USDOS User Manual

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Introduction to this User Manual

This user manual accompanies USDOS version 2 as described in Tsao, K. *et. al (in submission)*.

Style conventions used in this guide

`Text in this font is code`

Items in single quotes (' ') are file names

xx signifies a two-digit number (01 to 10)

** signifies text that can vary (such as a filename)

Requirements for using this guide

This manual assumes that the user

1) Is familiar with USDOS and has determined that it is a good fit for their question
2) Has access to a cluster (high-performance) computing environment
3) Has basic fluency in the use of a command line interface

If these do not apply, please consult these suggested resources:

To become familiar with USDOS and determine whether it is a good fit for the research question, please see Tsao, K. *et. al (in submission)* and Buhnerkempe et al (2014) "The Impact of Movements and Animal Density on Continental Scale Cattle Disease Outbreaks in the United States." Plos One 9(3): 10.

Foundational work building a cattle shipment model for the United States

- Buhnerkempe et al (2013) "A national-scale picture of US cattle movements obtained from Interstate Certificate of Veterinary Inspection data." Preventive Veterinary Medicine 112(3-4): 318-329.
- Gorsich et al (2018) "Model-guided suggestions for targeted surveillance based on cattle shipments in the US." Preventive Veterinary Medicine 150: 52-59.
- Lindstrom et al (2013) "A Bayesian Approach for Modeling Cattle Movements in the United States: Scaling up a Partially Observed Network." Plos One 8(1): 11.
- Portacci et al (2013) "Assessment of paper interstate certificates of veterinary inspection used to support disease tracing in cattle." Journal of the American Veterinary Medical Association 243(4): 555-560.

To gain access to a cluster computing environment or learning resources for the command line interface, check with your institution's IT department.

Quick start guide

This section provides a summary of the steps required to initialize and run USDOS. More detailed explainations for each of these steps can be found in subsequent sections of this User Manual.

Initial USDOS setup

Note: If USDOS is already initialized on your computing system, please proceed to the run-specific steps below

1. Download zipped USDOS folder from repository
2. Unzip USDOS folder into your working directory
3. Create object directory (`mkdir obj`)
4. Add any additional required files
5. Ensure USDOS compiles (using `make`) and modify 'makefile' if needed

Run-specific steps

1. Use 'createConfig_Function.R' to generate config, batch, and job files
2. Load required modules
3. Compile
4. Submit job
5. Export files
6. Generate results files with 'post_processing.R', and (if desired) results report with 'USDOS_Results_Report.Rmd'.

Initial USDOS setup in a high-performance computing environment

Note: These steps are only required once per model version

1. Download the zipped USDOS master folder ('usdos.zip') from the appropriate repository.

2. Transfer the zipped directory onto the desired working directory of your high-performance computing system.

3. Unzip the folder in the working directory: `unzip usdos.zip`

4. Enter the upzipped directory: `cd ./usdos`

5. Create an object directory: `mkdir obj`

6. Add any required files using SFTP
    i)   inputfiles Folder
        a. 'usammv1_beef.re's and 'usammv1_dairy.res'
        b. Projected landfill files (10 text files starting with 'landfills_flaps12_min_00')
    ii) FLAPS Folder
        a. Create a folder for the FLAPS: `mkdir FLAPS`
        b. Add desired FLAPS (default is 10 text files each starting with 'flaps12_min_00' and 'flaps12_max_00')
    iii) templates Folder
        a. Create a folder for the templates: `mkdir templates`
        b. config files (4 text files beginning with 'USDOS_CONFIG_TEMPLATE_')
        c. BATCH files ('SH_FILE_TEMPLATE.txt')
    iv) Main working directory
        a. 'createConfig_Function.R' (R script to generate the run-specific files)
7. Load required modules. The modules gcc and gsl are required to run USDOS. Versions 6.1.0 (gcc) and 2.1 (gsl) have been thoroughly tested with the code.
```
module load gcc/6.1.0
module load gsl/2.1
```

8. Compile USDOS using `make`. If it fails to compile, try these troubleshooting steps.

Simulation options

Run types

Several types of run are possible within USDOS. Definitions of terms used can be found here.

- **Base** runs do not include any control measures
- **Infected premises (IP) cull** runs include culling of the infected premises. Runs of this type are abbreviated "IP cull".
- **IP cull & Dangerous Contacts (DC) cull** runs include culling of both IPs and premises identified as dangerous contacts. Runs of this type are abbreviated "IP & DC cull".
- **IP cull & DC vaccination** runs include culling of IPs and vaccination of DCs. Runs of this type are abbreviated "IP cull & DC Vax".
- **IP cull & ring vaccination** runs include culling of IPs and vaccination within a ring around IPs. Standard ring vaccination radii are 3 and 10 kilometers. Runs of this type are abbreviated "IP cull & XXkm Vax".

A **movement ban** can be added to the control types above. As an example, you may have an IP & DC cull run with a 90% effective movement ban.

Configuration file contents

Control type (or lack thereof) and other run parameters are specified in the configuration file. Each line of the config file specifies an option or parameter for the run. These are grouped into sections: Output settings, General settings, Infection-related settings, Grid-related settings, Shipment-related settings, Control-related settings, and Reporting and Tracing (DC) settings.

An example configuration file is shown here. Below the file is a detailed description of each line and instructions for editing the configuration file during pre-processing.

```
## One variable per row, comments start with #
## Empty rows ignored. Rows with numbers and without descriptions are placeho
lders for future variables.
## Arguments not provided should be replaced with '*'.
## Values in parentheses are the index in the vector where value is stored.
## '~' after the value indicates that this value is required
## '+' after the value indicates that one of these adjacent options is requir
ed
## 'x' after the value indicates that this feature is not yet functional


####################### Output settings #######################
IP_VAX_3km_MvmtBan_90_flaps12_min_0001_01_20190513_ #(1) Batch name, used as
prefix for output files. Only letters, numbers and underscore.
1 #(2) Summary output on/off (1/0) - one line per replicate with # infected,
duration, seed info, run time
1 #(3) Detailed infection output on/off (1/0) - one line per exposed premises
```

with time, source of infection, route of infection
0 #(4) Print grid cells on/off
0 #(5)xAdditional functionality under development. Do not change default valu
e.
0 #(6)xAdditional functionality under development. Do not change default valu
e.
* #(7)
* #(8)
* #(9)
* #(10)

###################### General settings ######################
FLAPS/flaps12_min_0001.txt #(11)~Name of file containing premises ID, FIPS, x
, y, population - ie FLAPS_beefdairy_20151201_formatted.txt. Make sure the pr
emises file doesn't have numbers in 1e+05 format (may happen with IDs)
beef,dairy   #(12)~List of species for which counts are provided in pr
emises file, comma-separated
365 #(13)~Timesteps (days) to run
* #(14) Max infectious premises before stopping an outbreak (* = no limit)
1   #(15)~Verbose level: Output extra information to console as model runs (0
=off, 1=basic steps, 2=debug)
0   #(16)x~Disabled
0   #(17)~Reverse x/y option: in case input file is entered as lat/long (y/x)
(set to 1) instead of long/lat (x/y)(set to 0)
inputfiles/FIPS_20151805.txt #(18)~Name of file containing fips name, state n
ame, area (m2), x, y. Tab separated.
0   #(19) Day of the year to start simulation/generation on (jan 1 = day 1).
Must be 0 - 365. 0 = one random day [1-365].
* #(20)

###################### Infection-related settings ######################
allFips #(21)~Seed source, filename or "allFips". Filename is of file contain
ing identifiers (FIPS codes or premisesIDs) from which to seed infection, one
line per simulation. "allFips" specifies to choose from all counties containi
ng premises. To seed from multiple premises at once, provide comma-separated
premisesIDs in the file (one line per simulation).
fips #(22)~Seed file type - type of information provided per line of (21). "f
ips" = choose 1 premises at random within the FIPS code on a given line in (2
1) or in all FIPS, "singlePremises" = use the premisesID provided on a given
line in (21), "multiplePremises" = use all comma separated premisesIDs on a g
iven line in (21)
*   #(23)
1,1 #(24)~Susceptibility exponents(mu), species-specific & comma-separated in
order listed in (12) 0.42,0.49
1,1 #(25)~Infectiousness exponents(omega), species-specific & comma-separated
in order listed in (12) 0.41,0.2
1,1   #(26)~Susceptibility constants(a), species-specific & comma-separated
in order listed in (12) 5.7,1
10.252,10.252 #(27)~Infectiousness constants(b), species-specific & comma-sep
arated in order listed in (12)0.00082,0.00083

6

```
0          #(28)~Kernel type for local (diffusion) spread: 0: k1/(1 + (dista
nce/k2)^k3), 1: data file in (30), 2: k1/(1+d/k2)^k3
1.46e-08,1686.155,2.267 #(29)x~Kernel parameters k1, k2, k3
*       #(30) Name of file containing data-based local spread probabilities b
y distance, ie inputfiles/UKDataKernel.txt
5,0 #(31)~Mean, variance (around normal) days from premises exposure to infec
tiousness (latency duration)
7,0 #(32)~Mean, variance (around normal) days from premises infectiousness to
immunity (infectiousness duration)
0 #(33)+Additional functionality under development. Do not change default val
ue.
* #(34)+Additional functionality under development. Do not change default val
ue.
* #(35)


###################### Grid-related settings #######################
*           #(36)+Filename containing grid cells (will override other opt
ions)
*           #(37)+Length of cell side for uniform cells (will override de
nsity options)
500,100000  #(38)+Max farms per cell, cell size minimum side length in m
* #(39)
* #(40)


###################### Shipment-related settings #######################
1 #(41)~Method(s) to generate county-county shipments (USAMM), comma-separate
d (1 = USAMM version 1, -1 = shipments off)
1   #(42)~Timepoints at which to begin using each of the methods above (first
timepoint must be 1), comma-separated
0   #(43)xAdditional functionality under development. Do not change default v
alue.
inputfiles/usammv1_beef.res, inputfiles/usammv1_dairy.res #(44) Output files
from USAMM with parameters for a, b, N, s and covariates
Q1 #(45) Additional functionality under development. Do not change default va
lue.
1 #(46) Additional functionality under development. Do not change default val
ue.
*,* #(47) Origin covariates for all counties. One file for each species, comm
a separated. Must have header: FIPS, name1, name2... Names must match name co
mponent of covariate parameters in USAMM parameter file.
*,* #(48) Destination covariates for all counties. One file for each species,
comma separated. Must have header: FIPS, name1, name2... Names must match nam
e component of covariate parameters in USAMM parameter file.
*,* #(49) Disabled
1 #(50) Exposed shipments, shipping from a farm with status exposed will caus
e the receiver to become exposed as well. 1 = on, 0 = off


###################### Control-related settings #######################
shipBan,cull,vax #(51)~Names for unique control types, comma-separated (fixed
options: shipBan, cull, vax) '*' will turn off control.
```

