

# CASA-CNP Model Testbed

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User's Manual and Technical Documentation

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## 2 Overview of the CASA-CNP testbed

The CASA-CNP testbed (currently named *casacm\_mimics\_corpse*) has been developed to test different soil organic matter (SOM) cycling models with a common set of environmental conditions and litter input. At the heart of the testbed is the Carnegie-Aimes-Stanford Approach terrestrial biosphere model (CASA-CNP) (created by (Potter, Randerson et al. 1993), with modifications by (Randerson, Thompson et al. 1996, Randerson, Thompson et al. 1997); and with N and P biogeochemistry as implemented by (Wang, Law et al. 2010). We use the carbon-only calculations of CASA-CNP to calculate net primary productivity (NPP), carbon allocation to different tissues (roots, wood, and leaves), as well as the timing of plant mortality and litterfall. Currently, one of three different SOM cycling models can be selected to compute organic matter transformations, soil carbon stocks, and heterotrophic respiration (Figure 1). These SOM models include one first-order model, the SOM cycling model in CASA-CNP (Wang et al. 2010), and two microbial explicit models, the Microbial-Mineral Carbon Stabilization (MIMICS) model (Wieder, Grandy et al. 2014, Wieder, Grandy et al. 2015) and the Carbon, Organisms, Rhizosphere and Protection in the Soil Environment (CORPSE) model (Sulman, Phillips et al. 2014). If the CASA-CNP SOM model is selected, the testbed can be run with carbon only, with carbon and nitrogen only, or with carbon and nitrogen and phosphorus. Currently, the testbed is run in carbon-only mode when either MIMICS or CORPSE is selected since these models do not yet include N-cycling.

Data inputs were generated by the Community Land Model (CLM version 4.5) using a satellite phenology scheme forced with the Cru-NCEP climate reanalysis (Koven, Riley et al. 2013, Oleson, Lawrence et al. 2013). This standard configuration of CLM generated globally gridded daily output of gross primary productivity (GPP), air temperature, along with soil temperature, liquid soil moisture, and frozen soil moisture in 10 CLM soil layers (top 343 cm of soil) for the historical period (1901-2010). Static soil property inputs to the testbed including soil texture (sand, silt, clay fractions) and volumetric soil water content at wilting point, field capacity, and saturation inputs to the testbed were depth-weighted means in the top 50 cm of soil from the CLM surface data set (Oleson, Lawrence et al. 2013). The testbed assigned a single plant functional type (PFT) to each 2° x 2° grid cell, computed as the mode from the 1-

km International Geosphere–Biosphere Program Data and Information System (IGBP DISCover) data set with 18 vegetation types, including grassy tundra (Loveland, Reed et al. 2000) (National Center for Atmospheric Research Staff (Eds). Last modified 10 Feb 2017. "The Climate Data Guide: CERES: IGBP Land Classification." Retrieved from <https://climatedataguide.ucar.edu/climate-data/ceres-igbp-land-classification>) (Figure 2). CASA-CNP defines biome-specific parameters corresponding to each PFT (Table 6 to Table 21).

The daily time-dependent forcings required by the testbed include mean air temperature, atmospheric nitrogen deposition, Gross Primary Production (GPP), and soil temperature and volumetric soil water content for five soil layers in the top 150 cm of soil. CASA-CNP computes the depth-weighted mean soil temperature and depth-weighted volumetric soil water content in the rooting zone using to the PFT-specific root depth and root distribution to weight the contribution from each soil layer.

The testbed computes average soil temperature, liquid soil moisture, and frozen soil moisture as depth-weighted means in the rooting zone (50 to 150 cm) according to the PFT-specific root depth and root distribution within the six CASA-CNP soil layers (section "Fraction of root biomass in each CASA-CNP soil layer"). The three models in the testbed use only these mean soil moisture and mean soil temperature for their calculations rather than the vertically-resolved values. Only liquid soil moisture was considered when computing soil moisture limits on growth in the CASA-CNP vegetation model and soil moisture decomposition effects for both CASA-CNP and CORPSE soil organic models. Additionally, CORPSE required frozen soil moisture to calculate air-filled pore space. MIMICS does not consider soil moisture effects on decomposition.

