LandR Biomass Module Overview

Alex M. Chubaty

15/08/2019

## LandR Biomass module details

### Biomass\_regeneration

#### Required packages

## $Biomass\_regeneration  
## [1] "SpaDES.core"   
## [2] "crayon"   
## [3] "data.table"   
## [4] "PredictiveEcology/LandR@development"   
## [5] "PredictiveEcology/pemisc@development"  
## [6] "raster"

#### Parameters

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| paramName | paramClass | default | min | max | paramDesc |
| calibrate | logical | FALSE | NA | NA | Do calibration? Defaults to FALSE |
| fireInitialTime | numeric | NA | NA | NA | The event time that the first fire disturbance event occurs |
| fireTimestep | numeric | NA | NA | NA | The number of time units between successive fire events in a fire module |
| successionTimestep | numeric | 10 | NA | NA | defines the simulation time step, default is 10 years |

#### Input objects

|  |  |  |  |
| --- | --- | --- | --- |
| objectName | objectClass | desc | sourceURL |
| cohortData | data.table | age cohort-biomass table hooked to pixel group map by pixelGroupIndex at |  |
| succession time st | ep | NA |  |
| ecoregionMap | RasterLayer | ecoregion map that has mapcodes match ecoregion table and speciesEcoregion table | <https://github.com/LANDIS-II-Foundation/Extensions-Succession/raw/master/biomass-succession-archive/trunk/tests/v6.0-2.0/ecoregions.gis> |
| inactivePixelIndex | logical | internal use. Keeps track of which pixels are inactive | NA |
| pixelGroupMap | RasterLayer | updated community map at each succession time step | NA |
| rstCurrentBurn | RasterLayer | Binary raster of fires, 1 meaning ‘burned’, 0 or NA is non-burned | NA |
| species | data.table | a table that has species traits such as longevity… | <https://raw.githubusercontent.com/LANDIS-II-Foundation/Extensions-Succession/master/biomass-succession-archive/trunk/tests/v6.0-2.0/species.txt> |
| speciesEcoregion | data.table | table defining the maxANPP, maxB and SEP, which can change with both ecoregion and simulation time | <https://raw.githubusercontent.com/LANDIS-II-Foundation/Extensions-Succession/master/biomass-succession-archive/trunk/tests/v6.0-2.0/biomass-succession-dynamic-inputs_test.txt> |
| studyArea | SpatialPolygonsDataFrame | multipolygon to use as the study area, with attribute LTHFC describing the fire return interval. Defaults to a square shapefile in Southwestern Alberta, Canada. |  |
| sufficientLight | data.frame | table defining how the species with different shade tolerance respond to stand shadeness | <https://raw.githubusercontent.com/LANDIS-II-Foundation/Extensions-Succession/master/biomass-succession-archive/trunk/tests/v6.0-2.0/biomass-succession_test.txt> |
| treedFirePixelTableSinceLastDisp | data.table | 3 columns: pixelIndex, pixelGroup, and burnTime. Each row represents a forested pixel that was burned up to and including this year, since last dispersal event, with its corresponding pixelGroup and time it occurred | NA |

#### Output objects

|  |  |  |
| --- | --- | --- |
| objectName | objectClass | desc |
| cohortData | data.table | age cohort-biomass table hooked to pixel group map by pixelGroupIndex at succession time step |
| lastFireYear | numeric | Year of the most recent fire year |
| pixelGroupMap | RasterLayer | updated community map at each succession time step |
| serotinyResproutSuccessPixels | numeric | Pixels that were successfully regenerated via serotiny or resprouting. This is a subset of treedBurnLoci |
| postFireRegenSummary | data.table | summary table of species post-fire regeneration |
| treedFirePixelTableSinceLastDisp | data.table | 3 columns: pixelIndex, pixelGroup, and burnTime. Each row represents a forested pixel that was burned up to and including this year, since last dispersal event, with its corresponding pixelGroup and time it occurred |

### BiomassSpeciesData

#### Required packages

## $BiomassSpeciesData  
## [1] "SpaDES.core"   
## [2] "data.table"   
## [3] "gdalUtils"   
## [4] "googledrive"   
## [5] "magrittr"   
## [6] "PredictiveEcology/LandR@development"   
## [7] "PredictiveEcology/pemisc@development"  
## [8] "pryr"   
## [9] "raster"   
## [10] "reproducible"   
## [11] "SpaDES.tools"

