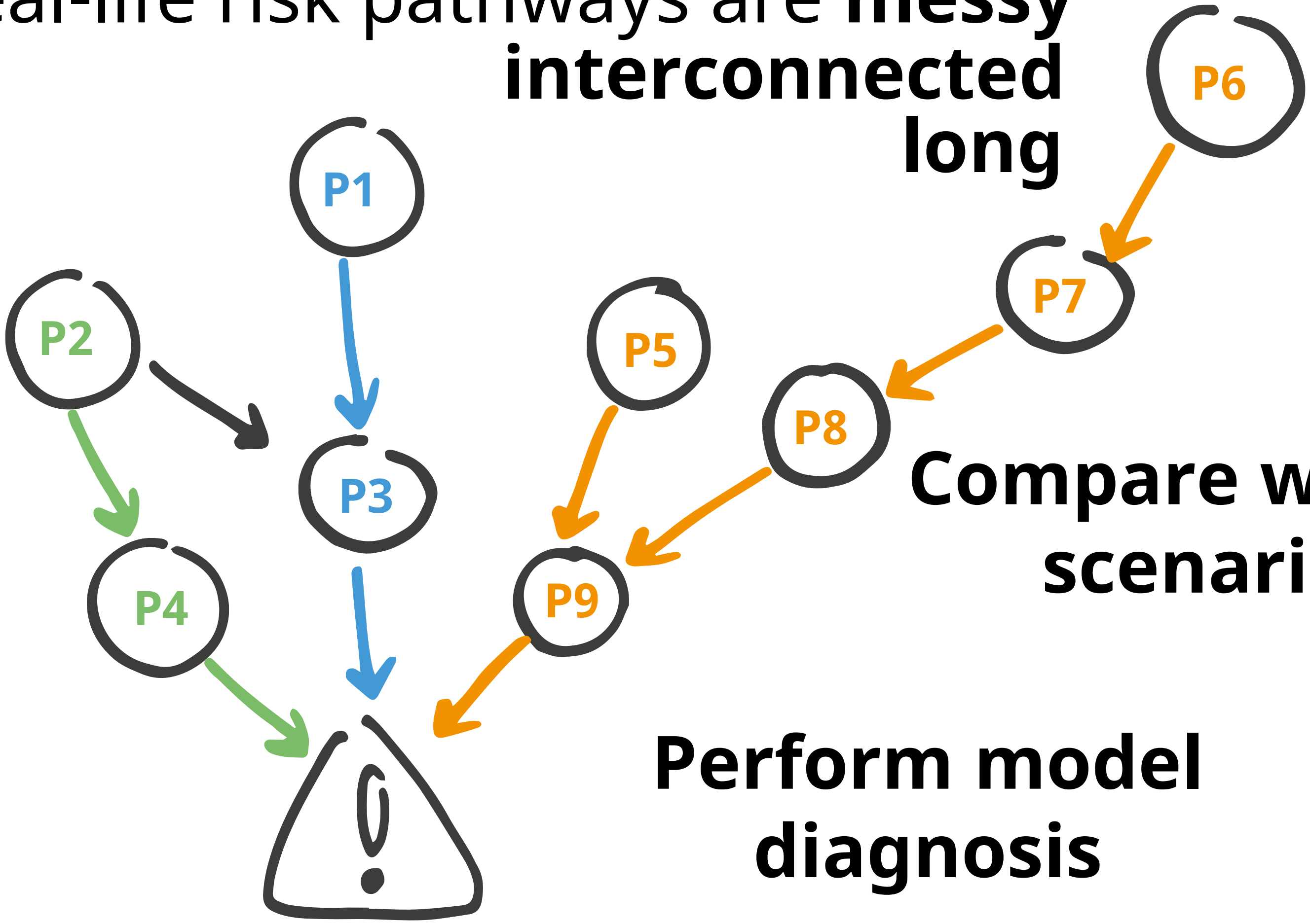
(many rows)

Not-aligned pathway variates

(different rows)

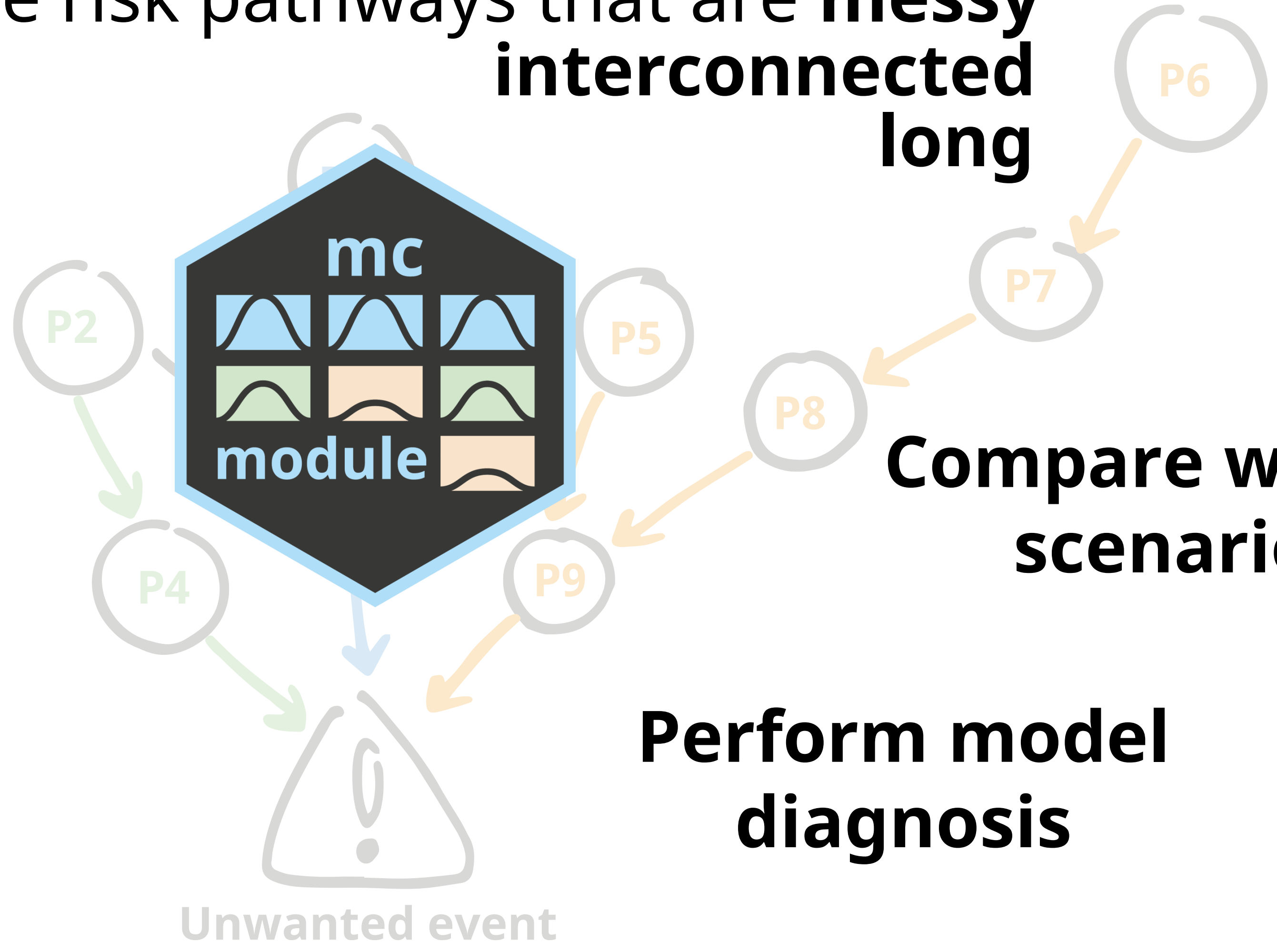
Compare what-if scenarios

Perform model diagnosis



Unwanted event

With `mcmodule`
Quantifying risk through stochastic probability steps
in real-life risk pathways that are **messy**
interconnected
long



Multi-variate
(many rows)

Not-aligned pathway variates
(different rows)

Compare what-if scenarios

Perform model diagnosis

With `mcmodule`
Quantifying risk through stochastic probability steps
in real-life risk pathways that are **messy**
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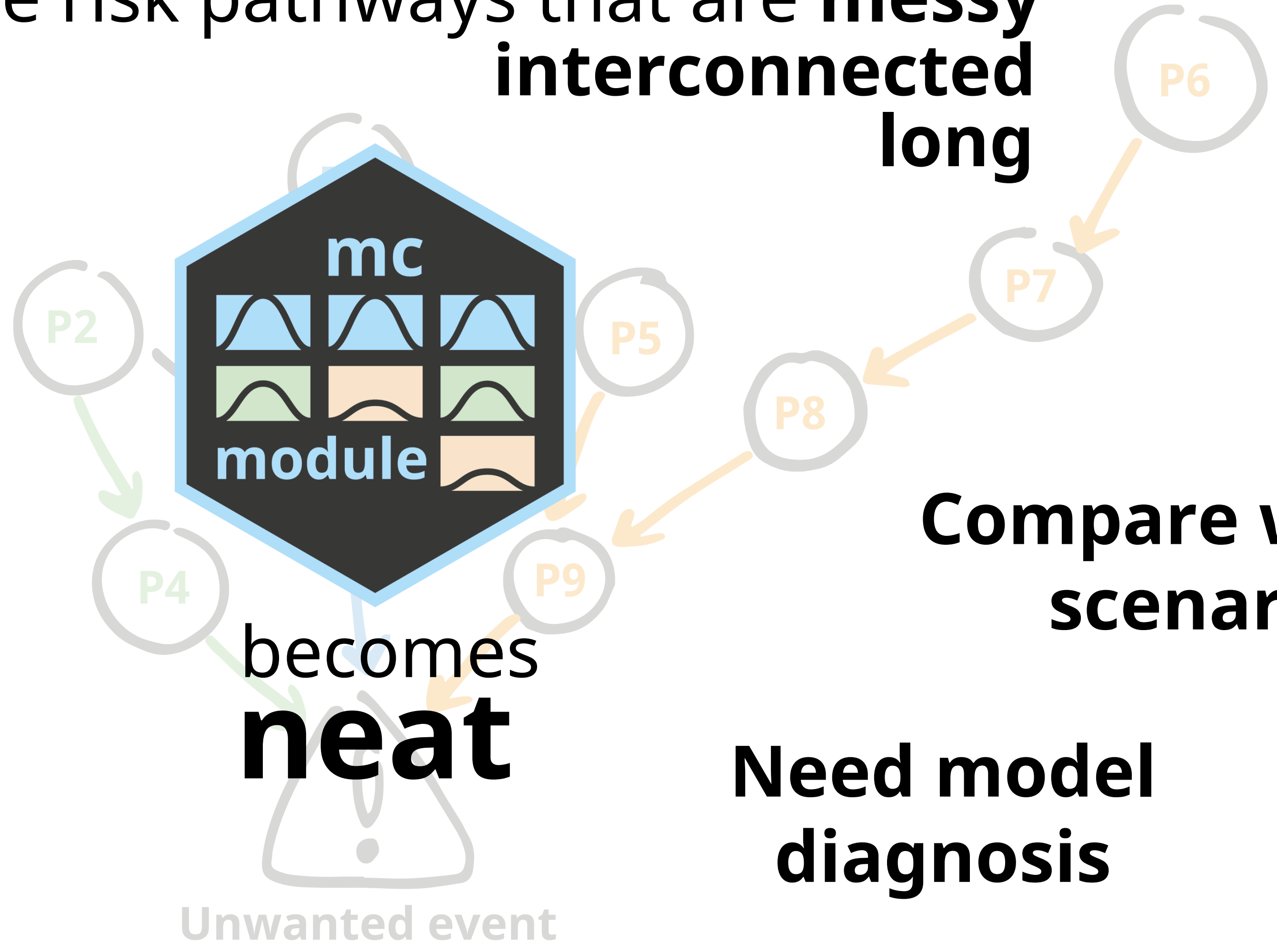
long



Multi-variate
(many rows)

Not-aligned pathway variates
(different rows)

becomes
neat

Compare what-if scenarios

Need model diagnosis

mcmodule::

Core components

mcmodule:: core components

Component	Purpose
Data	Table(s) with one row per variate and columns for input distribution parameters
Data keys	Unique identifiers of rows/variates
mctable	Table with node specifications (distributions, transformations)
Expressions	Mathematical risk calculations

This creates **metadata-rich modules** where:

- Nodes are created automatically from data
- Variates are identified by keys (country, species, scenario…)
- Operations align automatically
- Pathways combine safely
- Scenarios propagate through the model

mcmodule:: case study

Question

What is the probability of introducing sheep/goat pox to Spain through imports?