noLimit,stateSum,dailyLimit #(52) Control constraint function types, comma-se
parated
0;240,0;6804,0 #(53) Control constraint parameters, comma-separated parameter
s, SEMICOLON-separated by type. stateSum: constraint is mean/var max animals/
day/premises. 20 cows/hr*12 hrs/day = 240
state,premises,premises #(54)~Spatial scale at which control is applied, comm
a-separated (fixed options: premises, county (shipBan only), state (shipBan o
nly))
NA;inputfiles/landfills_flaps12_min_0001.txt;inputfiles/vaccineBankUpdated.tx
t #(55) List additional files here, comma-separated, SEMICOLON-separated by t
ype
NA;resourceLocs;resourceBoosts #(56) Specify file types for (55) here: (NA, r
esourceLocs) comma-separated, SEMICOLON-separated by type
0,0,11 #(57)~Implemented to effective: mean number of days, comma-separated f
or each control type
0,0,0 #(58)~Implemented to effective: variance number of days, comma-separate
d for each control type
366,366,183 #(59)~Effective to inactive: mean number of days, comma-separated
for each control type
0,0,0   #(60)~Effective to inactive: variance number of days, comma-separated
for each control type
0.9,0.9;1,1;0.9,0.9 #(61)~Effectiveness (including compliance) of control typ
es as proportion, comma-separated probability of preventing exposure given ex
posure and probability of transmission given infectiousness. SEMICOLON-separa
ted by type.
* #(62)
newRegionReportsOverX,newPremReportsOverX,newPremReportsOverX #(63)~Control t
riggers, comma-separated (fixed options). '*' will turn off control.
0,0,0 #(64)~Control trigger thresholds, comma-separated (numeric)
shipBan,cull,vax #(65)~Control trigger responses, comma-separated (must exist
in (51))
0,0,3000 #(66)~Control response targets, comma-separated. -1 = DCs, 0 = trigg
ers only, # = radius in units of x/y coordinates of premises
earliest,earliest,earliest #(67)~Control response priority, comma-separated.
Currently only accepts earliest for each control type.
* #(68)
* #(69)
* #(70)

######################## Reporting and Tracing (DC) settings ################
########
15,0 #(71)x~Mean, variance days from INDEX premises exposure to reporting
8,0 #(72)~Mean, variance days from (non-dangerous-contact) premises exposure
to reporting
2,0 #(73)~Mean, variance days from (dangerous-contact) premises exposure to r
eporting
sus,4;exp,5 #(74) Dangerous Contact scaling parameters relative to risk: stat
us, then scale, SEMICOLON-separated (only used if at least one of (66) is -1)
* #(75)

Configuration file guide

The line number in the config file is denoted by (#), along with a **brief descriptive variable name** and description including possible values.

Output settings (lines 1-10)

(1) **Batch name** A string containing only letters, numbers and underscore, used as prefix for output files. This is generated automatically based on selected options. The date and time of run start are appended to the end of the file name.

(2) **Summary output** Whether to generate the summary result file, which contains one line per replicate with number infected, duration, seed info, and run time.

- **1** = Summary output on [default]. File will be outputted in working directory with name [Batch name]_[date]_[time]_summary.txt

- **0** = Summary output off

(3) **Detailed output** Whether to generate the detail result file, which contains one line per exposed premises with time, source of infection, and route of infection.

- **1** = Detailed output on [default]. File will be outputted in working directory with name [Batch name]_[date]_[time]_detail.txt
- **0** = Detailed output off

(4) **Print grid cells** Whether to generate a file containing the grid cells used.

- **1** = Grid cells output on. File will be outputted in working directory with name [Batch name]_cells.txt
- **0** = Grid cells output off [default]

(5) Additional functionality under development. Do not change default value [0].

(6) Additional functionality under development. Do not change default value [0].

(7) Unused

(8) Unused

(9) Unused

(10) Unused

General settings (lines 11-20)

(11) **Premises file (FLAPS)** Path and name of file containing premises ID, FIPS (county ID), x, y, and population for each species- ie flaps12_min_0001.txt. By default this file is located in the FLAPS folder, and its path would thus be FLAPS/flaps12_min_0001.txt. Make sure there are no numbers in scientific notation (ex. 1e+05). This may happen with IDs in R-formatted files.

(12) **Species** List of species for which counts are provided in premises file, comma-separated. Default is "beef, dairy"

(13) **Timesteps (days) to run** Positive integer of maximum number of days to run each simulation. If an outbreak ends before this time, the simulation will end at that point instead. Default is 365.

(14) **Max infectious premises** Positive integer of threshold number of infectious premises allowed. If the total number of premises that have reached infectious status (not necessarily at the same time) surpasses this number, the simulation will end. The default value of * means there is no limit on the number of infectious premises

(15) **Verbose level** How much extra information to output to the console as model runs

- **0** = Output only critical information to console
- **1** = Output basic progress to console [default]
- **2** = Output debug-level information to console

(16) Disabled

(17) **Reverse x/y** This option allws you to specify if input files list locations as latitude(y) before longitude (x) (instead of the default, which is the reverse).

- **0** = Location input file for premises (line 11) lists longitude (x) before latitude (y) [default]
- **1** = Location input file for premises (line 11) lists latitude(y) before longitude (x)

(18) **FIPS info** Name and path of of file containing fips name, state name, area (in square meters), x coordinate, and y coordinate. Tab separated. Default is inputfiles/FIPS_20151805.txt

(19) **Day of the year to seed outbreak** January 1 = day 1. Must be an integer 0 - 365. The default of 0 selects one random day [1-365].

(20) Unused

Infection-related settings (lines 21-35)

(21) **Seed source** This line provides information on the seed sources (premises initially infected to begin simulations). The default of **allFips** will perform a simulation originating in each county present in the premises file (line 11, FLAPS), choosing a random premises within that county as the seed source. Alternatively, you can provide the name of a tab-delimited file containing identifiers (FIPS codes or premisesIDs) from which to seed infection, one line per simulation. You may also seed from multiple premises at once by providing comma-separated premisesIDs in the file (one line per simulation).

(22) **Seed file type** This describes the information provided in line 21.

- **fips** = choose 1 premises at random within the FIPS code on a given line in (21) or in all FIPS [default]

- **singlePremises** = use the premisesID provided on a given line in (21)
- **multiplePremises** = use all comma separated premisesIDs on a given line in (21)

(23) Unused

(24) **Susceptibility exponents (mu)** Comma-separated positive numeric values indicating the exponent value for susceptibility for each species/host type, in the same order as listed in line 12. This value is μ in calculating susceptibility of a premises with h animals of a given species as ah^{μ} (not including scaling adjustments). Default is 1,1.

(25) **Infectiousness exponents (omega)** Comma-separated positive numeric values indicating the exponent value for infectiousness for each species/host type, in the same order as listed in line 12. This value is ω in calculating infectiousness of a premises with h animals of a given species as bh^{ω} (not including scaling adjustments). Default is 1,1.

(26) **Susceptibility constants (a)** Comma-separated positive numeric values indicating the indicating the constant value for susceptibility for each species/host type, in the same order as listed in line 12. This value is a in calculating susceptibility of a premises with h animals of a given species as ah^{μ} (not including scaling adjustments). Default is 1,1.

(27) **Infectiousness constants (b)** Comma-separated positive numeric values indicating the constant value for infectiousness for each species/host type, in the same order as listed in line 12. This value is b in calculating infectiousness of a premises with h animals of a given species as bh^{ω} (not including scaling adjustments). Default is 5.8,5.8.

(28) **Kernel type for local (diffusion) spread**

- **0** = Form of kernel describing local spread is $k1/(1 + (distance/k2)^{k3})$ [default]
- **1** = Data-based kernel describing local spread is in file in line 30
- **2** = Form of kernel describing local spread is $k1/(1 + distance/k2)^{k3}$

(29) **Kernel parameters** Comma-separated positive numeric values for kernel parameters k1, k2, k3 as described in line 28, if applicable. Default is 1.293833e-08,2116.798,2.38

(30) **Data kernel file** Path and name of file containing data-based kernel referred to in line 28, with columns of distance (in same units as premises x/y) and associated probability of exposure.

(31) **Latency duration** Two comma-separated positive numeric values describing the mean and variance about a normal distribution for the number of days from premises exposure to infectiousness. Outcomes less than one are set equal to one. Default is 5,0.

(32) **Infectiousness duration** Two comma-separated positive numeric values describing the mean and variance about a normal distribution for the number of days from premises infectiousness to immunity. Outcomes less than one are set equal to one. Default is 7,0.

(33) Additional functionality under development. Do not change default value [0].

(34) Additional functionality under development. Do not change default value [*].

(35) Unused

(36) **Grid cell file** Filename containing grid cells (will override other options)

(37) **Grid cell length** Length of cell side for uniform cells (will override density options)

(38) **Grid cell options** Two comma-separated positive integers specifying a maximum number of premises per cell and minimum side length of a grid cell (same units as premises x/y). This is used to generate grid cells. Default is 500,100000.

(39) Unused

(40) Unused

(41) **Shipment generation method** Method(s) to generate county-county shipments using USAMM, comma-separated

- **1** = USAMM version 1 [default]
- **-1** = shipments off

(42) **Shipment method time** Comma-separated timepoints at which to begin using each of the methods above. First timepoint must be 1.

(43) Additional functionality under development. Do not change default value [0].

(44) **Parameter files** Output files from USAMM with parameters for a, b, N, s and covariates. Default is inputfiles/usammv1_beef.res, inputfiles/usammv1_dairy.res

(45) Additional functionality under development. Do not change default value [Q1].

(46) Additional functionality under development. Do not change default value [1].

(47) **Origin covariates** Covariates for all origin counties. One file for each species, comma separated. Must have header: FIPS, name1, name2... Names must match name component of covariate parameters in USAMM parameter file (line 44). Default is *,*.

(48) **Destination covariates** Covariates for all destination counties. One file for each species, comma separated. Must have header: FIPS, name1, name2... Names must match name component of covariate parameters in USAMM parameter file (line 44). Default is *,*.

(49) Disabled

(50) **Exposed shipments** If enabled, shipping from a farm with "exposed" status will cause the receiver to become exposed as well.

- **1** = on [default]
- **0** = off

There are two sections defining control actions. Lines 51-61 define attributes of particular control actions. Within this section, attributes for each control action must be listed in the same order as they initially appear in line 51. Lines 63-67 define how and when those control actions are applied.

(51) **Control types** Comma-separated names for unique control types. Options (which can be combined) are listed below. Based on this line's input there are restricted entries on other lines. These are also listed below.

- * turns off control. This option over-rides all others in this section.