#### Parameters

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| paramName | paramClass | default | min | max | paramDesc |
| sppEquivCol | character | Boreal | NA | NA | The column in sim$specieEquivalency data.table to use as a naming convention |
| types | character | KNN | NA | NA | The possible data sources. These must correspond to a function named paste0(‘prepSpeciesLayers\_’, type) |
| vegLeadingProportion | numeric | 0.8 | 0 | 1 | a number that define whether a species is leading for a given pixel |
| .plotInitialTime | numeric | NA | NA | NA | This describes the simulation time at which the first plot event should occur |
| .plotInterval | numeric | NA | NA | NA | This describes the simulation time interval between plot events |
| .saveInitialTime | numeric | NA | NA | NA | This describes the simulation time at which the first save event should occur |
| .saveInterval | numeric | NA | NA | NA | This describes the simulation time interval between save events |
| .useCache | logical | FALSE | NA | NA | Should this entire module be run with caching activated? This is generally intended for data-type modules, where stochasticity and time are not relevant |
| .useParallel | numeric | 64 | NA | NA | Used in reading csv file with fread. Will be passed to data.table::setDTthreads. |

#### Input objects

|  |  |  |  |
| --- | --- | --- | --- |
| objectName | objectClass | desc | sourceURL |
| rasterToMatch | RasterLayer | Raster layer of buffered study area used for cropping, masking and projecting. Defaults to the kNN biomass map masked with studyArea | <http://tree.pfc.forestry.ca/kNN-StructureBiomass.tar> |
| rasterToMatchReporting | RasterLayer | Raster layer of study area used for plotting and reporting only. Defaults to the kNN biomass map masked with studyArea | <http://tree.pfc.forestry.ca/kNN-StructureBiomass.tar> |
| sppColorVect | character | A named vector of colors to use for plotting. The names must be in simsppEquivCol]], and should also contain a color for ‘Mixed’ | NA |
| sppEquiv | data.table | table of species equivalencies. See LandR::sppEquivalencies\_CA. |  |
| studyArea | SpatialPolygonsDataFrame | Multipolygon to use as the study area. (studyArea is typically buffered to the actual study area of interest.) Defaults to an area in Southwestern Alberta, Canada. | NA |
| studyAreaReporting | SpatialPolygonsDataFrame | multipolygon (typically smaller/unbuffered than studyArea) to use for plotting/reporting. Defaults to an area in Southwestern Alberta, Canada. | NA |

#### Output objects

|  |  |  |
| --- | --- | --- |
| objectName | objectClass | desc |
| speciesLayers | RasterStack | biomass percentage raster layers by species in Canada species map |
| treed | data.table | one logical column for each species, indicating whether there were non-zero values |
| numTreed | numeric | a named vector with number of pixels with non-zero cover values |
| nonZeroCover | numeric | A single value indicating how many pixels have non-zero cover |

### Boreal\_LBMRDataPrep

#### Required packages

## $Boreal\_LBMRDataPrep  
## [1] "SpaDES.core"   
## [2] "achubaty/amc@development"   
## [3] "crayon"   
## [4] "data.table"   
## [5] "dplyr"   
## [6] "fasterize"   
## [7] "gdalUtils"   
## [8] "lme4"   
## [9] "plyr"   
## [10] "PredictiveEcology/LandR@development"   
## [11] "PredictiveEcology/pemisc@development"  
## [12] "raster"   
## [13] "rgeos"   
## [14] "sp"