Pathways

- Live animals (sheep and goat)
- Animal products with contamination risk (raw wool, hides)

Data

- Imports by commodity and country (COMTRADE + Spanish Cámara de Comercio)
- Disease status by country (WAHIS)
- Animal holdings and heads census by country (Eurostat + FAO)

mcmodule:: set-up

```r
# Load packages
library(mcmodule)
library(dplyr)
library(tidyr)
library(ggplot2)

ndvar(1001) # Uncertainty simulations

# Load data
imports_by_country_commodity <- read.csv("data/imports_by_country_commodity.csv", stringsAsFactors = TRUE)
disease_by_country <- read.csv("data/disease_by_country.csv", stringsAsFactors = TRUE)
census_by_country <- read.csv("data/census_by_country.csv", stringsAsFactors = TRUE)
```

mcmodule:: set-up

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```

If input parameters are provided at **different resolutions or aggregation levels**, it's recommended to load them in different tables. !

mcmodule:: set-up

```r
# Load packages
library(mcmodule)
library(dplyr)
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# Load data
imports_by_country_commodity <- read.csv("data/imports_by_country_commodity.csv", stringsAsFactors = TRUE)
disease_by_country <- read.csv("data/disease_by_country.csv", stringsAsFactors = TRUE)
census_by_country <- read.csv("data/census_by_country.csv", stringsAsFactors = TRUE)

# Combine data
imports_data <- imports_by_country_commodity %>%
  left_join(disease_by_country, by = "country_code") %>%
  left_join(census_by_country, by = c("country_code", "species"))
```

If input parameters are provided at **different resolutions or aggregation levels**, it's recommended to load them in different tables. !

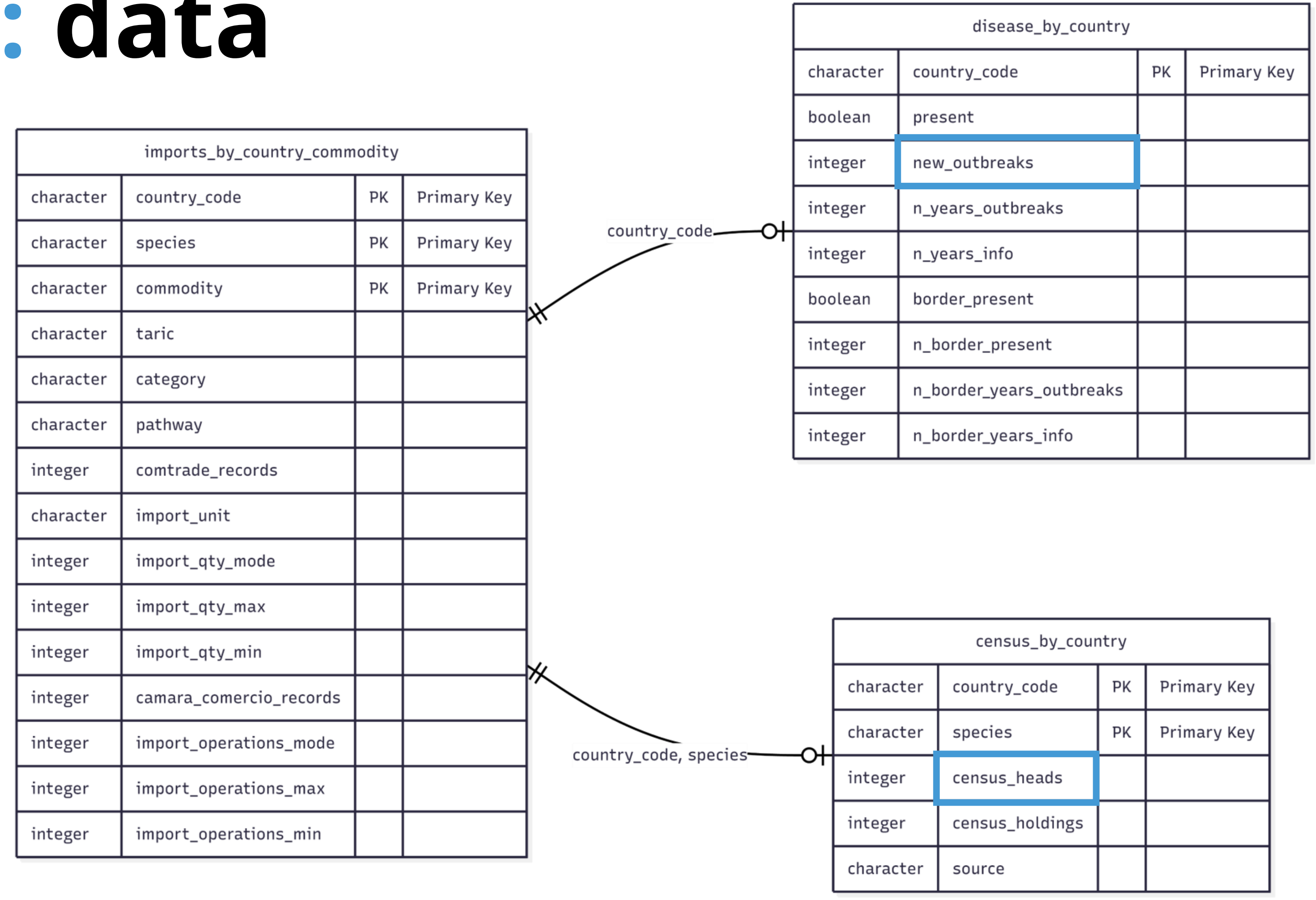
mcmodule:: **data**

Trace input **data resolution**

Good practice!

For example

- Parameter `census_heads` was provided at country and species level
- However `new_outbreaks` was provided at country level, no distinction between species



imports_by_country_commodity			
character	country_code	PK	Primary Key
character	species	PK	Primary Key
character	commodity	PK	Primary Key
character	taric		
character	category		
character	pathway		
integer	comtrade_records		
character	import_unit		
integer	import_qty_mode		
integer	import_qty_max		
integer	import_qty_min		
integer	camara_comercio_records		
integer	import_operations_mode		
integer	import_operations_max		
integer	import_operations_min		

disease_by_country			
character	country_code	PK	Primary Key
boolean	present		
integer	new_outbreaks		
integer	n_years_outbreaks		
integer	n_years_info		
boolean	border_present		
integer	n_border_present		
integer	n_border_years_outbreaks		
integer	n_border_years_info		

census_by_country			
character	country_code	PK	Primary Key
character	species	PK	Primary Key
integer	census_heads		
integer	census_holdings		
character	source		

mcmodule:: data

Trace input **data resolution**

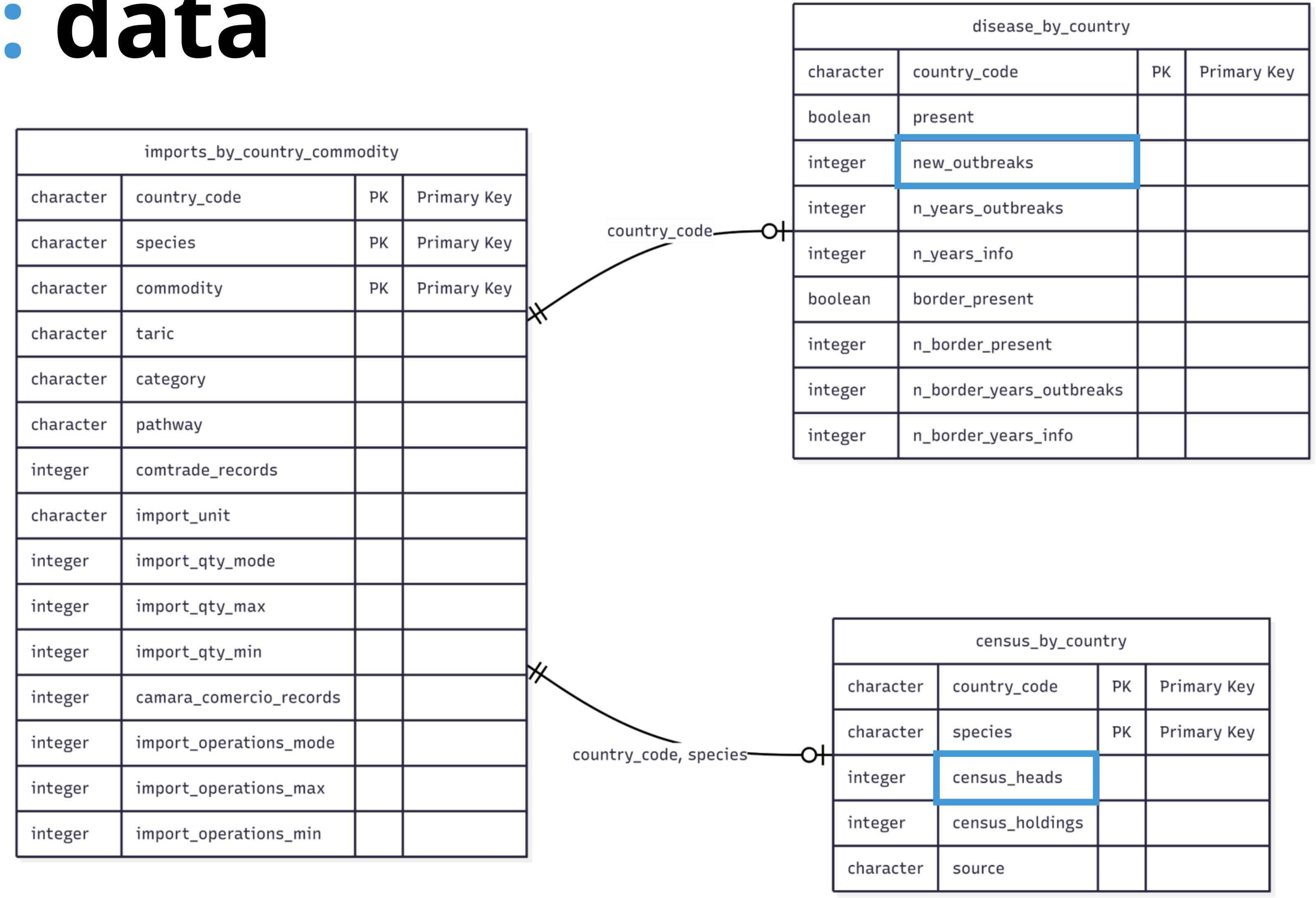
Good practice!

For example

- Parameter `census_heads` was provided at country and species level
- However `new_outbreaks` was provided at country level, no distinction between species

Saves memory use

Good practice!