- **shipBan**: Shipment (movement) ban
    - Line 52's section for this control type should be **noLimit**
    - Line 53's section for this control type should be **0**
    - Line 54's section for this control type should be either **county** or **state**
    - Lines 55 and 56's sections for this control type should be **NA**
- **cull**: Cull
    - Line 53's section for this control type will be interpreted as parameters for a daily per premises limit on numbers of animals that can be controlled
    - Line 54's section for this control type should be **premises**
- **vax**: Vaccination
    - Line 53's section for this control type will be interpreted as parameters for a daily per-premises limit on numbers of animals that can be controlled
    - Line 54's section for this control type should be **premises**

(52) **Constraint types** Comma-separated names for constraint types to apply to each control type, in the same order as listed in line 51. Options are listed below. Based on this line's input there are restricted entries on other lines. These are also listed below.

- **noLimit**: Any premises targeted for a particular control action will have that control type immediately implemented in the same timestep
    - Line 53's section for this control type should be **0**
    - Lines 55 and 56's sections for this control type should be **NA**
- **stateSum**: Premises within the same state all draw on a summed pool of resources for that state. Additionally, daily constraints will limit the number of animals per day that can be controlled.
    - Line 53's section for this control type should be the mean and variance for daily per premises limits on numbers of animals that can be controlled
    - Line 55's section for this control type should be resources to be summed by state
    - Line 56's section for this control type should be **resourceLocs**
- **dailyLimit**: Premises are limited to having some number of animals controlled per day, but there are no additional constraints.

- Line 53's section for this control type should be the mean and variance for daily per premises limits on numbers of animals that can be controlled
- **maxDistance**: A string combining "maxDistance" with a number denoting the radius for the farthest possible control resource, for example 'maxDistance50000'. This radius is in the same units as premises coordinates. For a given premises, the nearest available resource within the maximum distance will be assigned. Additionally, daily constraints will limit the number of animals per day that can be controlled. If no resources within the specified distance are available, control will not be performed for that premises
  - Line 53's section for this control type should be the mean and variance for daily per premises limits on numbers of animals that can be controlled
  - Line 55's section for this control type should be resources and their locations.
  - Line 56's section for this control type should be **resourceLocs**

(53) **Constraint parameters** Semicolon-separated list of numeric parameters to apply to control constraints, in the same order as listed in line 51. Multiple parameters to be applied to a given constraint should be comma-separated. Currently, the only constraint parameters provided here are the mean and variance of a daily per-premises limit on numbers of animals that can be controlled. The constraint parameters provided here are the mean and variance of animals that can be controlled. For example, the values for the stateSum constraint are the mean maximum number of animals per day per premises that can be culled, which is calcualted as 20 cows/hr*12 hrs/day = 240. The variance is set at 0. The default mean vaccination constraint is 6804, with variance 0.

(54) **Spatial scale** Scale at which each control type should be applied. Possible options are:

- **state**: Currently can only be specified with control type "shipBan"
- **county**: Currently can only be specified with control type "shipBan"
- **premises**: The only valid specification for control types "cull" and "vax"

(55) **Additional constraint files** Semicolon-separated list of paths and names of files containing additional information to use for control constraints, in the same order as listed in line 51. Multiple files to be applied to a given constraint should be comma-separated. Currently only accepts landfill locations for control type "cull". For control types other than "cull", enter **NA**.

(56) **Additional constraint type** Types of information provided in line 55, also semicolon separated by type and comma separated for multiple files to be applied to the same control type. Currently only accepts **resourceLocs** for landfill locations for control type "cull". For control types other than "cull", enter **NA**.

(57) **Mean effectiveness lag** Mean number of days from the control type being implemented to becoming effective (when transmission is affected). Comma-separated positive numeric values, one for each control type in the order listed in line 51, indicating the mean (about a normal distribution). The realized number of days will be drawn from a distribution based on this and line 58, and rounded to the nearest integer. Outcomes less than one are set equal to one. The default for **shipBan** and **cull** is 0, and for **vax** is 11.

(58) **Variance effectiveness lag** Variance in the number of days from the control type being implemented to becoming effective (when transmission is affected). Comma-separated positive numeric values, one for each control type in the order listed in line 51, indicating the variance (about a normal distribution). The realized number of days will be drawn from a distribution based on this and line 57, and rounded to the nearest integer. Outcomes less than one are set equal to one. Defaults are 0 for all control types.

(59) **Mean inactivation lag** Mean number of days for which the control type is effective before becoming inactive (when transmission is no longer affected). Comma-separated positive numeric values, one for each control type in the order listed in line 51, indicating the mean (about a normal distribution). The realized number of days will be drawn from a distribution based on this and line 60, and rounded to the nearest integer. Outcomes less than one are set equal to one. For control types that should be effectively permanent, set this value higher than the value in line 13. The default for **shipBan** and **cull** is 366, and for **vax** is 183.

(60) **Variance inactivation lag** Variance (about a normal distribution) in the number of days for which the control type is effective before becoming inactive (when transmission is no longer affected). Comma-separated positive numeric values, one for each control type in the order listed in line 51, indicating variance (about a normal distribution). The realized number of days will be drawn from a distribution based on this and line 59, and rounded to the nearest integer. Outcomes less than one are set equal to one. Defaults are 0 for all control types.

(61) **Control effectiveness** Effectiveness (including compliance) of control types. Pairs of proportions (numeric values in [0,1]) separated by commas, semicolon-separated by control type. The first value in the pair is the control type's probability of preventing exposure in a given transmission event. The second value in the pair is the control type's probability of preventing transmission from an infectious premises in a given transmission event. For control type "shipBan", the first and second numbers should be the same and indicate the probability of a a shipment not occurring due to the ban.

(62) Unused

(63) **Trigger type** Triggers that cause a control action to be applied. Options include

- **newPremReportsOverX** = Control will be triggered when the number of premises reported in a timestep exceeds the value specified in line 64.
- **newRegionReportsOverX** = Control will be triggered when the number of regions (counties or states as specified in line 54) reported in a timestep exceeds the value specified in line 64.

(64) **Trigger value** Comma-separated positive integer values, one for each trigger specified in line 63. Trigger thresholds over which control actions in line 63 should be applied.

(65) **Trigger control** Comma-separated control types to be applied for each trigger specified in line 63 (in the same order). Only control types specified in line 51 can be used.

Additional triggers may be added to apply the same control type in different situations (i.e. to cull both reported premises and dangerous contacts).

(66) **Response targets** Comma-separated control response targets, in the same order as the triggers specified in line 63.

- **-1** = apply triggered control type to dangerous contacts of reported farms
- **0** = apply triggered control type to reported farms
- **Positive integer** = radius in units of x/y coordinates of premises (usually meters)

(67) **Prioritization** Comma-separated prioritization methods for adding to control waitlists, in the same order as the triggers specified in line 63. Currently only accepts **earliest** for each control type.

(68) Unused

(69) Unused

(70) Unused

Reporting and Tracing (DC) settings (lines 71-75)

(71) **Index reporting lag** Two comma-separated positive numeric values describing the mean and variance about a normal distribution for the number of days from index premises exposure (the first case) to reporting. Outcomes less than one are set equal to one. Default is 15,0.

(72) **Reporting lag** Two comma-separated positive numeric values describing the mean and variance about a normal distribution for the number of days from premises exposure to reporting, if the premises has NOT been designated as a dangerous contact. Outcomes less than one are set equal to one. Default is 8,0.

(73) **DC reporting lag** Two comma-separated positive numeric values describing the mean and variance about a normal distribution for the number of days from premises exposure to reporting, if the premises HAS been designated as a dangerous contact. Outcomes less than one are set equal to one. Default is 2,0.

(74) **DC scaling** Dangerous contact scaling parameters relative to risk. Only used if at least one value in line 66 is -1, i.e. if dangerous contacts are a specified control target. Comma-separated pairs of a string and a numeric value >=1, semicolon separated. The string is the disease status for which the scaling constant will apply, and the number is the scaling constant. Generally, there will be two pairs, one each for statuses **sus** and **exp**. The value for 'exp' generally will be higher than the value for 'sus', indicating that premises are more likely to be identified as dangerous contacts if they truly are exposed at the time of this identification than if they are not. Default is **sus,4; exp,5**

(75) Unused

Generating input files

File types required to run the model

Each model run requires three types of files:

- config files, discussed above, include information about run type and the associated parameters. Each simulation requires a configuration file. A standard run, during which each of 10 FLAPS iterations is seeded 10 times per county, requires 100 configuration files. Most of the regularly-modified options in the config files can be changed using the pre-processing R script. Details for editing options using the script are below. An example configuration file was shown above, and an example file for each control type can be found in the Appendix.

- BATCH files are used in a high-performance, parallel computing environment to specify computing parameters, such as the run priority, memory allowed, and maximum runtime when running a config file. Each config file has a corresponding BATCH file. The BATCH files are generated automatically using the pre-processing script. Config file names are updated automatically, but if the user wishes to change run options (memory, etc.), that must be done manually by manipulating the template BATCH file (SH_FILE_TEMPLATE.txt in the templates folder). An example BATCH file is below.

```
#!/bin/bash

##SBATCH -J MI_f01_01

#SBATCH -t 24:00:00
#SBATCH -n 6
#SBATCH -o MI_f01_01.out
#SBATCH -e MI_f01_01.err
#SBATCH --partition smem

#

module load gcc/6.1.0
./USDOSv2_new config_IP_VAX_10km_MvmtBan90_flaps12_0001_min_01_20180925.txt


# End of script, no wait needed
```

- A job file is used to run all the BATCH files, which in turn run the config files. This file is also generated automatically using the pre-processing script. The first five lines of an example file are below.

```
sbatch BATCH_IP_VAX_10km_MvmtBan90_flaps12_0001_min_01_20180925.sh
sbatch BATCH_IP_VAX_10km_MvmtBan90_flaps12_0001_min_02_20180925.sh
sbatch BATCH_IP_VAX_10km_MvmtBan90_flaps12_0001_min_03_20180925.sh
```

```
sbatch BATCH_IP_VAX_10km_MvmtBan90_flaps12_0001_min_04_20180925.sh
sbatch BATCH_IP_VAX_10km_MvmtBan90_flaps12_0001_min_05_20180925.sh
```

Using the pre-processing code to generate required input files

All three types of file (config, batch, and job) are generated using the 'createConfig_Function.R' pre-processing script. The **options** listed below are items in the configuration file that can be set within the `createConfigs()` function in the 'createConfig_Function.R' pre-processing script. For example, the basic command to generate files for an IP & DC cull run with a 90% effective movement ban is `createConfigs(sim_type="IPDCcull",ban_eff = 0.9)`. The options below are grouped according to their location in the config file. Options in the first section, "File locations & run settings", are not found in the config file but are used to set general options for USDOS.