#### Parameters

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| paramName | paramClass | default | min | max | paramDesc |
| biomassModel | call | lme4::lmer(B ~ logAge \* speciesCode + cover \* speciesCode + (logAge + cover + speciesCode | ecoregionGroup)) | NA | NA | Model and formula for estimating biomass (B) from ecoregionGroup (currently ecoDistrict \* LandCoverClass), speciesCode, logAge (gives a downward curving relationship), and cover. Defaults to a LMEM, which can be slow if dealing with very large datasets (e.g. 36 000 points take 20min). For faster fitting try P(sim)$subsetDataBiomassModel == TRUE, or quote(RcppArmadillo::fastLm(formula = B ~ logAge \* speciesCode \* ecoregionGroup + cover \* speciesCode \* ecoregionGroup)). A custom model call can also be provided, as long as the ‘data’ argument is NOT included. |
| coverModel | call | lme4::glmer(cbind(coverPres, coverNum) ~ speciesCode + (1 | ecoregionGroup), family = binomial) | NA | NA | Model and formula used for estimating cover from ecoregion and speciesCode and potentially others. Defaults to a GLMEM if there are > 1 grouping levels. A custom model call can also be provided, as long as the ‘data’ argument is NOT included |
| forestedLCCClasses | numeric | c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 32, 34, 35) | 0 | 39 | The classes in the rstLCC layer that are ‘treed’ and will therefore be run in LBMR. |
| Defau | lts to forest | ed classes in LCC2005 map. |  |  |  |
| LCCClassesToReplaceNN | numeric | 34:35 | NA | NA | This will replace these classes on the landscape with the closest forest class P(sim)$forestedLCCClasses. If the user is using the default 2005 data product for rstLCC, then users may wish to include 36 (cities – if running a historic range of variation project), and 34:35 (burns) Since this is about estimating parameters for growth, it doesn’t make any sense to have unique estimates for transient classes in most cases |
| omitNonTreedPixels | logical | TRUE | FALSE | TRUE | Should this module use only treed pixels, as identified by P(sim)$forestedLCCClasses? |
| pixelGroupAgeClass | numeric | params(sim)successionTimestep | NA | NA | When assigning pixelGroup membership, this defines the resolution of ages that will be considered ‘the same pixelGroup’, e.g., if it is 10, then 6 and 14 will be the same |
| pixelGroupBiomassClass | numeric | 100 | NA | NA | When assigning pixelGroup membership, this defines the resolution of biomass that will be considered ‘the same pixelGroup’, e.g., if it is 100, then 5160 and 5240 will be the same |
| runName | character |  | NA | NA | A description for run. This will form the basis of cache path and output path, and affect dispersal parameterization. |
| speciesUpdateFunction | list | list(LandR::speciesTableUpdate(simspeciesTable, simsppEquivCol)) | NA | NA | Unnamed list of quoted functions that updates species table to customize values. |
| Defau | lt should alw | ays come first. |  |  |  |
| sppEquivCol | character | Boreal | NA | NA | The column in sim$specieEquivalency data.table to use as a naming convention |
| subsetDataAgeModel | numeric | NULL | NA | NA | the number of samples to use when subsampling the biomass data model; if TRUE, uses 50 |
| subsetDataBiomassModel | numeric | NULL | NA | NA | the number of samples to use when subsampling the biomass data model; if TRUE, uses 50 |
| successionTimestep | numeric | 10 | NA | NA | defines the simulation time step, default is 10 years |
| useCloudCacheForStats | logical | TRUE | NA | NA | Some of the statistical models take long (at least 30 minutes, likely longer). If this is TRUE, then it will try to get previous cached runs from googledrive |
| .plotInitialTime | numeric | NA | NA | NA | This describes the simulation time at which the first plot event should occur |
| .plotInterval | numeric | NA | NA | NA | This describes the simulation time interval between plot events |
| .saveInitialTime | numeric | NA | NA | NA | This describes the simulation time at which the first save event should occur |
| .saveInterval | numeric | NA | NA | NA | This describes the simulation time interval between save events |