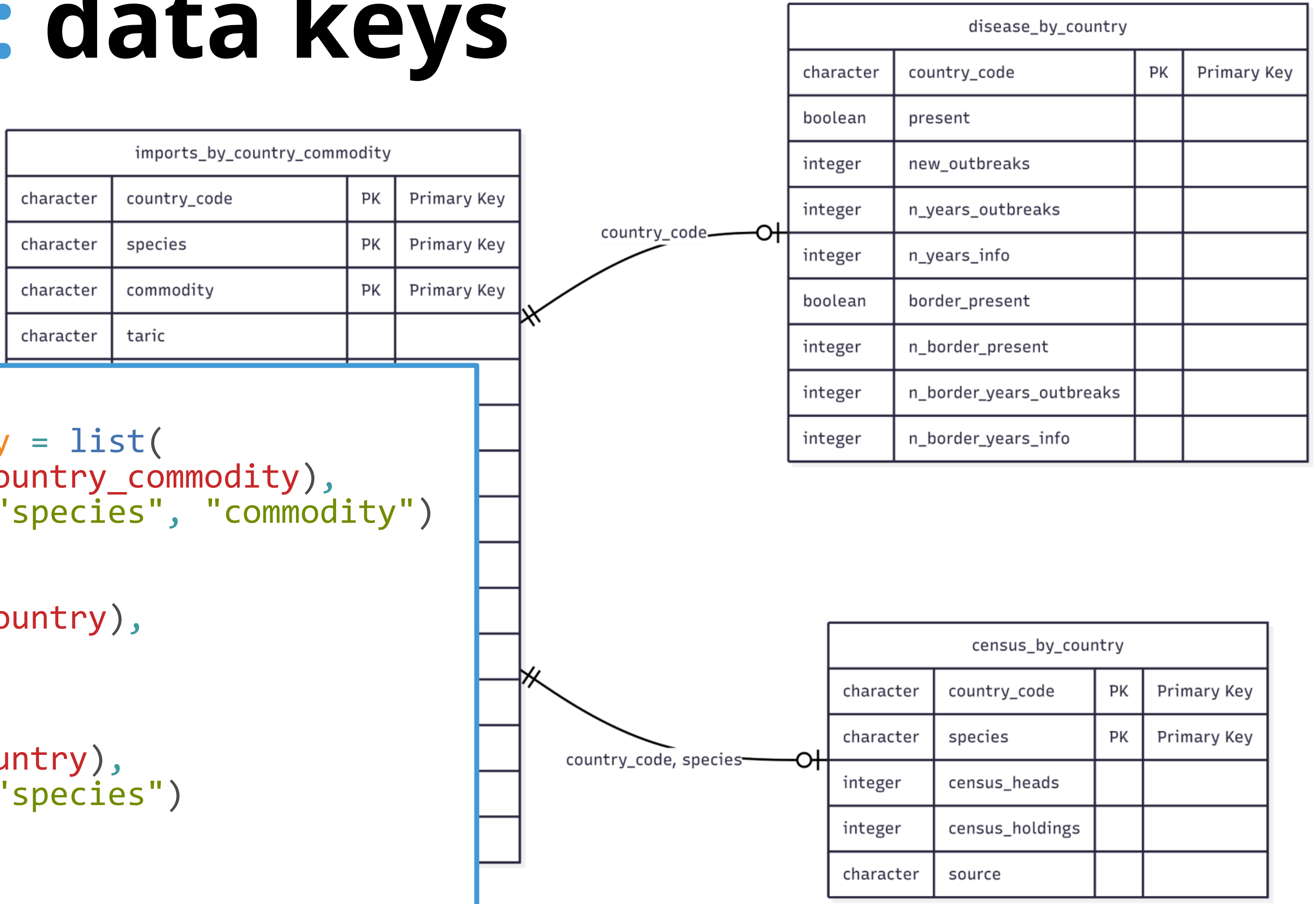


imports_by_country_commodity			
character	country_code	PK	Primary Key
character	species	PK	Primary Key
character	commodity	PK	Primary Key
character	taric		
character	category		
character	pathway		
integer	comtrade_records		
character	import_unit		
integer	import_qty_mode		
integer	import_qty_max		
integer	import_qty_min		
integer	camara_comercio_records		
integer	import_operations_mode		
integer	import_operations_max		
integer	import_operations_min		

disease_by_country			
character	country_code	PK	Primary Key
boolean	present		
integer	new_outbreaks		
integer	n_years_outbreaks		
integer	n_years_info		
boolean	border_present		
integer	n_border_present		
integer	n_border_years_outbreaks		
integer	n_border_years_info		

census_by_country			
character	country_code	PK	Primary Key
character	species	PK	Primary Key
integer	census_heads		
integer	census_holdings		
character	source		

mcmodule:: data keys



imports_by_country_commodity			
character	country_code	PK	Primary Key
character	species	PK	Primary Key
character	commodity	PK	Primary Key
character	taric		

disease_by_country			
character	country_code	PK	Primary Key
boolean	present		
integer	new_outbreaks		
integer	n_years_outbreaks		
integer	n_years_info		
boolean	border_present		
integer	n_border_present		
integer	n_border_years_outbreaks		
integer	n_border_years_info		

census_by_country			
character	country_code	PK	Primary Key
character	species	PK	Primary Key
integer	census_heads		
integer	census_holdings		
character	source		

Declare data keys

```r
sgp_data_keys <- list(
  imports_by_country_commodity = list(
    cols = names(imports_by_country_commodity),
    keys = c("country_code", "species", "commodity")
  ),
  disease_by_country = list(
    cols = names(disease_by_country),
    keys = "country_code"
  ),
  census_by_country = list(
    cols = names(census_by_country),
    keys = c("country_code", "species")
  )
)

set_data_keys(sgp_data_keys) # Set in the envir
```

mcmodule:: mctable

mcnode	description	mc_func	from_variable	transformation	sensi_baseline	sensi_variation
import_qty	Annual imports quantity (units for live animals, kilograms for animal products)	rpert	NA	NA	min = 2000, max = 8000	value * 1.5
import_operations	Annual imports operations	rpert	NA	NA	min = 30, max = 70	value * 1.5
n_years_outbreaks	Number of years with new outbreaks	NA	NA	NA	2	value * 1.5
n_years_info	Number of years with reported health status	NA	NA	NA	10	value * 1.5
census_heads	Number of animal heads in the country	NA	NA	NA	10000	value * 1.5
census_holdings	Number of animal holdings in the country	NA	NA	NA	500	value * 1.5
present	Disease was present in the country the last year reported	NA	NA	NA	0	pmin(1, pmax(0, value * 1.5))
border_present	TRUE if disease is present in any neighboring country	NA	NA	NA	1	pmin(1, pmax(0, value * 1.5))
n_border_present	Number of neighboring countries with disease present	NA	NA	NA	1	value * 1.5
n_border_years_info	Total years of health status information for neighboring countries	NA	NA	NA	10	value * 1.5
n_border_years_outbreaks	Total years of outbreaks in neighboring countries	NA	NA	NA	2	value * 1.5
live_animals	Live animals imports (TRUE if live animals, FALSE if animal products)	NA	pathway	value=='live_animals'	NA	pmin(1, pmax(0, value * 1.5))
p_herds_surveillance	Proportion of herds visited for surveillance at origin	runif	NA	NA	min = 0.25, max = 0.75	pmin(1, pmax(0, value * 1.5))
p_animals_inspected	Proportion of animals inspected per herd at origin	runif	NA	NA	min = 0.2, max = 0.4	pmin(1, pmax(0, value * 1.5))
clinical_se_origin	Sensitivity of clinical inspection at origin	runif	NA	NA	min = 0.5, max = 0.7	pmin(1, pmax(0, value * 1.5))
clinical_se_dest	Sensitivity of clinical inspection at destination	runif	NA	NA	min = 0.55, max = 0.75	pmin(1, pmax(0, value * 1.5))

mcmodule:: mctable

mcnode	description	mc_func	from_variable	transformation	sensi_baseline	sensi_variation
import_qty	Annual imports quantity (units for live animals, kilograms for animal products)	rpert	NA	NA	min = 2000, max = 8000	value * 1.5
import_operations	Annual imports operations	rpert	NA	NA	min = 30, max = 70	value * 1.5
n_years_outbreaks	Number of years with new outbreaks	NA	NA	NA	2	value * 1.5
n_years_info	Number of years with reported health status	NA	NA	NA	10	value * 1.5
census_heads	Number of animal heads in the country	NA	NA	NA	10000	value * 1.5
census_holdings	Number of animal holdings in the country	NA	N			
present	Disease was present in the country the last year reported	NA	N			
border_present	TRUE if disease is present in any neighboring country	NA	N			
n_border_present	Number of neighboring countries with disease present	NA	N			
n_border_years_info	Total years of health status information for neighboring countries	NA	N			
n_border_years_outbreaks	Total years of outbreaks in neighboring countries	NA	NA	NA	2	value * 1.5
live_animals	Live animals imports (TRUE if live animals, FALSE if animal products)	NA	pathway	value=='live_animals'	NA	pmin(1, pmax(0, value * 1.5))
p_herds_surveillance	Proportion of herds visited for surveillance at origin	runif	NA	NA	min = 0.25, max = 0.75	pmin(1, pmax(0, value * 1.5))
p_animals_inspected	Proportion of animals inspected per herd at origin	runif	NA	NA	min = 0.2, max = 0.4	pmin(1, pmax(0, value * 1.5))
clinical_se_origin	Sensitivity of clinical inspection at origin	runif	NA	NA	min = 0.5, max = 0.7	pmin(1, pmax(0, value * 1.5))
clinical_se_dest	Sensitivity of clinical inspection at destination	runif	NA	NA	min = 0.55, max = 0.75	pmin(1, pmax(0, value * 1.5))

Declare mctable

```r
sgp_mctable <- read.csv(
  "data/sgp_mctable.csv",
  stringsAsFactors = TRUE
)

set_mctable(sgp_mctable) # Set in the envir
```

mcmodule:: expressions

```r
origin_inf_exp <- quote({
  # Proportion of years with documented outbreaks
  p_years_outbreaks <- n_years_outbreaks / n_years_info

  # Surveillance sensitivity
  surveillance_se <- mcstoc(runif, min = 0.5, max = 0.9)

  # Probability origin is infected and not detected
  p_not_detected_origin <- p_years_outbreaks * (1 - surveillance_se)
})
```

mcmodule:: expressions

Input mcnodes will be created from data and mctable specifications

```
origin_inf_exp <- quote({
  # Proportion of years with documented outbreaks
  p_years_outbreaks <- n_years_outbreaks / n_years_info

  # Surveillance sensitivity
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```

mcmodule:: expressions

Input mcnodes will be created from data and mctable specifications

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origin_inf_exp <- quote({
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  surveillance_se <- mcstoc(runif, min = 0.5, max = 0.9)

  # Probability origin is infected and not detected
  p_not_detected_origin <- p_years_outbreaks * (1 - surveillance_se)
})
```

When they are evaluated, they will keep their metadata with them (their keys, the table they come from…)

mcmodule:: expressions

output mcnodes metadata will record their inputs and the combined keys of their inputs

```
origin_inf_exp <- quote({
  # Proportion of years with documented outbreaks
  p_years_outbreaks <- n_years_outbreaks / n_years_info

  # Surveillance sensitivity
  surveillance_se <- mcstoc(runif, min = 0.5, max = 0.9)

  # Probability origin is infected and not detected
  p_not_detected_origin <- p_years_outbreaks * (1 - surveillance_se)
})
```

mcmodule:: expressions

mcnodes can also be created **inline**

But variates are automatically assigned by data rows!