File locations & run settings

template.config.location The location of the template for the config file. Default is a 'templates' folder within the current working directory. The correct template will be selected based on the **sim_type** (see Control-related settings).

sh_template The location of the SH_FILE_TEMPLATE.txt file. Default is the 'templates' folder. Any changes to computing options (priority, memory allocation, etc.) should be made in this template. The relevant config file name will then be inserted by the pre-processing script.

jobfile.name The name of the jobfile to output. Default is 'USDOS_Sim.job'.

reps The number of times each FLAPS will be repeated. The default value is 10, for a total of 100 runs.

destination.folder The location to put all generated files. Folder must already exist. Default is the current working directory.

replacement.df The dataframe containing all information to use to modify the default config file. This is created with the time, date, and replacement_df as its title.

General settings

flaps The subname of the FLAPS version being used. For example, '12_min' will use the files 'flaps12_min_0001.txt' to 'flaps12_min_0010.txt'.

cutoff_days The number of timesteps (days) to run for each seeded outbreak. Default is 365. Corresponds to line 13 in the config file.

cutoff The max number of infectious premises to allow before stopping each outbreak. The default '*' indicates no limit. Corresponds to line 14 in the config file.

fips.info Name of file containing fips name, state name, area (m2), x, y. Tab separated. Default is "inputfiles/FIPS_20151805.txt" Corresponds to line 18 in the config file.

Infection-related settings

source The source FIPS to be seeded, filename, or 'allFips'. Filename is of the tab-delimited file containing the FIPS codes or premisesIDs from which to seed infection, one line per simulation. 'allFips' [default] will seed from all counties containing premises. Seeding from multiple premises at once requires comma-separated premisesIDs in a file, one line per simulation. Corresponds to line 21 in the config file.

filetype The seed file type - type of information provided per line of source. 'fips' [default] will choose 1 premises at random within the FIPS codes listed in the source parameter or in all FIPS, 'singlePremises' will use the premisesID provided by the source parameter, 'multiplePremises' will seed all comma separated premisesIDs in the source parameter. Corresponds to line 22 in the config file.

Tc The infectiousness constant. Default is 5.8. Corresponds to line 27 in the config file.

k1 Kernel parameter 1. Default is 1.293833e-08. Corresponds to the first value in line 29 of the config file.

k2 Kernel parameter 2. Default is 2116.798. Corresponds to the second value in line 29 of the config file.

k3 Kernel parameter 3. Default is 2.38. Corresponds to the third value in line 29 of the config file.

latency The mean days from premises exposure to infectiousness. Default is 5 days. Corresponds to the first value in line 31 in the config file.

infectious The mean days from premises infectiousness to immunity. Default is 7 days. Corresponds to the first value in line 32 in the config file.

Shipment-related settings

shipment.gen Method to generate county-to-county shipments with USAMM (1 = USAMM version 1, -1 = shipments off). Corresponds to line 41 in the config file.

Control-related settings

sim_type Specifies the control to be initiated. This value changes the default values for specific additional parameters. This modifies line 51 of the config file, as well as associated options listed below.

- The default value is 'base', indicating no controls will be implemented.

- 'IPcull' will by default change **ctrl_type** to 1, indicating cull of infected premises
- 'IPDCcull' will by default change **ctrl_type** to 2, indicating cull of infected premises and dangerous contacts, and will set **vax_range** to -1 to indicate an action for DCs
- 'cullVax' will change **ctrl_type** to 3, **vax_eff** to 1, **vax_delay** to 11, and **vax_range** to NULL.

- 'vax' will change **ctrl_type** to 4, **vax_eff** to 1, **vax_delay** to 11, and **vax_range** to NULL.

landfill.files Set to TRUE if there is a unique landfill file for each FLAPS file. TRUE will require landfill files named "landfill_{filename of flaps}.txt"
(e.g. 'landfills_flaps12_min_0001.txt'. Otherwise, set to FALSE and the file name listed in the config template file will be used. If the movement ban has a file associated, set to false and manually enter into the config file template. Used in line 55 of the config file.

ban_eff The effectiveness of the movement ban put into place on shipments. The value is between 0 and 1, with a default value of 0 for no movement ban. 1 indicates a 100% movement ban. Contributes to line 61 in the config file.

vax_eff The effectiveness of the vaccination. The value is between 0 and 1, and is only in effect if a vaccination control type is selected. The default value is 1 for 100% effectiveness. Contributes to line 61 in the config file.

vax_delay The length of time, in days, between vaccination and vaccine effectiveness. This is only in effect if a vaccination control type is selected. Contributes to line 57 in the config file.

vax_range The range of the vaccination ring. The default value is '-1', indicating that the vaccination is applied to dangerous contacts, not in a ring. A positive number indicates a ring vaccination, in meters. This is only in effect if a vaccination control type is selected. Used in line 66 of the config file.

Pre-processing steps

1. Edit the pre-processing R script using `nano createConfig_Function.R`

2. Run 'createConfig_Function.R' to generate the required config, batch, and job files

```
module load R/3.5.0
Rscript createConfig_Function.R
```

Additional simulation options

- Generate FLAPS files if not using nationwide FLAPS2007 or FLAPS2012 files
    - i) To select a subset of states, use 'CreateSubGeography.R'
    - ii) 'Reformat_FLAPS_realizations.R' is available to merge beef, dairy, and feedlot FLAPS files.
    - iii) FLAPS files should be contained in a /FLAPS/ folder in the directory containing the USDOS run program.
- Determine counties to be seeded from one of the following:
    - i) Use the default value of 'allFips' to seed all counties
    - ii) Generate random counties with 'County_Selection_USDOS_Sensitivity.R'
    - iii) Use previously generated sensitivity counties in 'County_Selection_shortlist_August2017.csv'
    - iv) Create a .csv list of desired counties to be seeded. This can be a custom list, or can be generated from subset geography using 'CreateSubGeography.R'
- To conduct sensitivity analysis, randomize parameters with 'LH_Parameters.R' or use the previously generated random parameter values with 'LHS_Parameters.csv.' The generated 'LHS_Parameter_Summary.csv' file gives information on the parameter values that were randomized.

Running the model

1. Make sure the job, batch, and config files are saved in the folder containing the USDOS run program. Note: This folder should also contain the /inputfiles, /include, and /FLAPS folders

2. Load required modules

```
module load gcc/6.1.0
module load gsl/2.1
```

3. Compile the run program with `make` *Note: if you have made changes since the previous run, use* `make clean` *to remove the previous program, then* `make` *to re-generate it*

4. Run the program

```
chmod a+x jobname.job
./jobname.job
```

Running the `./jobname.job` command above should result in a list of 100 (per run) lines reading "Submitted batch job [a number]"

5. Check that the run is working
    i)   Check your working directory for .err and .out files ('MI_**_fxx_xx.err/.out')
         a. If nothing is present, check your queue-your job may not have been allocated computing time yet.
         b. If present, check these files using `nano [file name]`
             1) .err files should be blank
             2) .out files should list steps the process has completed. *Note: These steps take some time to complete, so what you see in the .out file will vary depending on how far along the process is.*
    ii) If the .err and .out files look good, wait for the runs to complete.

Output files

Four types of files are generated by the model. Each of these output file types contains different information about the simulations.

The .err and .out files display information on the run itself: the .err file records any errors during model runs, while the .out file records step taken during the run. This includes the time to initialize various model components and information on the outbreaks resulting from the seeded infection. The information in these files is not intended for analysis, but is useful for diagnosing issues while running the models.

The detail and summary files contain the results. The detail file contains one line per exposure event, whereas the summary file contains one line per replicate.

The summary file contains information about the number of infected premises and counties, the outbreak duration, seed premises and FIPS, and whether control measures were implemented and effective. Summary file columns and descriptions are below. The first seven columns will be in the summary files for all run types, but the control-specific columns are ommitted if that control type is not used.

Summary file variable name	Description
Rep	The replicate number. One per seed unit (usually a county)
Num_Inf	The number of premises/animals infected
nAffCounties	The number of counties affected
Duration	The length (in days) of the simulation, from the first time a premises is infected until there are no more infectious premises.
Seed_Farms	The premises where infection was seeded (usually one per replicate, chosen randomly from within the seed county)
Seed_FIPS	The FIPS code of the county seeded with infection
RunTimeSec	The computation time (in seconds) taken to run the outbreak
shipBanImplemented	The number of geographical units (state or county, as specified by your parameters) in which a movement ban was implemented. This column is only present for runs with a Shipment Ban.
shipBanEffective	The number of geographical units (state or county, as specified by your parameters) in which a movement ban was effective. This column is only present for runs with a Shipment Ban.
cullImplemented	The number of premises on which culling was implemented. This column is only present for runs with Culling.

cullEffective	The number of premises on which culling was effective. This column is only present for runs with Culling.
vaxImplemented	The number of premises on which vaccination was implemented. This column is only present for runs with Vaccination.
vaxEffective	The number of premises on which vaccination was effective. This column is only present for runs with Vaccination.
cullImplementedDCSubset	The number of DC culls. This column is only present for runs with DC Culling.
meanDCsPerRP	The mean number of DCs identified per reported premises. This column is only present for runs with DC Culling.

The detail file contains information on the source and exposed premises and county, time and route of exposure, and whether/how the exposure was prevented. Detail file columns and descriptions are below.

Detail file variable name	Description
Rep	The replicate during which the exposure occurred
ExposedID	The exposed premises
atTime	The simulation day on which exposure occurred
SourceID	The infectious premises that exposed the ExposedID premises
InfRoute	The route of infection (0 = local spread, 1 = shipment spread)
ControlPrevented	Was this exposure prevented by a control measure. "none" signifies a successful exposure event, while the name of a control measure (ex "shipBan") indicates that the exposure was prevented by that control measure. "src" indicates the control measure was applied to the source premises, whereas "exp" indicates control applied to the exposed premises. "src:vax" therefore indicates a potential exposure that was prevented by vaccination of the source premises.
ExposedCounty	The FIPS code of the exposed county
SourceCounty	The FIPS code of the source county

Post-processing

When the run is completed, extract all run-associated files and save them in a directory with the 'post-processing.R' code:

- Input files
    - config
    - BATCH
    - .job
    - Runlog.txt
- Output files
    - .err
    - .out
    - _detail.txt
    - _summary.txt

You can process the detail and summary files using the post-processing code 'post-processing.R'. For each of the metrics described below, this code will generate a .csv file that contains metric-specific data from all summary and/or detail files and .jpeg files that include histograms, violin plots, and maps of the results for that metric. These files can be inserted into a Report that collates and describes the results using the 'USDOS_Results_Report.Rmd' file.