#### Input objects

|  |  |  |  |
| --- | --- | --- | --- |
| objectName | objectClass | desc | sourceURL |
| biomassMap | RasterLayer | total biomass raster layer in study area, default is Canada national biomass map | <http://tree.pfc.forestry.ca/kNN-StructureBiomass.tar> |
| cloudFolderID | character | The google drive location where cloudCache will store large statistical objects | NA |
| columnsForPixelGroups | character | The names of the columns in cohortData that define unique pixelGroups. Default is c(‘ecoregionGroup’, ‘speciesCode’, ‘age’, ‘B’) | NA |
| ecoDistrict | SpatialPolygonsDataFrame | ecodistricts in study area, default is Canada national ecodistricts | <http://sis.agr.gc.ca/cansis/nsdb/ecostrat/district/ecodistrict_shp.zip> |
| rstLCC | RasterLayer | A land classification map in study area. It must be ‘corrected’, in the sense that: |  |
| 1) Every class must not | conflict with any other ma | p in this module |  |
| (e.g., speciesLayer | s should not have data in L | CC classes that are non-treed); |  |
| 2) It can have treed an | d non-treed classes. The no | n-treed will be removed within this |  |
| module if P(sim)$om | itNonTreedPixels is TRUE; |  |  |
| 3) It can have transien | t pixels, such as ’young fi | re’. These will be converted to a |  |
| the nearest non-tra | nsient class, probabilistic | ally if there is more than 1 nearest |  |
| neighbour class, ba | sed on P(sim)$LCCClassesToR | eplaceNN. |  |
| The default layer used, | if not supplied, is Canada | national land classification in 2005 <https://drive.google.com/file/d/1g9jr0VrQxqxGjZ4ckF6ZkSMP-zuYzHQC/view?usp=sharing> |  |
| rasterToMatch | RasterLayer | DESCRIPTION NEEDED | NA |
| speciesLayers | RasterStack | cover percentage raster layers by species in Canada species map | <http://tree.pfc.forestry.ca/kNN-Species.tar> |
| speciesTable | data.table | species attributes table, default is from Dominic Cyr and Yan Boulanger’s project | <https://raw.githubusercontent.com/dcyr/LANDIS-II_IA_generalUseFiles/master/speciesTraits.csv> |
| sppColorVect | character | named character vector of hex colour codes corresponding to each species |  |
| sppEquiv | data.table | table of species equivalencies. See LandR::sppEquivalencies\_CA. |  |
| studyArea | SpatialPolygonsDataFrame | multipolygon to use as the study area, with attribute LTHFC describing the fire return interval. Defaults to a square shapefile in Southwestern Alberta, Canada. |  |
| studyAreaLarge | SpatialPolygonsDataFrame | multipolygon (larger area than studyArea) to use for parameter estimation, with attribute LTHFC describing the fire return interval. Defaults to a square shapefile in Southwestern Alberta, Canada. |  |
| standAgeMap | RasterLayer | stand age map in study area, default is Canada national stand age map | <http://tree.pfc.forestry.ca/kNN-StructureStandVolume.tar> |

#### Output objects

|  |  |  |
| --- | --- | --- |
| objectName | objectClass | desc |
| ecoDistrict |  |  |
| ecoregion | data.table | ecoregion look up table |
| ecoregionMap | RasterLayer | ecoregion map that has mapcodes match ecoregion table and speciesEcoregion table |
| cohortData | data.table | initial community table |
| pixelGroupMap | RasterLayer | initial community map that has mapcodes match initial community table |
| minRelativeB | data.frame | define the cut points to classify stand shadeness |
| species | data.table | a table that has species traits such as longevity… |
| speciesEcoregion | data.table | define the maxANPP, maxB and establishprob change with both ecoregion and simulation time |
| studyArea |  |  |
| sufficientLight | data.frame | define how the species with different shade tolerance respond to stand shadeness |

### LBMR

#### Required packages

## $LBMR  
## [1] "SpaDES.core"   
## [2] "compiler"   
## [3] "data.table"   
## [4] "dplyr"   
## [5] "fpCompare"   
## [6] "ggplot2"   
## [7] "grid"   
## [8] "PredictiveEcology/LandR@development"   
## [9] "PredictiveEcology/pemisc@development"   
## [10] "PredictiveEcology/reproducible@development"  
## [11] "PredictiveEcology/SpaDES.core@development"   
## [12] "PredictiveEcology/SpaDES.tools@development"  
## [13] "purrr"   
## [14] "quickPlot"   
## [15] "raster"   
## [16] "Rcpp"   
## [17] "scales"   
## [18] "sp"   
## [19] "tidyr"