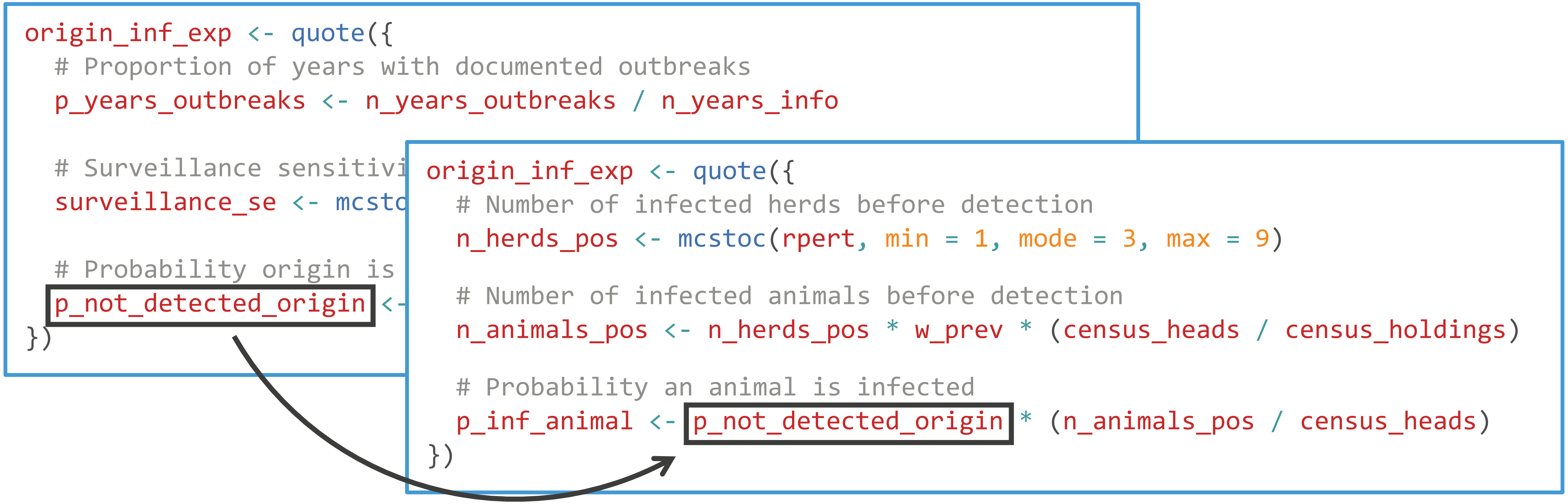
```
origin_inf_exp <- quote({
  # Proportion of years with documented outbreaks
  p_years_outbreaks <- n_years_outbreaks / n_years_info

  # Surveillance sensitivity
  surveillance_se <- mcstoc(runif, min = 0.5, max = 0.9)

  # Probability origin is infected and not detected
  p_not_detected_origin <- p_years_outbreaks * (1 - surveillance_se)
})
```

mcmodule:: expressions

One mcmodule can have **multiple expressions**



```
origin_inf_exp <- quote({
  # Proportion of years with documented outbreaks
  p_years_outbreaks <- n_years_outbreaks / n_years_info

  # Surveillance sensitivi
  surveillance_se <- mcsto

  # Probability origin is
  p_not_detected_origin <-
})
```

```
origin_inf_exp <- quote({
  # Number of infected herds before detection
  n_herds_pos <- mcstoc(rpert, min = 1, mode = 3, max = 9)

  # Number of infected animals before detection
  n_animals_pos <- n_herds_pos * w_prev * (census_heads / census_holdings)

  # Probability an animal is infected
  p_inf_animal <- p_not_detected_origin * (n_animals_pos / census_heads)
})
```

Expressions can use mcnodes from the previous expressions

mcmodule:: expressions

```r
origin_inf_exp <- quote({
  # Proport
  p_years_ou

  # Surveill
  surveillar

  # Probabil
  p_not_dete
})
```

```r
products_inf_exp <- quote({
  # Number c
  n_herds_pc

  # Number c
  n_products

  # Probabil
  p_inf_ pro
})
```

```r
animal_inf_exp <- quote({
  # Number of infected herds before detection
  n_herds_pos <- mcstoc(rpert, min = 1, mode = 3, max = 9)

  # Number of infected animals before detection
  n_animals_pos <- n_herds_pos * w_prev * (census_heads / census_holdings)

  # Probability an animal is infected
  p_inf_animal <- p_not_detected_origin * (n_animals_pos / census_heads)
})
```

```r
animal_import_exp <- list(
  origin_inf = origin_inf_exp,
  animal_inf = animal_inf_exp
)
```

```r
products_import_exp <- list(
  origin_inf = origin_inf_exp,
  products_inf = products_inf_exp
)
```

mcmodule:: expressions – case study

```r
# Probability that the origin country is infected with sheep/goat pox
inf_origin_exp <- quote({
  # Proportion of years with documented outbreaks
  p_years_outbreaks <- n_years_outbreaks / n_years_info


  # Number of herds visited for surveillance
  n_herd_surveillance <- p_herds_surveillance * census_holdings


  # Average herd size
  herd_size <- census_heads / census_holdings


  # Number of animals inspected
  n_animals_inspected <- p_animals_inspected * herd_size


  # Surveillance programme design prevalences
  herd_design_prev <- 0.1 # Herd-level target
  system_design_prev <- 0.001 # System-level target


  # Herd-level surveillance sensitivity
  herd_se <- 1 -
    (1 -
      (n_animals_inspected *
        clinical_se_origin /
```

mcmodule:: scenarios

```r
# Create baseline scenario with current surveillance parameters
baseline_data <- imports_by_country_commodity %>%
  left_join(disease_by_country, by = "country_code") %>%
  left_join(census_by_country, by = c("country_code", "species")) %>%
  mutate(scenario_id = "0") # Baseline must always be “0”


# Enhanced surveillance in destination scenario
enhanced_dest_data <- baseline_data %>%
  mutate(
    scenario_id = "Destination surveillance",
    clinical_se_dest_min = 0.85,
    clinical_se_dest_max = 0.95
  )
```

mcmodule::

Evaluate a module

mcmodule::eval_module()

```r
# Filter live animals data
live_animals_data <- bind_rows(
  baseline_data,
  enhanced_dest_data,
  enhanced_origin_data
) %>%
  filter(pathway == "live_animals")

# Combine expressions
live_animals_exp <- list(
  animal_inf_origin = inf_origin_exp,
  animal_entry = animal_entry_exp
)

# Evaluate live animals model
live_animals <- eval_module(
  exp = live_animals_exp,
  data = live_animals_data
)
```

mcmodule::eval_module()

```r
# Filter live animals data
live_animals_data <- bind_rows(
  baseline_data,
  enhanced_dest_data,
  enhanced_origin_data
) %>%
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# Combine expressions
live_animals_exp <- list(
  animal_inf_origin = inf_origin_exp,
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)

# Evaluate live animals model
live_animals <- eval_module(
  exp = live_animals_exp,
  data = live_animals_data
)
```
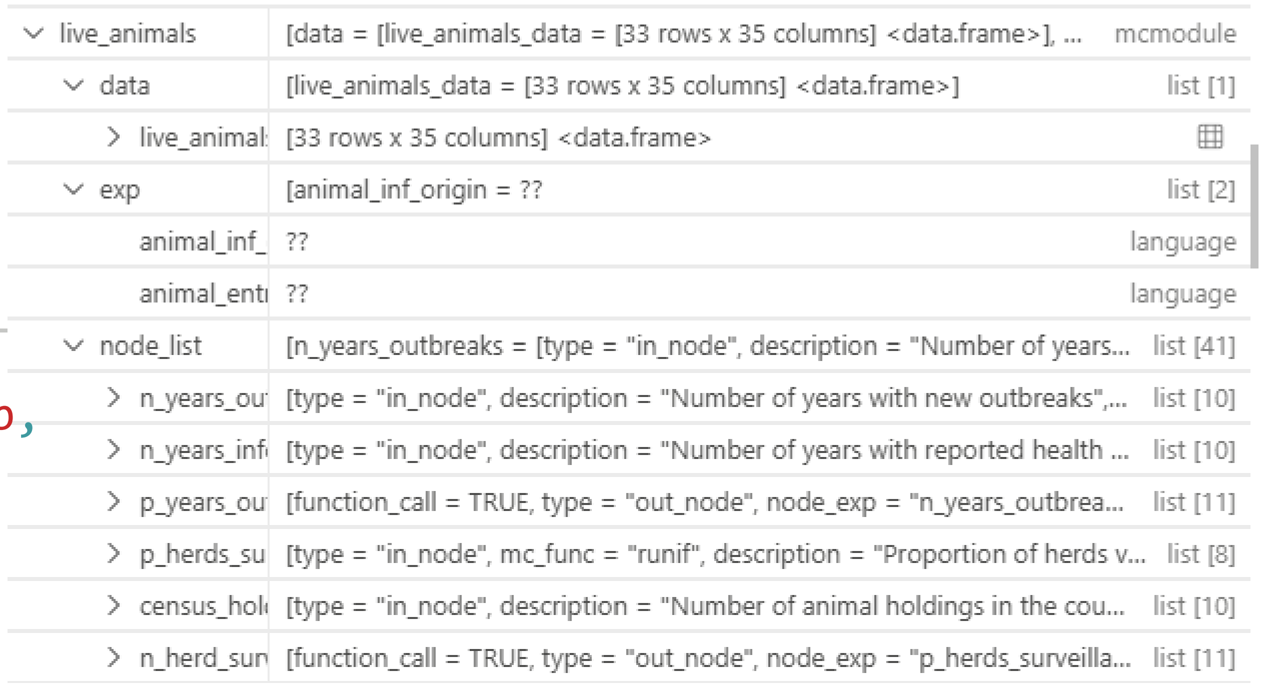
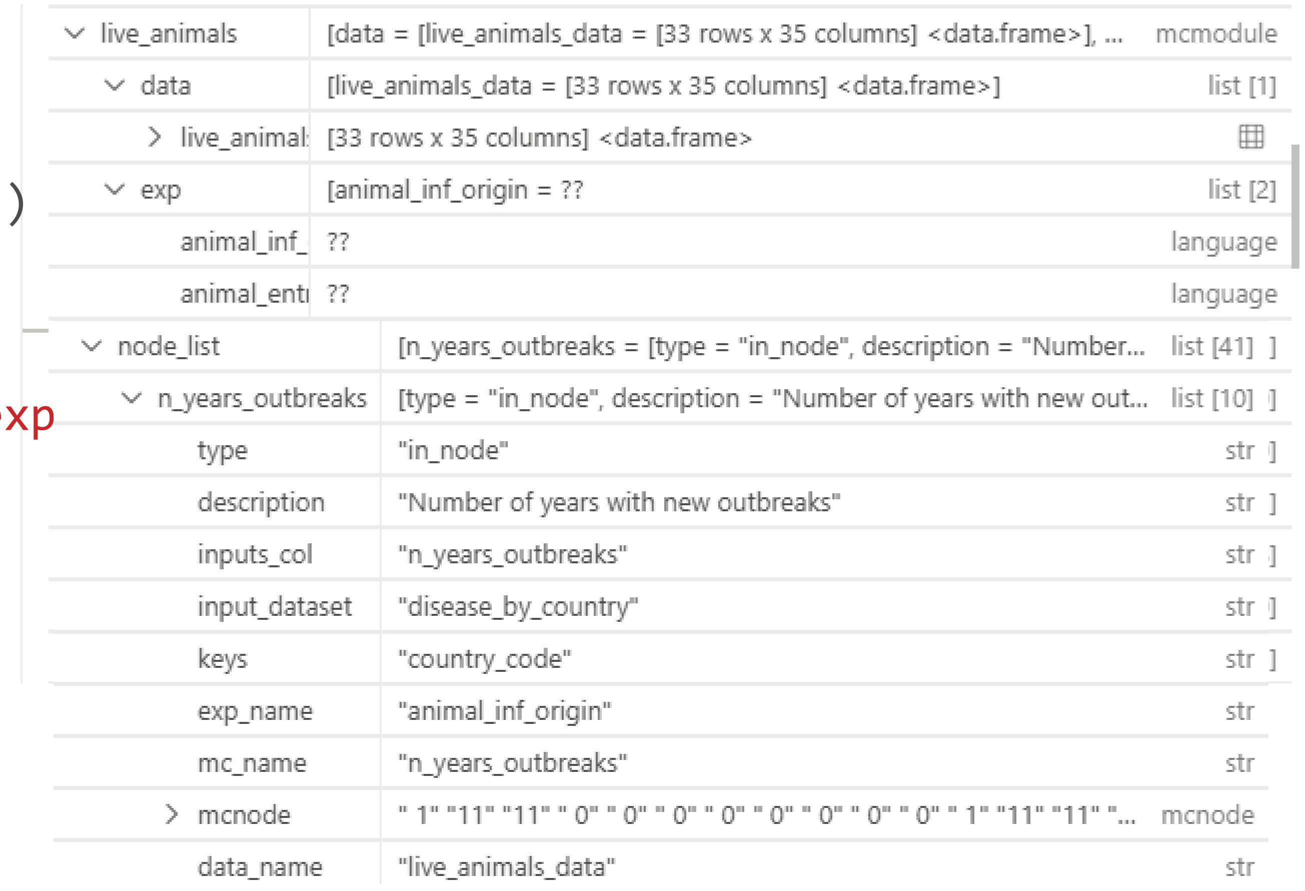