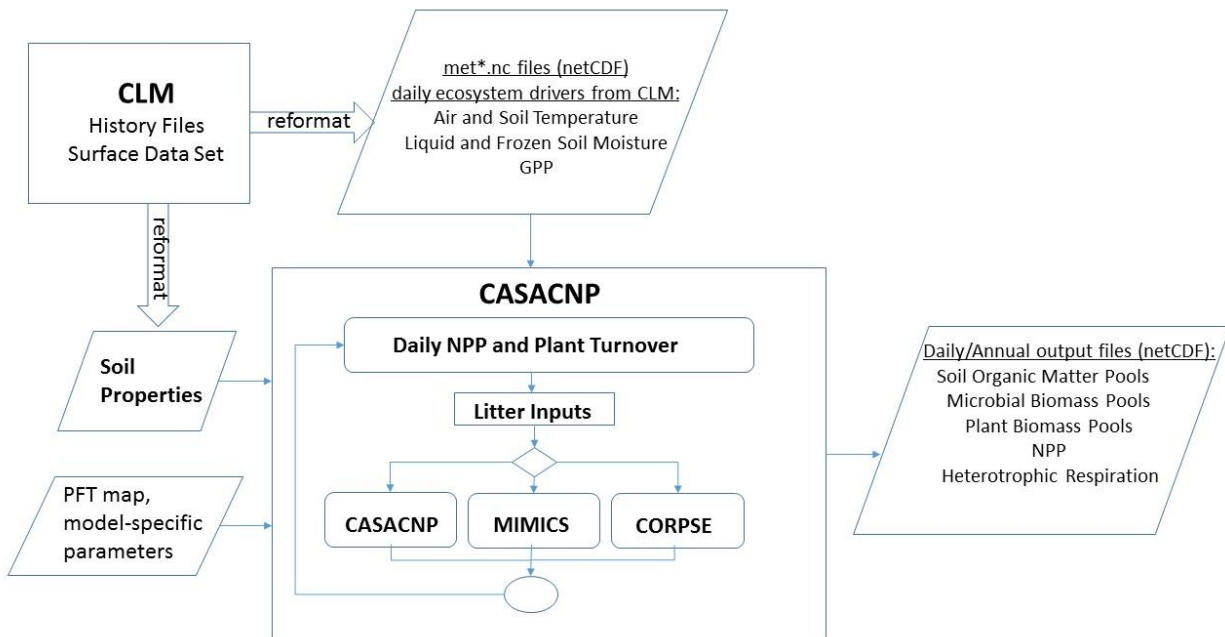


Figure 1. Schematic of the CASA-CNP testbed.



Currently the testbed is set up to run the land cells on the  $2^\circ \times 2^\circ$  global CLM grid. The grid resolution of the testbed is flexible and can be modified by updating the resolution of the input files; it can even be configured to run for a single point or field site. Although CLM defines multiple PFTs in each  $2^\circ \times 2^\circ$  grid cell, CASA-CNP defines only a single PFT per each grid cell. The testbed does not simulate cells that are designated as urban, wetlands, water, or ice. The daily GPP forcings are the total daily GPP that CLM reported for the grid cell even though CLM's results are the aggregate of multiple PFTs.

Post processing of CLM history files was required to format input data that could be read into the biogeochemical testbed ([see section on netCDFTools for instructions](#)). Other grid cell-specific properties, including Plant Functional Types (PFTs) and timing of phenology, were derived independent of the CLM model as described below.