#### Parameters

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| paramName | paramClass | default | min | max | paramDesc |
| calcSummaryBGM | character | end | NA | NA | A character vector describing when to calculate the summary of biomass, growth and mortality Currently any combination of 5 options is possible: ‘start’- as before vegetation succession events, i.e. before dispersal, ‘postDisp’ - after dispersal, ‘postRegen’ - after post-disturbance regeneration (currently the same as ‘start’), ‘postGM’ - after growth and mortality, ‘postAging’ - after aging, ‘end’ - at the end of vegetation succesion events, before plotting and saving. The ‘end’ option is always active, being also the default option. |
| calibrate | logical | FALSE | NA | NA | Do calibration? Defaults to FALSE |
| growthAndMortalityDrivers | character | LandR | NA | NA | package name where the following functions can be found: calculateClimateEffect, assignClimateEffect |
| growthInitialTime | numeric | start(sim) | NA | NA | Initial time for the growth event to occur |
| initialBiomassSource | character | cohortData | NA | NA | Currently, there are three options: ‘spinUp’, ‘cohortData’, ‘biomassMap’. If ‘spinUp’, it will derive biomass by running spinup derived from Landis-II. If ‘cohortData’, it will be taken from the ‘cohortData’ object, i.e., it is already correct, by cohort. If ‘biomassMap’, it will be taken from simspeciesLayers percent cover values `spinUp`` uses simbiomassMap is supplied |
| mixedType | numeric | 2 | NA | NA | How to define mixed stands: 1 for any species admixture; 2 for deciduous > conifer. See ?vegTypeMapGenerator. |
| seedingAlgorithm | character | wardDispersal | NA | NA | choose which seeding algorithm will be used among noDispersal, universalDispersal, and wardDispersal (default). |
| spinupMortalityfraction | numeric | 0.001 | NA | NA | defines the mortality loss fraction in spin up-stage simulation |
| sppEquivCol | character | Boreal | NA | NA | The column in sim$specieEquivalency data.table to use as a naming convention |
| successionTimestep | numeric | 10 | NA | NA | defines the simulation time step, default is 10 years. Note that growth and mortality always happen on a yearly basis. |
| vegLeadingProportion | numeric | 0.8 | 0 | 1 | a number that define whether a species is leading for a given pixel |
| .maxMemory | numeric | 5 | NA | NA | maximum amount of memory (in GB) to use for dispersal calculations. |
| .plotInitialTime | numeric | 0 | NA | NA | Vector of length = 1, describing the simulation time at which the first plot event should occur. Set to NA to turn plotting off. |
| .plotInterval | numeric | NA | NA | NA | defines the plotting time step. If NA, the default, .plotInterval is set to successionTimestep. |
| .plotMaps | logical | TRUE | NA | NA | Controls whether maps should be plotted or not |
| .saveInitialTime | numeric | NA | NA | NA | Vector of length = 1, describing the simulation time at which the first save event should occur. Set to NA if no saving is desired. If not NA, then saving will occur at .saveInitialTime with a frequency equal to .saveInterval |
| .saveInterval | numeric | NA | NA | NA | defines the saving time step. If NA, the default, .saveInterval is set to successionTimestep. |
| .useCache | logical | init | NA | NA | use caching for the spinup simulation? |
| .useParallel | ANY | 2 | NA | NA | Used only in seed dispersal. If numeric, it will be passed to data.table::setDTthreads and should be <= 2; If TRUE, it will be passed to parallel:makeCluster; and if a cluster object, it will be passed to parallel::parClusterApplyB. |

#### Input objects

|  |  |  |  |
| --- | --- | --- | --- |
| objectName | objectClass | desc | sourceURL |
| cohortData | data.table | Columns: B, pixelGroup, speciesCode, Indicating several features about ages and current vegetation of stand | NA |
| ecoregion | data.table | ecoregion look up table | <https://raw.githubusercontent.com/LANDIS-II-Foundation/Extensions-Succession/master/biomass-succession-archive/trunk/tests/v6.0-2.0/ecoregions.txt> |
| ecoregionMap | RasterLayer | ecoregion map that has mapcodes match ecoregion table and speciesEcoregion table. Defaults to a dummy map matching rasterToMatch with two regions | NA |
| minRelativeB | data.frame | table defining the cut points to classify stand shadeness | NA |
| pixelGroupMap | RasterLayer | initial community map that has mapcodes match initial community table | NA |
| rasterToMatch | RasterLayer | Raster layer of buffered study area used for cropping, masking and projecting. Defaults to the kNN biomass map masked with studyArea | <http://tree.pfc.forestry.ca/kNN-StructureBiomass.tar> |
| rasterToMatchReporting | RasterLayer | Raster layer of study area used for plotting and reporting only. Defaults to the kNN biomass map masked with studyArea | <http://tree.pfc.forestry.ca/kNN-StructureBiomass.tar> |
| species | data.table | a table that has species traits such as longevity, shade tolerance, etc. Default is partially based on Dominic Cir and Yan’s project | <https://raw.githubusercontent.com/dcyr/LANDIS-II_IA_generalUseFiles/master/speciesTraits.csv> |
| speciesEcoregion | data.table | table defining the maxANPP, maxB and SEP, which can change with both ecoregion and simulation time. Defaults to a dummy table based on dummy data os biomass, age, ecoregion and land cover class | NA |
| sppColorVect | character | A named vector of colors to use for plotting. The names must be in simsppEquivCol]], and should also contain a color for ‘Mixed’ | NA |
| sppEquiv | data.table | table of species equivalencies. See LandR::sppEquivalencies\_CA. |  |
| studyArea | SpatialPolygonsDataFrame | multipolygon to use as the study area, with attribute LTHFC describing the fire return interval. Defaults to a square shapefile in Southwestern Alberta, Canada. |  |
| studyAreaReporting | SpatialPolygonsDataFrame | multipolygon (typically smaller/unbuffered than studyArea) to use for plotting/reporting. Defaults to an area in Southwestern Alberta, Canada. | NA |
| sufficientLight | data.frame | table defining how the species with different shade tolerance respond to stand shadeness. Default is based on LANDIS-II Biomass Succession v6.2 parameters | <https://raw.githubusercontent.com/LANDIS-II-Foundation/Extensions-Succession/master/biomass-succession-archive/trunk/tests/v6.0-2.0/biomass-succession_test.txt> |
| treedFirePixelTableSinceLastDisp | data.table | 3 columns: pixelIndex, pixelGroup, and burnTime. Each row represents a forested pixel that was burned up to and including this year, since last dispersal event, with its corresponding pixelGroup and time it occurred |  |