⌄ live_animals	[data = [live_animals_data = [33 rows x 35 columns] <data.frame>], ...	mcmodule
⌄ data	[live_animals_data = [33 rows x 35 columns] <data.frame>]	list [1]
› live_animal	[33 rows x 35 columns] <data.frame>	▦
⌄ exp	[animal_inf_origin = ??	list [2]
animal_inf_	??	language
animal_entı	??	language
⌄ node_list	[n_years_outbreaks = [type = "in_node", description = "Number of years...	list [41]
› n_years_ou	[type = "in_node", description = "Number of years with new outbreaks",...	list [10]
› n_years_inf	[type = "in_node", description = "Number of years with reported health ...	list [10]
› p_years_ou	[function_call = TRUE, type = "out_node", node_exp = "n_years_outbrea...	list [11]
› p_herds_su	[type = "in_node", mc_func = "runif", description = "Proportion of herds v...	list [8]
› census_hol	[type = "in_node", description = "Number of animal holdings in the cou...	list [10]
› n_herd_sur	[function_call = TRUE, type = "out_node", node_exp = "p_herds_surveilla...	list [11]

mcmodule::eval_module()

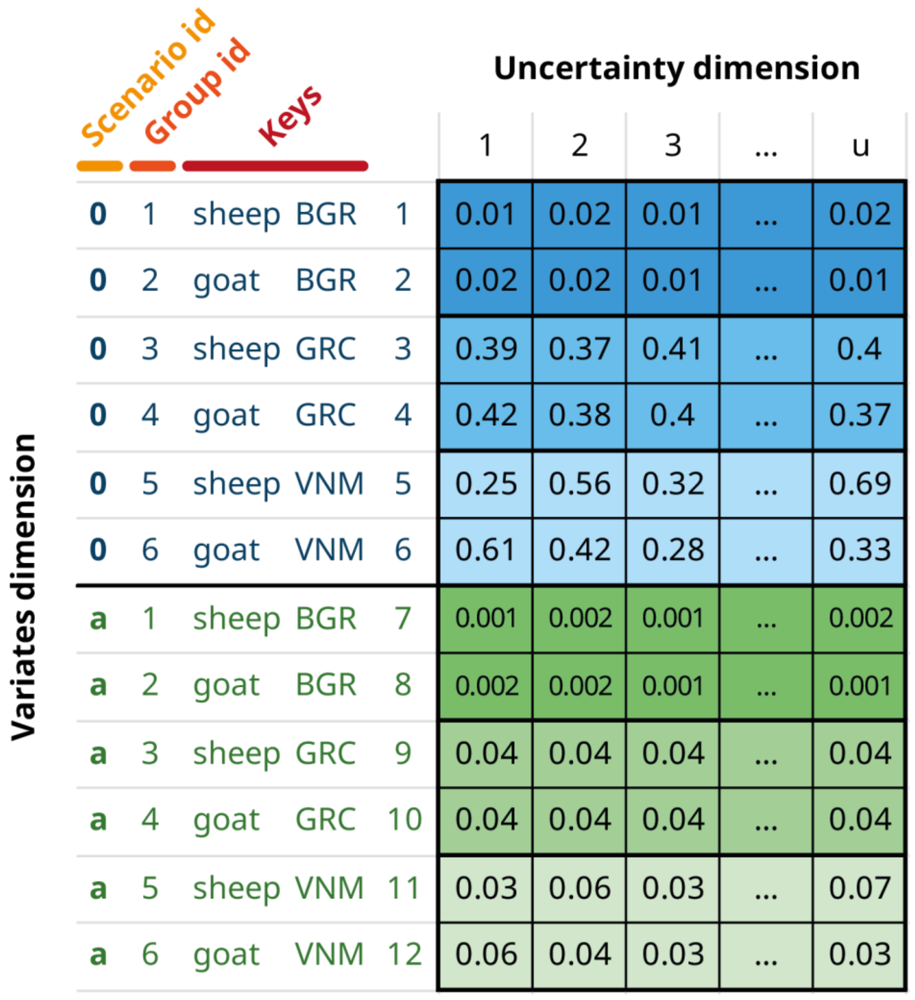
```r
# Filter live animals data
live_animals_data <- bind_rows(
  baseline_data,
  enhanced_dest_data,
  enhanced_origin_data
) %>%
  filter(pathway == "live_animals")

# Combine expressions
live_animals_exp <- list(
  animal_inf_origin = inf_origin_exp
  animal_entry = animal_entry_exp
)

# Evaluate live animals model
live_animals <- eval_module(
  exp = live_animals_exp,
  data = live_animals_data
)
```



⌄ live_animals	[data = [live_animals_data = [33 rows x 35 columns] <data.frame>], ...	mcmodule
⌄ data	[live_animals_data = [33 rows x 35 columns] <data.frame>]	list [1]
› live_animal	[33 rows x 35 columns] <data.frame>	▦
⌄ exp	[animal_inf_origin = ??	list [2]
animal_inf_	??	language
animal_entı	??	language
⌄ node_list	[n_years_outbreaks = [type = "in_node", description = "Number...	list [41]]
⌄ n_years_outbreaks	[type = "in_node", description = "Number of years with new out...	list [10]]
type	"in_node"	str]
description	"Number of years with new outbreaks"	str]
inputs_col	"n_years_outbreaks"	str]
input_dataset	"disease_by_country"	str]
keys	"country_code"	str]
exp_name	"animal_inf_origin"	str
mc_name	"n_years_outbreaks"	str
› mcnode	" 1" "11" "11" " 0" " 0" " 0" " 0" " 0" " 0" " 0" " 0" " 1" "11" "11" "...	mcnode
data_name	"live_animals_data"	str

mcmodule::eval_module()

```r
# Filter live animals data
live_animals_data <- bind_rows(
  baseline_data,
  enhanced_dest_data,
  enhanced_origin_data
) %>%
  filter(pathway == "live_animals")

# Combine expressions
live_animals_exp <- list(
  animal_inf_origin = inf_origin_exp,
  animal_entry = animal_entry_exp
)

# Evaluate live animals model
live_animals <- eval_module(
  exp = live_animals_exp,
  data = live_animals_data
)
```



Scenario id
Group id
Keys
Uncertainty dimension
Variates dimension

Scenario id	Group id	Keys			1	2	3	...	u
0	1	sheep	BGR	1	0.01	0.02	0.01	...	0.02
0	2	goat	BGR	2	0.02	0.02	0.01	...	0.01
0	3	sheep	GRC	3	0.39	0.37	0.41	...	0.4
0	4	goat	GRC	4	0.42	0.38	0.4	...	0.37
0	5	sheep	VNM	5	0.25	0.56	0.32	...	0.69
0	6	goat	VNM	6	0.61	0.42	0.28	...	0.33
a	1	sheep	BGR	7	0.001	0.002	0.001	...	0.002
a	2	goat	BGR	8	0.002	0.002	0.001	...	0.001
a	3	sheep	GRC	9	0.04	0.04	0.04	...	0.04
a	4	goat	GRC	10	0.04	0.04	0.04	...	0.04
a	5	sheep	VNM	11	0.03	0.06	0.03	...	0.07
a	6	goat	VNM	12	0.06	0.04	0.03	...	0.03

mcmodule::

Calculate trial totals

mcmodule:: simple trial totals

```r
# Probability for introducing at least one infected animal
# in one import operations
live_animals <- trial_totals(
  mcmodule = live_animals,
  mc_names = "p_entry_animal",
  trials_n = "import_size”
)
```

mcmodule:: simple trial totals

```r
# Probability for introducing at least one infected animal
# in one import operations
live_animals <- trial_totals(
  mcmodule = live_animals,
  mc_names = "p_entry_animal",
  trials_n = "import_size”
)
```

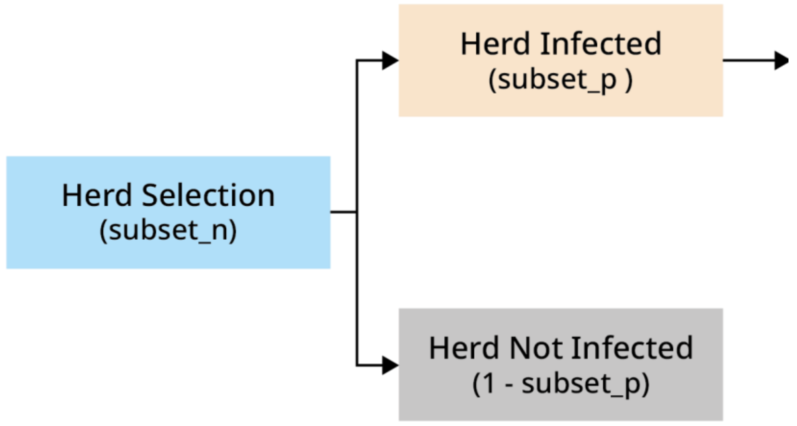
```
> animal_products$node_list$p_product_inf_animal_set$summary
                  mc_name country_code species       commodity         mean           sd Min 2.5% 25%
1  p_product_inf_animal_set          BGR   sheep Raw wool, sheep 1.165756e-14 4.858792e-14   0    0   0 0.0
2  p_product_inf_animal_set          EGY   sheep Raw wool, sheep 0.000000e+00 0.000000e+00   0    0   0 0.0
3  p_product_inf_animal_set          GRC    goat  Raw hide, goat 2.084691e-15 6.891559e-15   0    0   0 0.0
4  p_product_inf_animal_set          GRC   sheep Raw wool, sheep 1.774582e-18 1.560022e-17   0    0   0 0.0
5  p_product_inf_animal_set          TUN   sheep Raw wool, sheep 0.000000e+00 0.000000e+00   0    0   0 0.0
```

mcmodule:: hierarchical trial totals

```r
# Probability for introducing at least one infected animal
# in at least one import operations
live_animals <- trial_totals(
  mcmodule = live_animals,
  mc_names = "p_entry_animal",
  trials_n = "import_size",
  subsets_p = "p_inf_origin",
  subsets_n = "import_operations"
)
```

mcmodule:: hierarchical trial totals

```r
# Probability for introducing at least one infected animal
# in at least one import operations
live_animals <- trial_totals(
  mcmodule = live_animals,
  mc_names = "p_entry_animal",
  trials_n = "import_size",
  subsets_p = "p_inf_origin",
  subsets_n = "import_operations"
)
```