Metrics generated during post-processing:

- **Number of infected premises**: The national total number of infected and reported premises.
- **Number of cattle infected**: The national total number of infected and reported cattle.
- **Number of infected counties**: The total number of counties infected when infection is seeded in that county, also known as epidemic extent.
- **County risk**: The proportion of simulations in which a county is infected, not including simulations in which infection was seeded in that county.
- **Duration**: The bumer of days between the initial seed infection and when there are no more infected premises, or 365 days, whichever happens sooner.
- **Proportion local transmission**: The proportion of transmission events at the county level that result from local transmission (as opposed to shipment spread)

Additional Information

Abbreviations & Acronyms

Base: A run with no control implemented

DC: Dangerous Contact

FIPS: Federal Information Processing Standard

FLAPS: Farm Location and Animal Population Simulator

IP: Infected Premises

IP cull: A type of control run that implements culling of IPs

IP & DC cull: A type of control run that implements culling of IPs and DCs

IP cull & DC vax: A type of control run that implements culling of IPs and vaccination of DCs

IP cull & XXkm vax: A type of control run that implements culling of IPs and vaccination of premises with a radius of XX kilometers.

SFTP: Secure File Transfer Protocol

USAMM: United States Animal Movement Model

USDOS: United States Disease Outbreak Simulation

VAX: Vaccine/vaccinated/vaccination

Definitions

Cull: To depopulate the animals on a permises.

Dangerous Contact (DC): Premises that have an epidemiological link to the infected premises or are at a higher risk of infection from infected premises.

FIPS code: A five-digit code assigned to each US county. The first two digits indicate the state, and the final three are county-specific.

Infected Premises (IP): Premises that are infected and have been detected and reported.

Movement ban: A prohibition on animal movements, here implemented at the state or county level.

(Ring) Vaccination: Vaccination in a solid circle centered on the IP. Rings of radius 3 or 10 kilometers are commonly used in modeling studies and encompass a good range of possible ring sizes. The optimum ring size for controlling the UK 2001 outbreak was predicted to be around 10Km (Tildesley, et al. 2006). Currently, vaccinations are prioritized by the time when a premises was identified as requiring vaccination. This does not follow either the 'outside-in' or 'inside-out' vaccination method. Vaccination is currently vaccination to die.

Model file descriptions

File Group	File Type	File Naming Pattern	File Contents
Input files			
	Config(uration)	config_**.txt	The parameters used for a set of model runs.
	Batch	BATCH_**.sh	The computing options for the runs. There is one batch file per config file.
	Job	**.job	The master queuing file that runs all the batch files.
Output files			
	Error	MI_**_fxx_xx.err	The errors generated while running a given config file. Will be empty for a successful run.
	Out	MI_**_fxx_xx.out	Information on the steps for each config file and the time they took. Will be large for a successful run. May also contain helpful error messages showing where a run stopped.
	Detail	**_detail.txt	One line per exposure containing information the replicate generating the exposure, the source and exposed premises and county, time and route of exposure, and whether/how the exposure was prevented. Additional details on this file's contents can be found here.
	Summary	**_summary.txt	One line per replicate containing information replicate runtime, the number of infected premises and counties, the outbreak duration, seed premises and FIPS, and whether control measures were implemented and effective. Additional details on this file's contents can be found here.

Troubleshooting

Pre-processing

">50 warnings of"In readLines(template.config.location) : incomplete final line found on templates/USDOS_CONFIG_TEMPLATE_NoControls_workaround.txt'"

- Incomplete final line in template: open the file, hit return after last line, save and close.

Running the model

Can't access BATCH files

- Check in R code that `allFips` is correctly capitalized (is not "allfips")
- Make sure FLAPS names are right in R code ("12_min")

Compile fail

- Check that your makefile shows the following, and edit if not using `nano makefile`:

```
CC        =g++
CFLAGS    =-c -std=gnu++11 -Wall -O3 -I/curc/sw/gsl/2.1/gcc/6.1.0/include
LDFLAGS   =-lstdc++ -L/curc/sw/gsl/2.1/gcc/6.1.0/lib -lgsl -lgslcblas -lm
INCLUDE   =-I./include/
OBJDIR    =obj/

# Backslash for linebreak, and comment is #, but beware, it affects the *whol
e* line.
OBJLIST   = Point.o Farm.o Alias_table.o Shipment_kernel.o \
                    Region.o County.o State.o Grid_cell.o Grid_checker.o
\
                    Grid_manager.o Status_manager.o shared_functions.o \
                    File_manager.o main.o Control_manager.o Shipment_mana
ger.o \
                    Local_spread.o Control_resource.o USAMM_parameters.o
Population_manager.o

OBJECTS   = $(addprefix $(OBJDIR), $(OBJLIST) )

all:USDOSv2_new

USDOSv2_new: $(OBJECTS)
        $(CC) $(LDFLAGS) $(OBJECTS) -o $@

$(OBJECTS): ./$(OBJDIR)%.o: src/%.cpp
        $(CC) $(CFLAGS) $? -o $@ $(INCLUDE)

clean:
        rm obj/*.o
```

- If your makefile is correct and it is still failing to compile, you will need to change the #include <gsl_xxxx.h> and #include "gsl_xxxx.h" lines to #include <gsl/gsl_xxxx.h> and #include "gsl/gsl_xxxx.h" in the following files:
    - include/County.h
    - include/State.h
    - include/Shipment_manager.h
    - src/County.cpp
    - src/State.cpp
    - src/Shipment_manager.cpp
    - *Note: If the error looks anything like items that you are supposed to change when updating, follow these instructions*
- Always double check the makefile if you get further errors. Any time it errors and a restart of 'make' is needed, use:

```
make clean
make
```

The model runs, but only produces .err and .out files

- Look into these files
- If the last line refers to a file, re-download it and try again (might have an end of line error)

Appendix: Example configuration files

This section includes an example configuration file for each of the standard run types: Base (no control), IP culling, IP & DC culling, IP Culling & DC vaccination, and IP culling & ring vaccination

Base (no control)

```
## One variable per row, comments start with #
## Empty rows ignored. Rows with numbers and without descriptions are placeho
lders for future variables.
## Arguments not provided should be replaced with '*'.
## Values in parentheses are the index in the vector where value is stored.
## '~' after the value indicates that this value is required
## '+' after the value indicates that one of these adjacent options is requir
ed
## 'x' after the value indicates that this feature is not yet functional


###################### Output settings #######################
base_flaps12_min_0001_01_20190513_ #(1) Batch name, used as prefix for output
files. Only letters, numbers and underscore.
1 #(2) Summary output on/off (1/0) - one line per replicate with # infected,
duration, seed info, run time
1 #(3) Detailed infection output on/off (1/0) - one line per exposed premises
with time, source of infection, route of infection
0 #(4) Print grid cells on/off
0 #(5)xAdditional functionality under development. Do not change default valu
e.
0 #(6)xAdditional functionality under development. Do not change default valu
e.
* #(7)
* #(8)
* #(9)
* #(10)


###################### General settings #######################
FLAPS/flaps12_min_0001.txt #(11)~Name of file containing premises ID, FIPS, x
, y, population - ie FLAPS_beefdairy_20151201_formatted.txt. Make sure the pr
emises file doesn't have numbers in 1e+05 format (may happen with IDs)
beef,dairy          #(12)~List of species for which counts are provided in pr
emises file, comma-separated
365 #(13)~Timesteps (days) to run
* #(14) Max infectious premises before stopping an outbreak (* = no limit)
1    #(15)~Verbose level: Output extra information to console as model runs (0
=off, 1=basic steps, 2=debug)
0    #(16)x~Disabled
0    #(17)~Reverse x/y option: in case input file is entered as lat/long (y/x)
(set to 1) instead of long/lat (x/y)(set to 0)
inputfiles/FIPS_20151805.txt #(18)~Name of file containing fips name, state n
ame, area (m2), x, y. Tab separated.
```

0   #(19) Day of the year to start simulation/generation on (jan 1 = day 1). Must be 0 - 365. 0 = one random day [1-365].
* #(20)

####################### Infection-related settings #######################
allFips #(21)~Seed source, filename or "allFips". Filename is of file containing identifiers (FIPS codes or premisesIDs) from which to seed infection, one line per simulation. "allFips" specifies to choose from all counties containing premises. To seed from multiple premises at once, provide comma-separated premisesIDs in the file (one line per simulation).
fips #(22)~Seed file type - type of information provided per line of (21). "fips" = choose 1 premises at random within the FIPS code on a given line in (21) or in all FIPS, "singlePremises" = use the premisesID provided on a given line in (21), "multiplePremises" = use all comma separated premisesIDs on a given line in (21)
*   #(23)
1,1 #(24)~Susceptibility exponents(mu), species-specific & comma-separated in order listed in (12) 0.42,0.49
1,1 #(25)~Infectiousness exponents(omega), species-specific & comma-separated in order listed in (12) 0.41,0.2
1,1   #(26)~Susceptibility constants(a), species-specific & comma-separated in order listed in (12) 5.7, 1
10.252,10.252 #(27)~Infectiousness constants(b), species-specific & comma-separated in order listed in (12)0.00082,0.00083
0   #(28)~Kernel type for local (diffusion) spread: 0: k1/(1 + (distance/k2)^k3), 1: data file in (30), 2: k1/(1+d/k2)^k3
1.46e-08,1686.155,2.267 #(29)x~Kernel parameters k1, k2, k3
*   #(30) Name of file containing data-based local spread probabilities by distance, ie inputfiles/UKDataKernel.txt
5,0 #(31)~Mean, variance (around normal) days from premises exposure to infectiousness (latency duration)
7,0 #(32)~Mean, variance (around normal) days from premises infectiousness to immunity (infectiousness duration)
0 #(33)+Additional functionality under development. Do not change default value.
* #(34)+Additional functionality under development. Do not change default value.
* #(35)

####################### Grid-related settings #######################
*   #(36)+Filename containing grid cells (will override other options)
*   #(37)+Length of cell side for uniform cells (will override density options)
500,100000 #(38)+Max farms per cell, cell size minimum side length in m
* #(39)
* #(40)

####################### Shipment-related settings #######################
1 #(41)~Method(s) to generate county-county shipments (USAMM), comma-separated (1 = USAMM version 1, -1 = shipments off)

1   #(42)~Timepoints at which to begin using each of the methods above (first timepoint must be 1), comma-separated
0   #(43)xAdditional functionality under development. Do not change default value.
inputfiles/usammv1_beef.res, inputfiles/usammv1_dairy.res #(44) Output files from USAMM with parameters for a, b, N, s and covariates
Q1 #(45) Additional functionality under development. Do not change default value.
1 #(46) Additional functionality under development. Do not change default value.
, #(47) Origin covariates for all counties. One file for each species, comma separated. Must have header: FIPS, name1, name2... Names must match name component of covariate parameters in USAMM parameter file.
, #(48) Destination covariates for all counties. One file for each species, comma separated. Must have header: FIPS, name1, name2... Names must match name e component of covariate parameters in USAMM parameter file.
, #(49) Disabled
1 #(50) Exposed shipments, shipping from a farm with status exposed will cause the receiver to become exposed as well. 1 = on, 0 = off