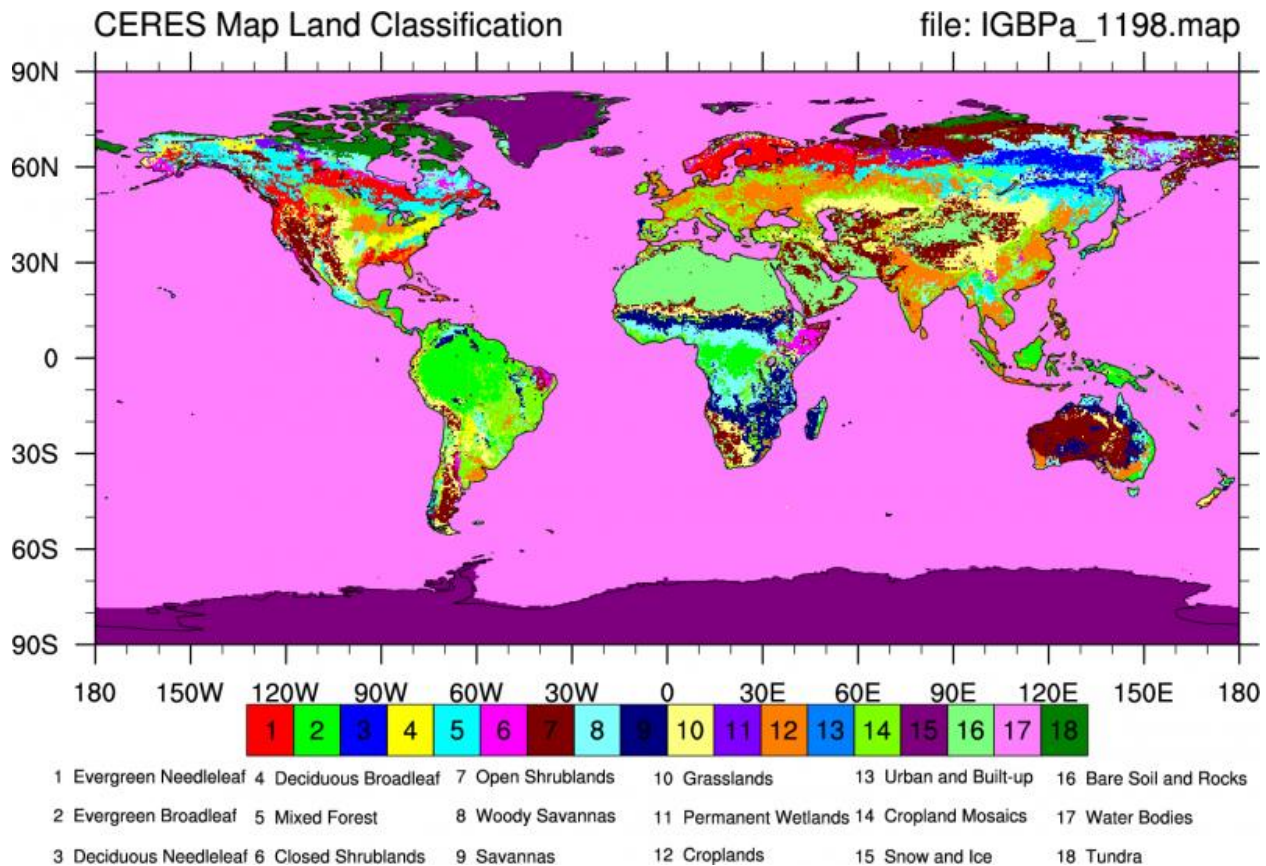


Figure 2. CERES land classification from IGBPa\_1198.map.nc. Surface types 1 - 17 correspond to those defined by IGBP (International Geosphere Biosphere Programme). The 18th surface type (tundra) was defined for CERES. The IGBP surface type for snow and ice number 15, is for permanent snow and ice. (Climate Data Guide; D. Shea). <https://climatedataguide.ucar.edu/climate-data/ceres-igbp-land-classification>.

Given daily meteorological inputs and daily gross primary production (GPP) as forcings, the primary modifications to CASA-CNP to develop this testbed were:

- MIMICS and CORPSE were added as alternative SOM models to the CASA-CNP first-order model
- The testbed specifies soil properties by grid cell instead of assigning a soil type to each grid cell. Originally CASA-CNP had 9 soil *types* where each type hard-coded values for soil texture and water holding capacities.
- Gridded daily input for meteorological and other time-dependent data is through netCDF (met.nc) files instead of text files.
- N deposition is a time-dependent daily input instead of a single average annual input.
- The testbed has capability to run transient simulations. Transient simulations read a series of annual forcing files and maintain the state of the model between each year; no stop/restart is required. In this way, the model can be driven with a long continuous climate record instead of recycling a meteorological record with a finite number of years. Transient runs require one met.nc file for each calendar year of the transient simulation. Non-transient runs require a single met.nc file that is read over and over; this file can contain up to five complete years of daily inputs.
- The testbed saves daily or mean annual output each year to netCDF files. Formerly output was saved at the end of the simulation only to .csv files.
- As with CASA-CNP, the testbed outputs the state of vegetation and soil pools at the end of the simulation to .csv files. These “restart” files can be used to initialize subsequent runs.

Run-time options for the testbed are specified in a text file (fCASA-CNP\_clm\_testbed.lst). These run-time options include the frequency of output (annual or daily), the names of the model-specific parameter files, the names of meteorological forcing files, the SOM cycling model to run (i.e. CASA-CNP, MIMICS, or CORPSE), the type of simulation (spinup or transient), the name of the restart files to initialize the models, and the names of the output files.

CASA-CNP calculates NPP from GPP by accounting for autotrophic respiration losses and nutrient limitation (Wang, Law et al. 2010). Nutrient limitation is not relevant when CASA-CNP is run in carbon-only mode. CASA-CNP computes the exact same NPP and litter inputs regardless of SOM model selected; in the carbon-only mode there is no feedback of the SOM model to the plant model.

The testbed provides the ability to perturb soil temperatures and/or air temperatures as a step increment during a simulation. Soil temperature perturbations affect soil organic matter turnover rates and heterotrophic respiration (all SOM models), root maintenance and growth respiration (and therefore NPP and litterfall rates), and N mineralization and N leaching when CASA-CNP simulates N cycling. Air temperature perturbations affect wood maintenance and growth respiration (and therefore NPP and litterfall rates), labile C (carbohydrate) storage (and therefore NPP and litterfall rates), and cold effects on leaf litter fall.

The simulations for each SOM model are usually carried out in three steps.