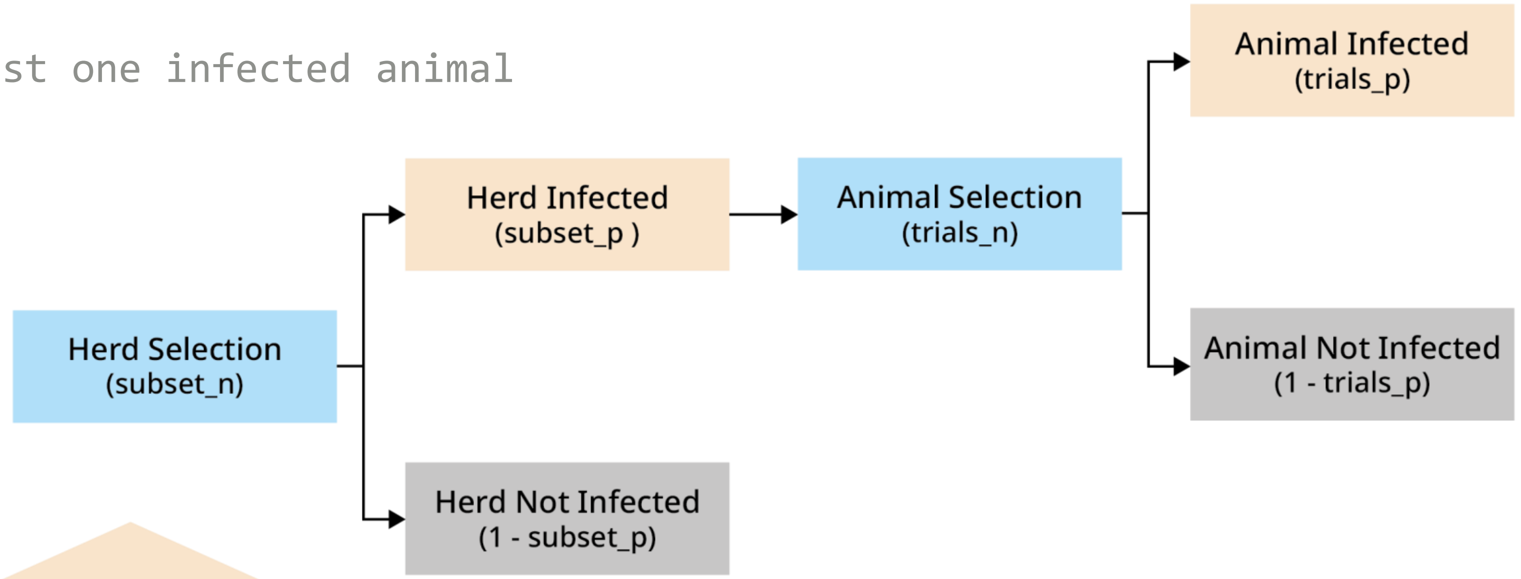


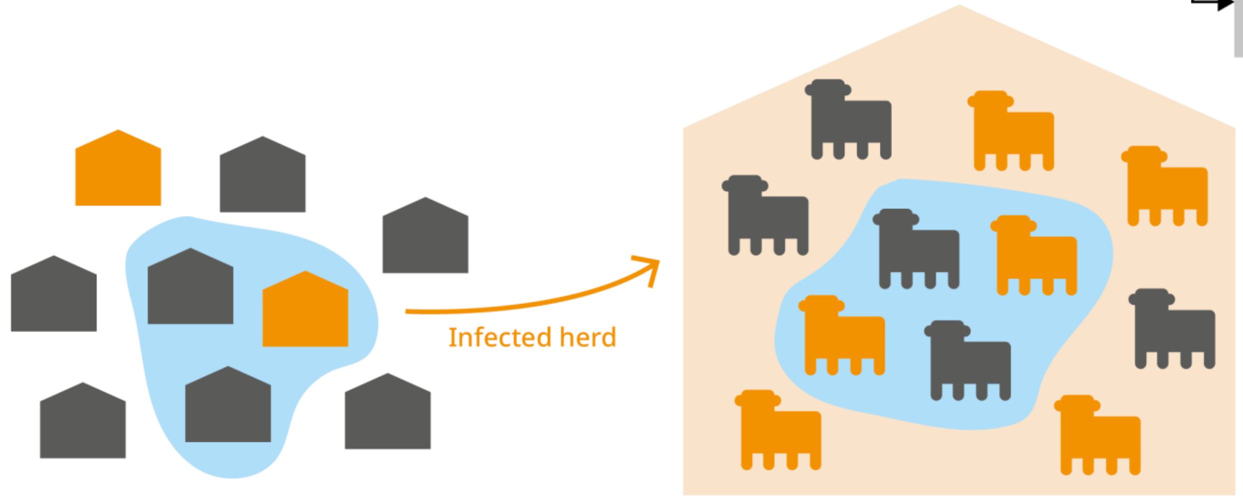
Infected herd

subset_n = 3, subset_p = 0.2

mcmodule:: hierarchical trial totals

```r
# Probability for introducing at least one infected animal
# in at least one import operations
live_animals <- trial_totals(
  mcmodule = live_animals,
  mc_names = "p_entry_animal",
  trials_n = "import_size",
  subsets_p = "p_inf_origin",
  subsets_n = "import_operations"
)
```





subset_n = 3, subset_p = 0.2

trials_n = 4, trials_p = 0.5

mcmodule::

Combine modules

mcmodule:: add_prefix()

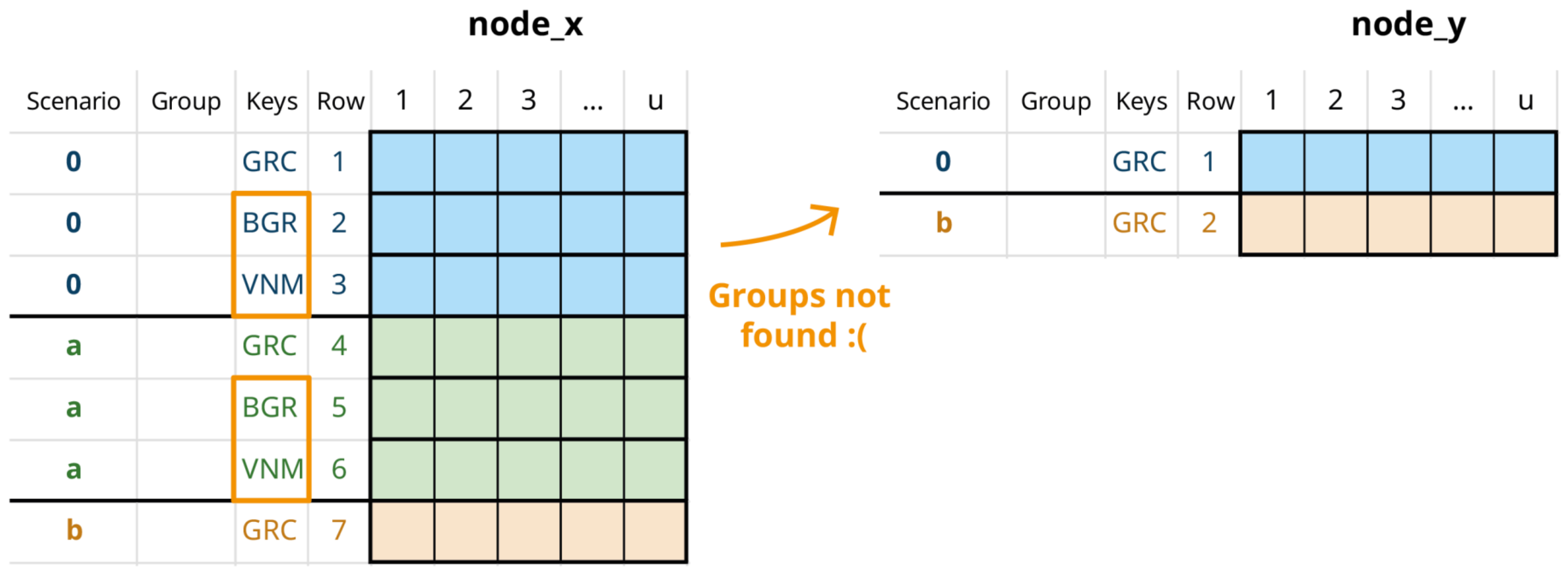
```r
# Evaluate live animals pathway
live_animals <- eval_module(
  exp = live_animals_exp,
  data = live_animals_data
)

# Evaluate animal products pathway
animal_products <- eval_module(
  exp = animal_products_exp,
  data = animal_products_data
)

# Add prefixes to distinguish pathway nodes
live_animals <- add_prefix(live_animals, prefix = "live")
animal_products <- add_prefix(animal_products, prefix = "products")
```

mcmodule:: combine_modules()

```r
# Evaluate live animals pathway
live_animals <- eval_module(
  exp = live_animals_exp,
  data = live_animals_data
)

# Evaluate animal products pathway
animal_products <- eval_module(
  exp = animal_products_exp,
  data = animal_products_data
)

# Add prefixes to distinguish pathway nodes
live_animals <- add_prefix(live_animals, prefix = "live")
animal_products <- add_prefix(animal_products, prefix = "products")


# Combine modules
animal_imports <- combine_modules(live_animals, animal_products)
```

mcmodule:: at_least_one()

```r
# Calculate combined probability of entry from either pathway
animal_imports <- at_least_one(
  mcmodule = animal_imports,
  mc_names = c("products_p_product_inf_animal_set", "live_p_entry_animal_set"),
  name = "p_entry_total"
)
```



node_x

Scenario	Group	Keys	Row	1	2	3	...	u
0		GRC	1	🟦	🟦	🟦	🟦	🟦
0		BGR	2	🟦	🟦	🟦	🟦	🟦
0		VNM	3	🟦	🟦	🟦	🟦	🟦
a		GRC	4	🟩	🟩	🟩	🟩	🟩
a		BGR	5	🟩	🟩	🟩	🟩	🟩
a		VNM	6	🟩	🟩	🟩	🟩	🟩
b		GRC	7	🟧	🟧	🟧	🟧	🟧

node_y

Scenario	Group	Keys	Row	1	2	3	...	u
0		GRC	1	🟦	🟦	🟦	🟦	🟦
b		GRC	2	🟧	🟧	🟧	🟧	🟧

mcmodule:: at_least_one()

```r
# Calculate combined probability of entry from either pathway
animal_imports <- at_least_one(
  mcmodule = animal_imports,
  mc_names = c("products_p_product_inf_animal_set", "live_p_entry_animal_set"),
  name = "p_entry_total"
)
```

Node x			Node y		
Scenario	Group	Row	Scenario	Group	Row
0	1	1	**0**	1	1
0	2	2	**null**	2	
0	3	3	**null**	3	
a	1	4	**0**	1	1
a	2	5	**null**	2	
a	3	6	**null**	3	
0	1	1	**b**	1	2

mcmodule:: at_least_one()

```r
# Calculate combined probability of entry from either pathway
animal_imports <- at_least_one(
  mcmodule = animal_imports,
  mc_names = c("products_p_product_inf_animal_set", "live_p_entry_animal_set"),
  name = "p_entry_total"
)
```

Node x			Node y		
Scenario	Group	Row	Scenario	Group	Row
0	1	1	**0**	1	1
0	2	2	**null**	2	
0	3	3	**null**	3	
a	1	4	**0**	1	1
a	2	5	**null**	2	
a	3	6	**null**	3	
0	1	1	**b**	1	2

node_xy

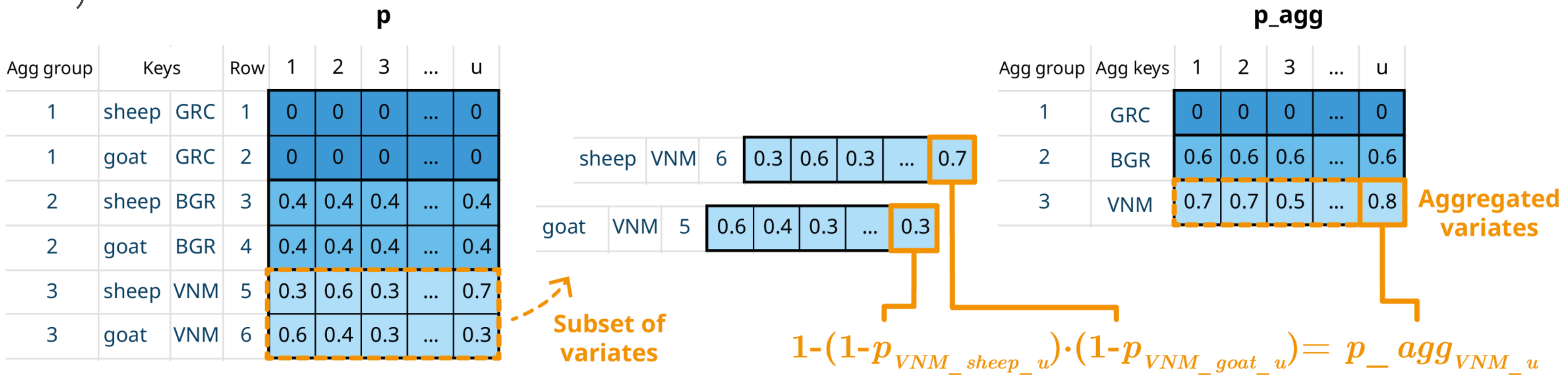
Scenario	Group	Keys	Row	1	2	3	...	u
0	1	GRC	1	🟦	🟦	🟦	🟦	🟦
0	2	BGR	2	🟦	🟦	🟦	🟦	🟦
0	3	VNM	3	🟦	🟦	🟦	🟦	🟦
a	1	GRC	4	🟩	🟩	🟩	🟩	🟩
a	2	BGR	5	🟩	🟩	🟩	🟩	🟩
a	3	VNM	6	🟩	🟩	🟩	🟩	🟩
b	1	GRC	7	🟧	🟧	🟧	🟧	🟧

mcmodule::