###################### Control-related settings ######################
* #(51)~Names for unique control types, comma-separated (fixed options: shipBan, cull, vax) '*' will turn off control.
noLimit,stateSum   #(52) Control constraint function types, comma-separated
0;240,0 #(53) Control constraint parameters, comma-separated parameters, SEMICOLON-separated by type. stateSum: constraint is mean/var max animals/day/premises. 20 cows/hr*12 hrs/day = 240
state,premises #(54)~Spatial scale at which control is applied, comma-separated (fixed options: premises, county (shipBan only), state (shipBan only))
NA;inputfiles/landfills_flaps12_min_0001.txt #(55) List additional files here, comma-separated, SEMICOLON-separated by type
NA;resourceLocs #(56) Specify file types for (55) here: (NA, resourceLocs) comma-separated, SEMICOLON-separated by type
0,0 #(57)~Implemented to effective: mean number of days, comma-separated for each control type
0,0 #(58)~Implemented to effective: variance number of days, comma-separated for each control type
366,366 #(59)~Effective to inactive: mean number of days, comma-separated for each control type
0,0 #(60)~Effective to inactive: variance number of days, comma-separated for each control type
0,0;1,1 #(61)~Effectiveness (including compliance) of control types as proportion, comma-separated probability of preventing exposure given exposure and probability of transmission given infectiousness. SEMICOLON-separated by type.
* #(62)
* #(63)~Control triggers, comma-separated (fixed options). '*' will turn off control.
0,0 #(64)~Control trigger thresholds, comma-separated (numeric)
shipBan,cull #(65)~Control trigger responses, comma-separated (must exist in (51))

```
0,0 #(66)~Control response targets, comma-separated. -1 = DCs, 0 = triggers o
nly, # = radius in units of x/y coordinates of premises
earliest,earliest #(67)~Control response priority, comma-separated. Currently
only accepts earliest for each control type.
* #(68)
* #(69)
* #(70)


####################### Reporting and Tracing (DC) settings ################
########
15,0 #(71)x~Mean, variance days from INDEX premises exposure to reporting
8,0 #(72)~Mean, variance days from (non-dangerous-contact) premises exposure
to reporting
2,0 #(73)~Mean, variance days from (dangerous-contact) premises exposure to r
eporting
sus,4;exp,5 #(74) Dangerous Contact scaling parameters relative to risk: stat
us, then scale, SEMICOLON-separated (only used if at least one of (66) is -1)
* #(75)
```

IP cull

```
## One variable per row, comments start with #
## Empty rows ignored. Rows with numbers and without descriptions are placeho
lders for future variables.
## Arguments not provided should be replaced with '*'.
## Values in parentheses are the index in the vector where value is stored.
## '~' after the value indicates that this value is required
## '+' after the value indicates that one of these adjacent options is requir
ed
## 'x' after the value indicates that this feature is not yet functional


####################### Output settings #######################
IP_MvmtBan_90_flaps12_min_0001_01_20190513_ #(1) Batch name, used as prefix f
or output files. Only letters, numbers and underscore.
1 #(2) Summary output on/off (1/0) - one line per replicate with # infected,
duration, seed info, run time
1 #(3) Detailed infection output on/off (1/0) - one line per exposed premises
with time, source of infection, route of infection
0 #(4) Print grid cells on/off
0 #(5)xAdditional functionality under development. Do not change default valu
e.
0 #(6)xAdditional functionality under development. Do not change default valu
e.
* #(7)
* #(8)
* #(9)
* #(10)


####################### General settings #######################
FLAPS/flaps12_min_0001.txt #(11)~Name of file containing premises ID, FIPS, x
```

, y, population - ie FLAPS_beefdairy_20151201_formatted.txt. Make sure the pr
emises file doesn't have numbers in 1e+05 format (may happen with IDs)
beef,dairy   #(12)~List of species for which counts are provided in pr
emises file, comma-separated
365 #(13)~Timesteps (days) to run
* #(14) Max infectious premises before stopping an outbreak (* = no limit)
1   #(15)~Verbose level: Output extra information to console as model runs (0
=off, 1=basic steps, 2=debug)
0   #(16)x~ Disabled
0   #(17)~Reverse x/y option: in case input file is entered as lat/long (y/x)
(set to 1) instead of long/lat (x/y)(set to 0)
inputfiles/FIPS_20151805.txt #(18)~Name of file containing fips name, state n
ame, area (m2), x, y. Tab separated.
0   #(19) Day of the year to start simulation/generation on (jan 1 = day 1).
Must be 0 - 365. 0 = one random day [1-365].
* #(20)

####################### Infection-related settings #######################
allFips #(21)~Seed source, filename or "allFips". Filename is of file contain
ing identifiers (FIPS codes or premisesIDs) from which to seed infection, one
line per simulation. "allFips" specifies to choose from all counties containi
ng premises. To seed from multiple premises at once, provide comma-separated
premisesIDs in the file (one line per simulation).
fips #(22)~Seed file type - type of information provided per line of (21). "f
ips" = choose 1 premises at random within the FIPS code on a given line in (2
1) or in all FIPS, "singlePremises" = use the premisesID provided on a given
line in (21), "multiplePremises" = use all comma separated premisesIDs on a g
iven line in (21)
*   #(23)
1,1 #(24)~Susceptibility exponents(mu), species-specific & comma-separated in
order listed in (12) 0.42,0.49
1,1 #(25)~Infectiousness exponents(omega), species-specific & comma-separated
in order listed in (12) 0.41,0.2
1,1   #(26)~Susceptibility constants(a), species-specific & comma-separated
in order listed in (12) 5.7,1
10.252,10.252 #(27)~Infectiousness constants(b), species-specific & comma-sep
arated in order listed in (12)0.00082,0.00083
0   #(28)~Kernel type for local (diffusion) spread: 0: k1/(1 + (dista
nce/k2)^k3), 1: data file in (30), 2: k1/(1+d/k2)^k3
1.46e-08,1686.155,2.267 #(29)x~Kernel parameters k1, k2, k3
*   #(30) Name of file containing data-based local spread probabi
lities by distance, ie inputfiles/UKDataKernel.txt
5,0 #(31)~Mean, variance (around normal) days from premises exposure to infec
tiousness (latency duration)
7,0 #(32)~Mean, variance (around normal) days from premises infectiousness to
immunity (infectiousness duration)
0 #(33)+Additional functionality under development. Do not change default val
ue.
* #(34)+Additional functionality under development. Do not change default val
ue.

* #(35)

###################### Grid-related settings ########################
*   #(36)+Filename containing grid cells (will override other opt
ions)
*   #(37)+Length of cell side for uniform cells (will override de
nsity options)
500,100000 #(38)+Max farms per cell, cell size minimum side length in m
* #(39)
* #(40)

###################### Shipment-related settings ########################
1 #(41)~Method(s) to generate county-county shipments (USAMM), comma-separate
d (1 = USAMM version 1, -1 = shipments off)
1   #(42)~Timepoints at which to begin using each of the methods above (first
timepoint must be 1), comma-separated
0   #(43)xAdditional functionality under development. Do not change default v
alue.
inputfiles/usammv1_beef.res, inputfiles/usammv1_dairy.res #(44) Output files
from USAMM with parameters for a, b, N, s and covariates
Q1 #(45) Additional functionality under development. Do not change default va
lue.
1 #(46) Additional functionality under development. Do not change default val
ue.
, #(47) Origin covariates for all counties. One file for each species, comm
a separated. Must have header: FIPS, name1, name2... Names must match name co
mponent of covariate parameters in USAMM parameter file.
, #(48) Destination covariates for all counties. One file for each species,
comma separated. Must have header: FIPS, name1, name2... Names must match nam
e component of covariate parameters in USAMM parameter file.
, #(49) Disabled
1 #(50) Exposed shipments, shipping from a farm with status exposed will caus
e the receiver to become exposed as well. 1 = on, 0 = off

###################### Control-related settings ########################
shipBan,cull #(51)~Names for unique control types, comma-separated (fixed opt
ions: shipBan, cull, vax) '*' will turn off control.
noLimit,stateSum   #(52) Control constraint function types, comma-separated
0;240,0 #(53) Control constraint parameters, comma-separated parameters, SEMI
COLON-separated by type. stateSum: constraint is mean/var max animals/day/pre
mises. 20 cows/hr*12 hrs/day = 240
state,premises #(54)~Spatial scale at which control is applied, comma-separat
ed (fixed options: premises, county (shipBan only), state (shipBan only))
NA;inputfiles/landfills_flaps12_min_0001.txt #(55) List additional files here
, comma-separated, SEMICOLON-separated by type
NA;resourceLocs #(56) Specify file types for (55) here: (NA, resourceLocs) co
mma-separated, SEMICOLON-separated by type
0,0 #(57)~Implemented to effective: mean number of days, comma-separated for
each control type
0,0 #(58)~Implemented to effective: variance number of days, comma-separated

```
for each control type
366,366 #(59)~Effective to inactive: mean number of days, comma-separated for
each control type
0,0 #(60)~Effective to inactive: variance number of days, comma-separated for
each control type
0.9,0.9;1,1 #(61)~Effectiveness (including compliance) of control types as pr
oportion, comma-separated probability of preventing exposure given exposure a
nd probability of transmission given infectiousness. SEMICOLON-separated by t
ype.
* #(62)
newRegionReportsOverX,newPremReportsOverX #(63)~Control triggers, comma-separ
ated (fixed options). '*' will turn off control.
0,0 #(64)~Control trigger thresholds, comma-separated (numeric)
shipBan,cull #(65)~Control trigger responses, comma-separated (must exist in
(51))
0,0 #(66)~Control response targets, comma-separated. -1 = DCs, 0 = triggers o
nly, # = radius in units of x/y coordinates of premises
earliest,earliest #(67)~Control response priority, comma-separated. Currently
only accepts earliest for each control type.
* #(68)
* #(69)
* #(70)


######################### Reporting and Tracing (DC) settings ################
#########
15,0 #(71)x~Mean, variance days from INDEX premises exposure to reporting
8,0 #(72)~Mean, variance days from (non-dangerous-contact) premises exposure
to reporting
2,0 #(73)~Mean, variance days from (dangerous-contact) premises exposure to r
eporting
sus,4;exp,5 #(74) Dangerous Contact scaling parameters relative to risk: stat
us, then scale, SEMICOLON-separated (only used if at least one of (66) is -1)
* #(75)
```