#### Output objects

|  |  |  |
| --- | --- | --- |
| objectName | objectClass | desc |
| activePixelIndex | integer | internal use. Keeps track of which pixels are active |
| activePixelIndexReporting | integer | internal use. Keeps track of which pixels are active in the reporting study area |
| ANPPMap | RasterLayer | ANPP map at each succession time step |
| cohortData | data.table | age cohort-biomass table hooked to pixel group map by pixelGroupIndex at succession time step |
| inactivePixelIndex | logical | internal use. Keeps track of which pixels are inactive |
| inactivePixelIndexReporting | integer | internal use. Keeps track of which pixels are inactive in the reporting study area |
| initialCommunities | character | Because the initialCommunities object can be LARGE, it is saved to disk with this filename |
| lastFireYear | numeric | Year of the most recent fire year |
| lastReg | numeric | an internal counter keeping track of when the last regeneration event occurred |
| minRelativeB | data.frame | define the cut points to classify stand shadeness |
| mortalityMap | RasterLayer | Mortality map at each succession time step |
| pixelGroupMap | RasterLayer | updated community map at each succession time step |
| regenerationOutput | data.table | TODO: description needed |
| reproductionMap | RasterLayer | Regeneration map at each succession time step |
| simulatedBiomassMap | RasterLayer | Biomass map at each succession time step |
| simulationOutput | data.table | contains simulation results by ecoregion (main output) |
| simulationTreeOutput | data.table | Summary of several characteristics about the stands, derived from cohortData |
| species | data.table | a table that has species traits such as longevity, shade tolerance, etc. Currently obtained from LANDIS-II Biomass Succession v.6.0-2.0 inputs |
| speciesEcoregion | data.table | define the maxANPP, maxB and SEP change with both ecoregion and simulation time |
| spinupOutput | data.table | Spin-up output |
| summaryBySpecies | data.table | The total species biomass, average age and aNPP across the landscape (used for plotting and reporting). |
| summaryBySpecies1 | data.table | No. pixels of each leading vegetation type (used for plotting and reporting). |
| summaryLandscape | data.table | The averages of total biomass, age and aNPP across the landscape (used for plotting and reporting). |

## LandR module integration

modules\_landr <- c("BiomassSpeciesData", modules[c(1, 2, 4)])  
  
mySim\_landr <- Cache(simInit, times = times,  
 params = parameters,  
 modules = modules\_landr,  
 outputs = outputs,  
 objects = objects,  
 paths = paths3,  
 loadOrder = unlist(modules),  
 useCloud = FALSE,  
 cloudFolderID = cloudCacheFolderID,  
 omitArgs = c("debug", "paths", ".plotInitialTime")  
)  
  
png(file.path("docs", "LandR\_module\_diagram.png"), height = 800, width = 800)  
 moduleDiagram(mySim\_landr)  
dev.off()  
  
## currently not working: see https://github.com/rich-iannone/DiagrammeR/issues/207  
## workaround is to use Rstudio's manual export ability :S  
objectDiagram(mySim\_landr, height = 2500, width = 1250) # %>%  
# DiagrammeRsvg::export\_svg() %>%  
# charToRaw() %>%  
# rsvg::rsvg() %>%  
# png::writePNG(file.path("docs", "LandWeb\_object\_diagram.png"))