Calculate aggregation totals

mcmodule:: aggregation totals

```r
# 1. Total probability by country and scenario
animal_imports <- agg_totals(
  mcmodule = animal_imports,
  mc_name = "p_entry_total",
  agg_keys = c("country_code", "scenario_id"),
  name = "p_entry_total_by_country"
)
```



p

Agg group	Keys		Row	1	2	3	...	u
1	sheep	GRC	1	0	0	0	...	0
1	goat	GRC	2	0	0	0	...	0
2	sheep	BGR	3	0.4	0.4	0.4	...	0.4
2	goat	BGR	4	0.4	0.4	0.4	...	0.4
3	sheep	VNM	5	0.3	0.6	0.3	...	0.7
3	goat	VNM	6	0.6	0.4	0.3	...	0.3

sheep	VNM	6	0.3	0.6	0.3	...	0.7
goat	VNM	5	0.6	0.4	0.3	...	0.3

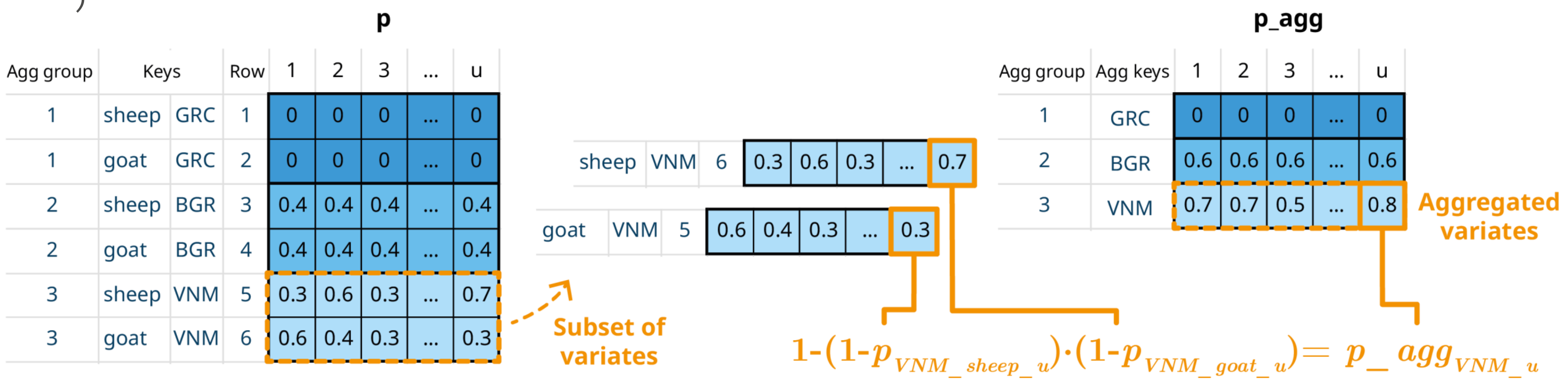
p_agg

Agg group	Agg keys	1	2	3	...	u
1	GRC	0	0	0	...	0
2	BGR	0.6	0.6	0.6	...	0.6
3	VNM	0.7	0.7	0.5	...	0.8

$$1\text{-}(1\text{-}p_{VNM\_sheep\_u})\cdot(1\text{-}p_{VNM\_goat\_u}) = p\_agg_{VNM\_u}$$

mcmodule:: aggregation totals

```r
# 1. Total probability by country and scenario
animal_imports <- agg_totals(
  mcmodule = animal_imports,
  mc_name = "p_entry_total",
  agg_keys = c("country_code", "scenario_id"),
  name = "p_entry_total_by_country"
)
```



p

Agg group	Keys		Row	1	2	3	...	u
1	sheep	GRC	1	0	0	0	...	0
1	goat	GRC	2	0	0	0	...	0
2	sheep	BGR	3	0.4	0.4	0.4	...	0.4
2	goat	BGR	4	0.4	0.4	0.4	...	0.4
3	sheep	VNM	5	0.3	0.6	0.3	...	0.7
3	goat	VNM	6	0.6	0.4	0.3	...	0.3

sheep	VNM	6	0.3	0.6	0.3	...	0.7
goat	VNM	5	0.6	0.4	0.3	...	0.3

p_agg

Agg group	Agg keys	1	2	3	...	u
1	GRC	0	0	0	...	0
2	BGR	0.6	0.6	0.6	...	0.6
3	VNM	0.7	0.7	0.5	...	0.8

$$1\text{-}(1\text{-}p_{VNM\_sheep\_u})\cdot(1\text{-}p_{VNM\_goat\_u}) = p\_agg_{VNM\_u}$$

By default, it calculates the **combined probability of independent events**, but it can take functions such as sum, product, average...

mcmodule:: aggregation totals

```r
# 1. Total probability by country and scenario
animal_imports <- agg_totals(
  mcmodule = animal_imports,
  mc_name = "p_entry_total",
  agg_keys = c("country_code", "scenario_id"),
  name = "p_entry_total_by_country"
)

# 2. Total probability by commodity and scenario
animal_imports <- agg_totals(
  mcmodule = animal_imports,
  mc_name = "p_entry_total",
  agg_keys = c("commodity", "scenario_id"),
  name = "p_entry_total_by_commodity"
)

# 3. Total probability by scenario only (overall risk aggregation)
animal_imports <- agg_totals(
  mcmodule = animal_imports,
  mc_name = "p_entry_total",
  agg_keys = "scenario_id",
  name = "p_entry_total_by_scenario"
)
```

mcmodule::

Analysis and visualization

mcmodule::mc_summary()

```
> # Summary statistics by scenario (overall risk)
+ mc_summary(animal_imports, "p_entry_total_by_scenario")
```

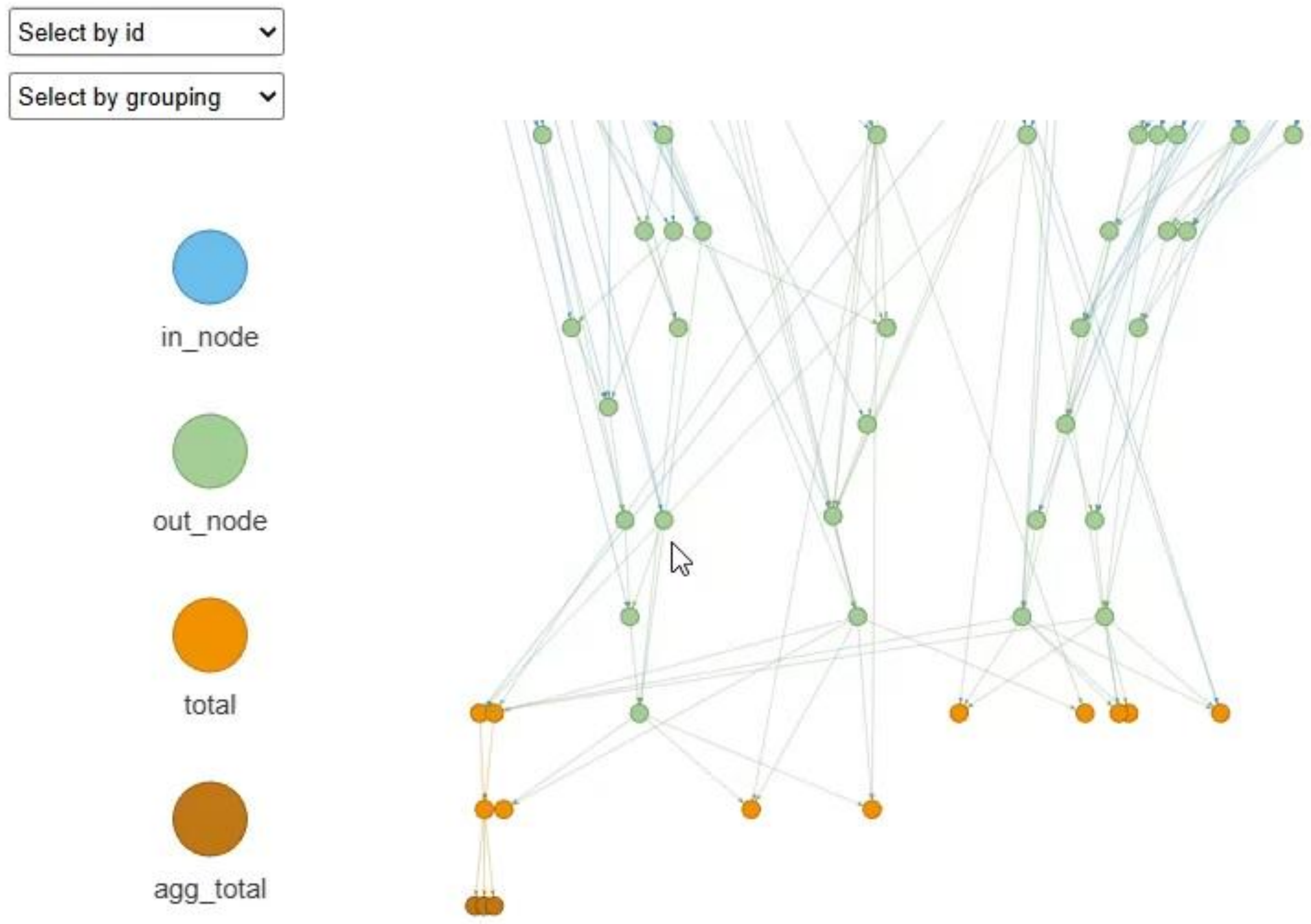
```
                   mc_name              scenario_id         mean           sd          Min         2.5%          25%          50%
1  p_entry_total_by_scenario                       0 1.461221e-06 1.366041e-06 3.860955e-08 1.439198e-07 5.241053e-07 1.048014e-06
41 p_entry_total_by_scenario Destination surveillance 4.097420e-07 4.304603e-07 3.552278e-09 3.282649e-08 1.436553e-07 2.842297e-07
81 p_entry_total_by_scenario      Origin surveillance 1.515106e-06 1.530098e-06 4.697465e-08 1.826068e-07 5.593250e-07 1.085713e-06
            75%        97.5%          Max  nsv Na's
1  1.954708e-06 5.084258e-06 1.014417e-05 1001    0
41 5.271032e-07 1.572215e-06 5.311798e-06 1001    0
81 1.983311e-06 5.188272e-06 2.017941e-05 1001    0
```

mcmodule::mc_summary()

```
> # Summary statistics by scenario (overall risk)
+ mc_summary(animal_imports, "p_entry_total_by_scenario")
```