IP & DC cull

```
## One variable per row, comments start with #
## Empty rows ignored. Rows with numbers and without descriptions are placeho
lders for future variables.
## Arguments not provided should be replaced with '*'.
## Values in parentheses are the index in the vector where value is stored.
## '~' after the value indicates that this value is required
## '+' after the value indicates that one of these adjacent options is requir
ed
## 'x' after the value indicates that this feature is not yet functional


######################### Output settings #########################
IP_DC_MvmtBan_90_flaps12_min_0001_01_20190513_ #(1) Batch name, used as prefi
x for output files. Only letters, numbers and underscore.
1 #(2) Summary output on/off (1/0) - one line per replicate with # infected,
```

duration, seed info, run time
1 #(3) Detailed infection output on/off (1/0) - one line per exposed premises
with time, source of infection, route of infection
0 #(4) Print grid cells on/off
0 #(5)xAdditional functionality under development. Do not change default valu
e.
0 #(6)xAdditional functionality under development. Do not change default valu
e.
* #(7)
* #(8)
* #(9)
* #(10)

####################### General settings #######################
FLAPS/flaps12_min_0001.txt #(11)~Name of file containing premises ID, FIPS, x
, y, population - ie FLAPS_beefdairy_20151201_formatted.txt. Make sure the pr
emises file doesn't have numbers in 1e+05 format (may happen with IDs)
beef,dairy   #(12)~List of species for which counts are provided in pr
emises file, comma-separated
365 #(13)~Timesteps (days) to run
* #(14) Max infectious premises before stopping an outbreak (* = no limit)
1   #(15)~Verbose level: Output extra information to console as model runs (0
=off, 1=basic steps, 2=debug)
0   #(16)x~Disabled
0   #(17)~Reverse x/y option: in case input file is entered as lat/long (y/x)
(set to 1) instead of long/lat (x/y)(set to 0)
inputfiles/FIPS_20151805.txt #(18)~Name of file containing fips name, state n
ame, area (m2), x, y. Tab separated.
0   #(19) Day of the year to start simulation/generation on (jan 1 = day 1).
Must be 0 - 365. 0 = one random day [1-365].
* #(20)

####################### Infection-related settings #######################
allFips #(21)~Seed source, filename or "allFips". Filename is of file contain
ing identifiers (FIPS codes or premisesIDs) from which to seed infection, one
line per simulation. "allFips" specifies to choose from all counties containi
ng premises. To seed from multiple premises at once, provide comma-separated
premisesIDs in the file (one line per simulation).
fips #(22)~Seed file type - type of information provided per line of (21). "f
ips" = choose 1 premises at random within the FIPS code on a given line in (2
1) or in all FIPS, "singlePremises" = use the premisesID provided on a given
line in (21), "multiplePremises" = use all comma separated premisesIDs on a g
iven line in (21)
*   #(23)
1,1 #(24)~Susceptibility exponents(mu), species-specific & comma-separated in
order listed in (12) 0.42,0.49
1,1 #(25)~Infectiousness exponents(omega), species-specific & comma-separated
in order listed in (12) 0.41,0.2
1,1   #(26)~Susceptibility constants(a), species-specific & comma-separated
in order listed in (12) 5.7,1

```
10.252,10.252 #(27)~Infectiousness constants(b), species-specific & comma-sep
arated in order listed in (12) 0.00082,0.00083
0          #(28)~Kernel type for local (diffusion) spread: 0: k1/(1 + (dista
nce/k2)^k3), 1: data file in (30), 2: k1/(1+d/k2)^k3
1.46e-08,1686.155,2.267 #(29)x~Kernel parameters k1, k2, k3
*              #(30) Name of file containing data-based local spread probabi
lities by distance, ie inputfiles/UKDataKernel.txt
5,0 #(31)~Mean, variance (around normal) days from premises exposure to infec
tiousness (latency duration)
7,0 #(32)~Mean, variance (around normal) days from premises infectiousness to
immunity (infectiousness duration)
0 #(33)+Additional functionality under development. Do not change default val
ue.
* #(34)+Additional functionality under development. Do not change default val
ue.
* #(35)


###################### Grid-related settings ######################
*              #(36)+Filename containing grid cells (will override other opt
ions)
*              #(37)+Length of cell side for uniform cells (will override de
nsity options)
500,100000  #(38)+Max farms per cell, cell size minimum side length in m
* #(39)
* #(40)


###################### Shipment-related settings ######################
1 #(41)~Method(s) to generate county-county shipments (USAMM), comma-separate
d (1 = USAMM version 1, -1 = shipments off)
1   #(42)~Timepoints at which to begin using each of the methods above (first
timepoint must be 1), comma-separated
0   #(43)xAdditional functionality under development. Do not change default v
alue.
inputfiles/usammv1_beef.res, inputfiles/usammv1_dairy.res #(44) Output files
from USAMM with parameters for a, b, N, s and covariates
Q1 #(45) Additional functionality under development. Do not change default va
lue.
1 #(46) Additional functionality under development. Do not change default val
ue.
*,* #(47) Origin covariates for all counties. One file for each species, comm
a separated. Must have header: FIPS, name1, name2... Names must match name co
mponent of covariate parameters in USAMM parameter file.
*,* #(48) Destination covariates for all counties. One file for each species,
comma separated. Must have header: FIPS, name1, name2... Names must match nam
e component of covariate parameters in USAMM parameter file.
*,* #(49) Disabled
1 #(50) Exposed shipments, shipping from a farm with status exposed will caus
e the receiver to become exposed as well. 1 = on, 0 = off


###################### Control-related settings ######################
```

shipBan,cull #(51)~Names for unique control types, comma-separated (fixed opt
ions: shipBan, cull, vax) '*' will turn off control.
noLimit,stateSum   #(52) Control constraint function types, comma-separated
0;240,0 #(53) Control constraint parameters, comma-separated parameters, SEMI
COLON-separated by type. stateSum: constraint is mean/var max animals/day/pre
mises. 20 cows/hr*12 hrs/day = 240
state,premises #(54)~Spatial scale at which control is applied, comma-separat
ed (fixed options: premises, county (shipBan only), state (shipBan only))
NA;inputfiles/landfills_flaps12_min_0001.txt #(55) List additional files here
, comma-separated, SEMICOLON-separated by type
NA;resourceLocs #(56) Specify file types for (55) here: (NA, resourceLocs) co
mma-separated, SEMICOLON-separated by type
0,0 #(57)~Implemented to effective: mean number of days, comma-separated for
each control type
0,0 #(58)~Implemented to effective: variance number of days, comma-separated
for each control type
366,366 #(59)~Effective to inactive: mean number of days, comma-separated for
each control type
0,0 #(60)~Effective to inactive: variance number of days, comma-separated for
each control type
0.9,0.9;1,1 #(61)~Effectiveness (including compliance) of control types as pr
oportion, comma-separated probability of preventing exposure given exposure a
nd probability of transmission given infectiousness. SEMICOLON-separated by t
ype.
* #(62)
newRegionReportsOverX,newPremReportsOverX,newPremReportsOverX #(63)~Control t
riggers, comma-separated (fixed options). '*' will turn off control.
0,0,0 #(64)~Control trigger thresholds, comma-separated (numeric)
shipBan,cull,cull #(65)~Control trigger responses, comma-separated (must exis
t in (51))
0,0,-1 #(66)~Control response targets, comma-separated. -1 = DCs, 0 = trigger
s only, # = radius in units of x/y coordinates of premises
earliest,earliest,earliest #(67)~Control response priority, comma-separated.
Currently only accepts earliest for each control type.
* #(68)
* #(69)
* #(70)

###################### Reporting and Tracing (DC) settings ################
########
15,0 #(71)x~Mean, variance days from INDEX premises exposure to reporting
8,0 #(72)~Mean, variance days from (non-dangerous-contact) premises exposure
to reporting
2,0 #(73)~Mean, variance days from (dangerous-contact) premises exposure to r
eporting
sus,4;exp,5 #(74) Dangerous Contact scaling parameters relative to risk: stat
us, then scale, SEMICOLON-separated (only used if at least one of (66) is -1)
* #(75)

IP cull & DC vaccination

```
## One variable per row, comments start with #
## Empty rows ignored. Rows with numbers and without descriptions are placeho
lders for future variables.
## Arguments not provided should be replaced with '*'.
## Values in parentheses are the index in the vector where value is stored.
## '~' after the value indicates that this value is required
## '+' after the value indicates that one of these adjacent options is requir
ed
## 'x' after the value indicates that this feature is not yet functional


######################## Output settings ########################
IP_VAX_MvmtBan_90_flaps12_min_0001_01_20190513_ #(1) Batch name, used as pref
ix for output files. Only letters, numbers and underscore.
1 #(2) Summary output on/off (1/0) - one line per replicate with # infected,
duration, seed info, run time
1 #(3) Detailed infection output on/off (1/0) - one line per exposed premises
with time, source of infection, route of infection
0 #(4) Print grid cells on/off
0 #(5)xAdditional functionality under development. Do not change default valu
e.
0 #(6)xAdditional functionality under development. Do not change default valu
e.
* #(7)
* #(8)
* #(9)
* #(10)


######################## General settings ########################
FLAPS/flaps12_min_0001.txt #(11)~Name of file containing premises ID, FIPS, x
, y, population - ie FLAPS_beefdairy_20151201_formatted.txt. Make sure the pr
emises file doesn't have numbers in 1e+05 format (may happen with IDs)
beef,dairy          #(12)~List of species for which counts are provided in pr
emises file, comma-separated
365 #(13)~Timesteps (days) to run
* #(14) Max infectious premises before stopping an outbreak (* = no limit)
1    #(15)~Verbose level: Output extra information to console as model runs (0
=off, 1=basic steps, 2=debug)
0    #(16)x~Disabled
0    #(17)~Reverse x/y option: in case input file is entered as lat/long (y/x)
(set to 1) instead of long/lat (x/y)(set to 0)
inputfiles/FIPS_20151805.txt #(18)~Name of file containing fips name, state n
ame, area (m2), x, y. Tab separated.
0    #(19) Day of the year to start simulation/generation on (jan 1 = day 1).
Must be 0 - 365. 0 = one random day [1-365].
* #(20)


######################## Infection-related settings ########################
allFips #(21)~Seed source, filename or "allFips". Filename is of file contain
ing identifiers (FIPS codes or premisesIDs) from which to seed infection, one
line per simulation. "allFips" specifies to choose from all counties containi
```

ng premises. To seed from multiple premises at once, provide comma-separated premisesIDs in the file (one line per simulation).
fips #(22)~Seed file type - type of information provided per line of (21). "fips" = choose 1 premises at random within the FIPS code on a given line in (21) or in all FIPS, "singlePremises" = use the premisesID provided on a given line in (21), "multiplePremises" = use all comma separated premisesIDs on a given line in (21)
*   #(23)
1,1 #(24)~Susceptibility exponents(mu), species-specific & comma-separated in order listed in (12) 0.42,0.49
1,1 #(25)~Infectiousness exponents(omega), species-specific & comma-separated in order listed in (12) 0.41,0.2
1,1   #(26)~Susceptibility constants(a), species-specific & comma-separated in order listed in (12) 5.7,1
10.252,10.252 #(27)~Infectiousness constants(b), species-specific & comma-separated in order listed in (12)0.00082,0.00083
0   #(28)~Kernel type for local (diffusion) spread: 0: k1/(1 + (distance/k2)^k3), 1: data file in (30), 2: k1/(1+d/k2)^k3
1.46e-08,1686.155,2.267 #(29)x~Kernel parameters k1, k2, k3
*   #(30) Name of file containing data-based local spread probabilities by distance, ie inputfiles/UKDataKernel.txt
5,0 #(31)~Mean, variance (around normal) days from premises exposure to infectiousness (latency duration)
7,0 #(32)~Mean, variance (around normal) days from premises infectiousness to immunity (infectiousness duration)
0 #(33)+Additional functionality under development. Do not change default value.
* #(34)+Additional functionality under development. Do not change default value.
* #(35)

######################## Grid-related settings ########################
*   #(36)+Filename containing grid cells (will override other options)
*   #(37)+Length of cell side for uniform cells (will override density options)
500,100000 #(38)+Max farms per cell, cell size minimum side length in m
* #(39)
* #(40)

######################## Shipment-related settings ########################
1 #(41)~Method(s) to generate county-county shipments (USAMM), comma-separated (1 = USAMM version 1, -1 = shipments off)
1   #(42)~Timepoints at which to begin using each of the methods above (first timepoint must be 1), comma-separated
0   #(43)xAdditional functionality under development. Do not change default value.
inputfiles/usammv1_beef.res, inputfiles/usammv1_dairy.res #(44) Output files from USAMM with parameters for a, b, N, s and covariates
Q1 #(45) Additional functionality under development. Do not change default va

lue.
1 #(46) Additional functionality under development. Do not change default val
ue.
, #(47) Origin covariates for all counties. One file for each species, comm
a separated. Must have header: FIPS, name1, name2... Names must match name co
mponent of covariate parameters in USAMM parameter file.
, #(48) Destination covariates for all counties. One file for each species,
comma separated. Must have header: FIPS, name1, name2... Names must match nam
e component of covariate parameters in USAMM parameter file.
, #(49) Disabled
1 #(50) Exposed shipments, shipping from a farm with status exposed will caus
e the receiver to become exposed as well. 1 = on, 0 = off

###################### Control-related settings ######################
shipBan,cull,vax #(51)~Names for unique control types, comma-separated (fixed
options: shipBan, cull, vax) '*' will turn off control.
noLimit,stateSum,dailyLimit #(52) Control constraint function types, comma-se
parated
0;240,0;6804,0 #(53) Control constraint parameters, comma-separated parameter
s, SEMICOLON-separated by type. stateSum: constraint is mean/var max animals/
day/premises. 20 cows/hr*12 hrs/day = 240
state,premises,premises #(54)~Spatial scale at which control is applied, comm
a-separated (fixed options: premises, county (shipBan only), state (shipBan o
nly))
NA;inputfiles/landfills_flaps12_min_0001.txt;inputfiles/vaccineBankUpdated.tx
t #(55) List additional files here, comma-separated, SEMICOLON-separated by t
ype
NA;resourceLocs;resourceBoosts #(56) Specify file types for (55) here: (NA, r
esourceLocs) comma-separated, SEMICOLON-separated by type
0,0,11 #(57)~Implemented to effective: mean number of days, comma-separated f
or each control type
0,0,0 #(58)~Implemented to effective: variance number of days, comma-separate
d for each control type
366,366,183 #(59)~Effective to inactive: mean number of days, comma-separated
for each control type
0,0,0   #(60)~Effective to inactive: variance number of days, comma-separated
for each control type
0.9,0.9;1,1;0.9,0.9 #(61)~Effectiveness (including compliance) of control typ
es as proportion, comma-separated probability of preventing exposure given ex
posure and probability of transmission given infectiousness. SEMICOLON-separa
ted by type.
* #(62)
newRegionReportsOverX,newPremReportsOverX,newPremReportsOverX #(63)~Control t
riggers, comma-separated (fixed options). '*' will turn off control.
0,0,0 #(64)~Control trigger thresholds, comma-separated (numeric)
shipBan,cull,vax #(65)~Control trigger responses, comma-separated (must exist
in (51))
0,0,-1 #(66)~Control response targets, comma-separated. -1 = DCs, 0 = trigger
s only, # = radius in units of x/y coordinates of premises
earliest,earliest,earliest #(67)~Control response priority, comma-separated.

Currently only accepts earliest for each control type.
* #(68)
* #(69)
* #(70)

####################### Reporting and Tracing (DC) settings ################
########
15,0 #(71)x~Mean, variance days from INDEX premises exposure to reporting
8,0 #(72)~Mean, variance days from (non-dangerous-contact) premises exposure
to reporting
2,0 #(73)~Mean, variance days from (dangerous-contact) premises exposure to r
eporting
sus,4;exp,5 #(74) Dangerous Contact scaling parameters relative to risk: stat
us, then scale, SEMICOLON-separated (only used if at least one of (66) is -1)
* #(75)

IP cull & ring vaccination

One variable per row, comments start with
Empty rows ignored. Rows with numbers and without descriptions are placeho
lders for future variables.
Arguments not provided should be replaced with '*'.
Values in parentheses are the index in the vector where value is stored.
'~' after the value indicates that this value is required
'+' after the value indicates that one of these adjacent options is requir
ed
'x' after the value indicates that this feature is not yet functional

####################### Output settings #######################
IP_VAX_3km_MvmtBan_90_flaps12_min_0001_01_20190513_ #(1) Batch name, used as
prefix for output files. Only letters, numbers and underscore.
1 #(2) Summary output on/off (1/0) - one line per replicate with # infected,
duration, seed info, run time
1 #(3) Detailed infection output on/off (1/0) - one line per exposed premises
with time, source of infection, route of infection
0 #(4) Print grid cells on/off
0 #(5)xAdditional functionality under development. Do not change default valu
e.
0 #(6)xAdditional functionality under development. Do not change default valu
e.
* #(7)
* #(8)
* #(9)
* #(10)

####################### General settings #######################
FLAPS/flaps12_min_0001.txt #(11)~Name of file containing premises ID, FIPS, x
, y, population - ie FLAPS_beefdairy_20151201_formatted.txt. Make sure the pr
emises file doesn't have numbers in 1e+05 format (may happen with IDs)
beef,dairy   #(12)~List of species for which counts are provided in pr

emises file, comma-separated
365 #(13)~Timesteps (days) to run
* #(14) Max infectious premises before stopping an outbreak (* = no limit)
1   #(15)~Verbose level: Output extra information to console as model runs (0
=off, 1=basic steps, 2=debug)
0   #(16)x~Disabled
0   #(17)~Reverse x/y option: in case input file is entered as lat/long (y/x)
(set to 1) instead of long/lat (x/y)(set to 0)
inputfiles/FIPS_20151805.txt #(18)~Name of file containing fips name, state n
ame, area (m2), x, y. Tab separated.
0   #(19) Day of the year to start simulation/generation on (jan 1 = day 1).
Must be 0 - 365. 0 = one random day [1-365].
* #(20)

###################### Infection-related settings ######################
allFips #(21)~Seed source, filename or "allFips". Filename is of file contain
ing identifiers (FIPS codes or premisesIDs) from which to seed infection, one
line per simulation. "allFips" specifies to choose from all counties containi
ng premises. To seed from multiple premises at once, provide comma-separated
premisesIDs in the file (one line per simulation).
fips #(22)~Seed file type - type of information provided per line of (21). "f
ips" = choose 1 premises at random within the FIPS code on a given line in (2
1) or in all FIPS, "singlePremises" = use the premisesID provided on a given
line in (21), "multiplePremises" = use all comma separated premisesIDs on a g
iven line in (21)
*   #(23)
1,1 #(24)~Susceptibility exponents(mu), species-specific & comma-separated in
order listed in (12) 0.42,0.49
1,1 #(25)~Infectiousness exponents(omega), species-specific & comma-separated
in order listed in (12) 0.41,0.2
1,1   #(26)~Susceptibility constants(a), species-specific & comma-separated
in order listed in (12) 5.7,1
10.252,10.252 #(27)~Infectiousness constants(b), species-specific & comma-sep
arated in order listed in (12)0.00082,0.00083
0   #(28)~Kernel type for local (diffusion) spread: 0: k1/(1 + (dista
nce/k2)^k3), 1: data file in (30), 2: k1/(1+d/k2)^k3
1.46e-08,1686.155,2.267 #(29)x~Kernel parameters k1, k2, k3
*   #(30) Name of file containing data-based local spread probabilities b
y distance, ie inputfiles/UKDataKernel.txt
5,0 #(31)~Mean, variance (around normal) days from premises exposure to infec
tiousness (latency duration)
7,0 #(32)~Mean, variance (around normal) days from premises infectiousness to
immunity (infectiousness duration)
0 #(33)+Additional functionality under development. Do not change default val
ue.
* #(34)+Additional functionality under development. Do not change default val
ue.
* #(35)

###################### Grid-related settings ######################

```
*               #(36)+Filename containing grid cells (will override other opt
ions)
*               #(37)+Length of cell side for uniform cells (will override de
nsity options)
500,100000  #(38)+Max farms per cell, cell size minimum side length in m
* #(39)
* #(40)


###################### Shipment-related settings ######################
1 #(41)~Method(s) to generate county-county shipments (USAMM), comma-separate
d (1 = USAMM version 1, -1 = shipments off)
1   #(42)~Timepoints at which to begin using each of the methods above (first
timepoint must be 1), comma-separated
0   #(43)xAdditional functionality under development. Do not change default v
alue.
inputfiles/usammv1_beef.res, inputfiles/usammv1_dairy.res #(44) Output files
from USAMM with parameters for a, b, N, s and covariates
Q1 #(45) Additional functionality under development. Do not change default va
lue.
1 #(46) Additional functionality under development. Do not change default val
ue.
*,* #(47) Origin covariates for all counties. One file for each species, comm
a separated. Must have header: FIPS, name1, name2... Names must match name co
mponent of covariate parameters in USAMM parameter file.
*,* #(48) Destination covariates for all counties. One file for each species,
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```

Acknowledgements & Contact Information

If you have questions or comments regarding USDOS or this User Manual, please contact Dr. Colleen Webb at Colleen.Webb@colostate.edu.