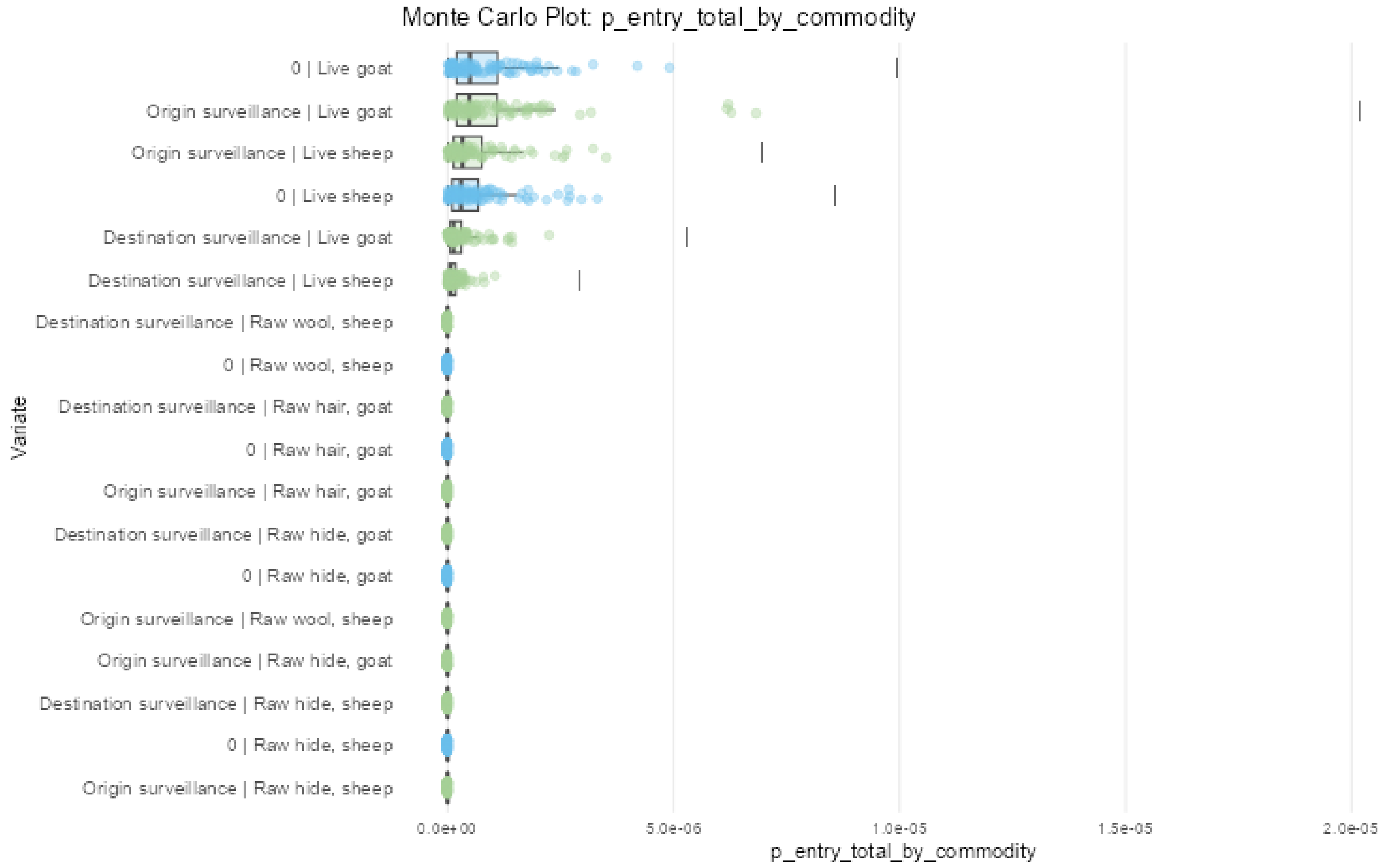
```
                     mc_name             scenario_id         mean           sd          Min         2.5%          25%          50%
1  p_entry_total_by_scenario                       0 1.461221e-06 1.366041e-06 3.860955e-08 1.439198e-07 5.241053e-07 1.048014e-06
41 p_entry_total_by_scenario Destination surveillance 4.097420e-07 4.304603e-07 3.552278e-09 3.282649e-08 1.436553e-07 2.842297e-07
81 p_entry_total_by_scenario      Origin surveillance 1.515106e-06 1.530098e-06 4.697465e-08 1.826068e-07 5.593250e-07 1.085713e-06
            75%        97.5%          Max  nsv Na's
1  1.954708e-06 5.084258e-06 1.014417e-05 1001    0
41 5.271032e-07 1.572215e-06 5.311798e-06 1001    0
81 1.983311e-06 5.188272e-06 2.017941e-05 1001    0
```

mcmodule::mcmodule_network()



mcmodule::mc_plot()

```r
# Plot total probability of entry by commodity
mc_plot(animal_imports, "p_entry_total_by_commodity", order_by = "median")
```



mcmodule::mcmodule_corr()

```r
# Correlation betwen inputs
# and total output
corr_analysis <- mcmodule_corr(
  mcmodule = animal_imports,
  output = "p_entry_total",
  progress = TRUE,
  print_summary = TRUE,
  method = "spearman"
)
```

```
Analysis Parameters:
- Analysis type: Global output
- Output node: p_entry_total
- Correlation method(s): spearman
- Missing value handling: all.obs

Results Summary:
- Total correlations calculated: 1836
- Top 5 most influential inputs (by absolute
mean correlation):
1. products_import_qty: 0.0790
2. products_clinical_se_origin: -0.0383
3. live_import_operations: 0.0120
4. live_clinical_se_origin: -0.0105
5. live_clinical_se_dest: -0.0103

Inputs by Correlation Strength:
- Moderate: products_import_qty
- Weak: products_import_qty
```

mcmodule::mcmodule_converg()

```r
# Analyse convergence of live animals pathway
converg_live <- mcmodule_converg(
  mcmodule = live_animals,
  from_quantile = 0.95,
  to_quantile = 1.0,
  print_summary = TRUE
)
```

```
     Analysis Parameters:
     - Number of simulations: 1001
     - Simulation quantile range: 0.95 to 1
     - Simulations range: 950 to 1001 (51 simulations)

     Convergence Results:
     - Total nodes analyzed: 711
     - Nodes with divergence below 0.001: 427 (60.06%)
     - Nodes with divergence below 1% of their mean: 520 (73.14%)
     - Nodes with divergence below 0.001 or 1% of their mean: 613 (86.22%)
     - Nodes with divergence below 0.001 or 2.5% of their mean: 679 (95.50%)
     - Nodes with divergence below 0.001 or 5% of their mean: 705 (99.16%)

     6 (0.84%) nodes did not converge at 5% threshold :(
```

mcmodule::

Tricks and tweaks

mcmodule:: tricks and tweaks

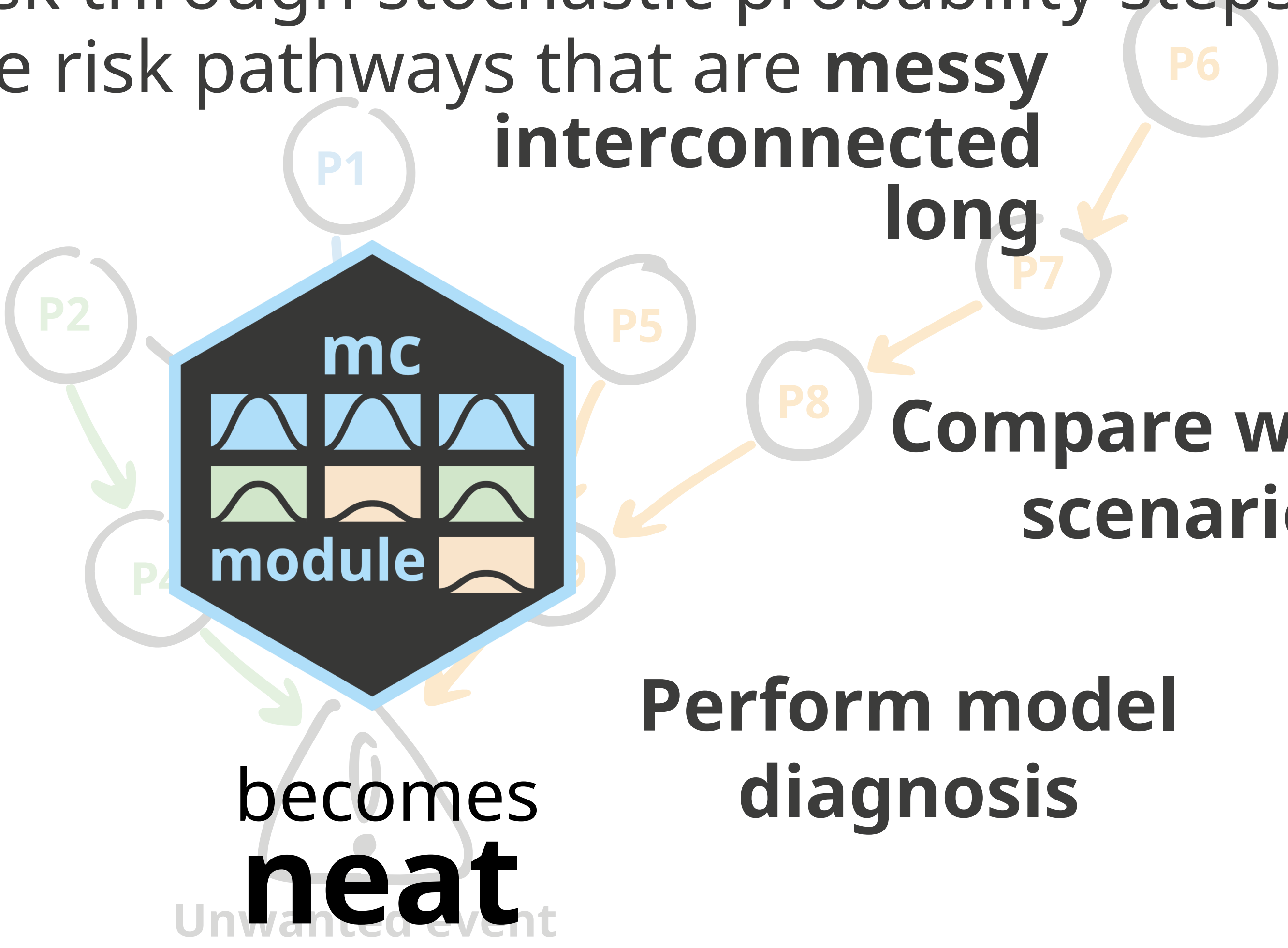
- Replace missing or infinite values to prevent calculation errors using `mcnode_na_rm()`
- Use the `name` parameter in functions like `at_least_one()` and `agg_totals()` to customize output node name
- Some functions can work outside modules: `create_mcnodes()` and `mc_summary()` (useful for prototyping)
- Convert to other formats: Transform mcmodules into matrices or mc objects with `mcmodule_to_matrices()` and `mcmodule_to_mc()`

mcmodule::

Conclusion

mcmodule:: conclusion

Quantifying risk through stochastic probability steps in real-life risk pathways that are **messy**
interconnected
long



Multi-variate

Not-aligned pathway variates

Compare what-if scenarios

Perform model diagnosis

becomes
neat

mcmodule:: conclusion

Modularity

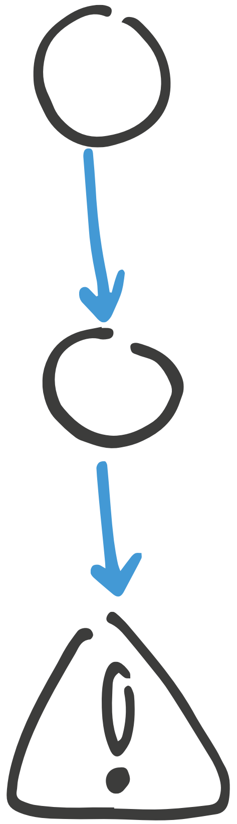
Scalability

Transparency & traceability

Communication

Diagnosis

mcmodule:: next directions



- We are currently planning to add **global sensitivity analysis** based on Morris screening, using the existing local sensitivity (OAT) support
- We are working on building **compatibility with other R packages**, to facilitate integration with broader risk assessment workflows
- To stay updated watch our repository: https://github.com/NataliaCiria/mcmodule
- We encourage you to explore the package further, adapt it to your own use cases, report bugs, and contribute feedback or improvements.

mcmodule:: acknowledgments

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GitHub: https://github.com/NataliaCiria