1. Initialize CASA-CNP vegetation pools with a “pre-spin” simulation. We ran the testbed with 1901 climate for 100 years. This pre-spin creates more stable vegetation pools and litter inputs for subsequent simulations; the microbial pools of MIMICS and CORPSE are sensitive to changes in litter inputs. The state of the vegetation pools (but not SOM pools) from this pre-spin simulation is used to initialize spinup runs for all SOM models.
2. We executed spinup simulations by driving each SOM model with 1901-1920 forcings over and over until organic matter pools reached equilibrium. An SOM model was considered to be in equilibrium when all three of the following criteria were met between 20-year cycles: global

litter plus soil carbon stocks changed less than 0.01Pg, total litter plus soil carbon in less than 2% of grid cells changed more than 1 g C m<sup>-2</sup>, and total litter plus soil carbon in less than 2% of grid cells changed more than 0.1%. Spinup times varied between models: a) CASA-CNP required 10,000 years of an accelerated spinup followed by 10,000 years of normal spinup in order to reach equilibrium. The passive pool, the pool with the slowest turnover rate, required the longest spinup time. For the accelerated spinup, the decomposition rates were increased 10 times. Pools were multiplied by 10 before starting the normal spinup phase; b) MIMICS organic matter pools required 12,000 years to reach equilibrium. The physically protected pool required the longest spinup time; c) CORPSE organic matter pools required 50,000 years to reach equilibrium. The recalcitrant litter pool required the longest spinup time.

3. Run transient simulations using CRU/NCEP weather from 1901 – 2010. The transient simulations were initialized from restart files created by the spinup runs.

## 2.1 Creating input files for the CASA testbed with netcdfTools

The *netcdfTools* program can be used to create several input files for the testbed by reformatting CLM history files. The following are three files that netcdfTools creates. More information about the format of these files can be found in the next section.

### 2.1.1 Meteorological inputs (met\*.nc files)

*The testbed requires* meteorological input files in netCDF format (the *met\*.nc files*). These files are extracted from CLM history files. Non-transient runs require either a single (multi-year) *met.nc* file or a subset of consecutive single-year *met.nc* files that are read over and over. Transient runs require one *met.nc* file for each calendar year of the transient simulation. *Met.nc* files that contain data for the entire grid are limited to a maximum of 5 years since this amount of data is about 2GB, the maximum size of a netCDF file. *Met.nc* files for point simulations can have hundreds of years.

### 2.1.2 Grid cell locations and PFT coverage (gridinfo\_igbpz.csv)

For each grid cell in the CLM grid, this file contains one row with a grid cell id, latitude, longitude, PFT, land area, and some other information. Note that the Ndep (Nitrogen deposition) column in this file is now ignored; since August 22, 2016 daily Ndep is stored in the *met.nc* file.

### 2.1.3 Grid cell soil properties (gridinfo\_soil.csv)

For each grid cell in the CLM grid, this file contains one row with the cell's soil properties. Soil properties are derived from the CLM surface data set and include sand, clay, and silt, fractions and volumetric soil water content at wilting point (wwilt), field capacity (wfiel), and saturation (wsat).

### 2.1.4 Compiling the netcdfTools executable

If the *netcdfTools* executable does not exist or needs to be recompiled for any reason, change to the CASACLM/NetCDFTools/SOURCE directory, remove any object files (to be safe), and type the following "make" command:

```
cd CASACLM/NetCDFTools/SOURCE
rm *.o *.mod
make -f Makefile.txt netcdfTools
```

If the code fails to compile, the makefile, Makefile.txt, may need to be updated with the specifics (compiler and pathnames) for your system. Next, copy the *netcdfTools* executable to the location where it will be run. The Linux *chmod* command will make it executable in case the file permissions get changed when it is copied. For example

```
cp netcdfTools ..
cd ..
chmod 755 netcdfTools
```

The *netcdfTools* program reads a text file named *files.ini* and a .csv file named *clmGrid\_IGBP.csv*. It creates one *met\_yyyy\_yyyy.nc* file (yyyy and yyyy are the starting and ending years of data stored in the file) and two .csv files (*gridinfo\_igbpz.csv* and *gridinfo\_soil.csv*) per simulation.

Example of *files.ini*:

```
h1          ! file type (h0=monthly, h1=daily)
19010101    ! start (yyyymmdd)
19071231    ! end (yyyymmdd)
/project/bgc01/bonan/casa-cnp/clm/clm45sp_2deg4506_hist.clm2.h1.1901-01-01-00000.nc
/project/bgc01/melannie/surfddata_1.9x2.5_simyr1850_c130421.nc
/project/bgc01/melannie/fndep_clm_hist_simyr1849-2006_1.9x2.5_c100428.nc
./CO2_1768-2010.txt
```

#### 2.1.4.1 Explanation of *files.ini* content

Line 1: Use h1, h0 no longer works.  
 Line 2: First day for *met\_yyyy\_yyyy.nc* file (best to start Jan. 1<sup>st</sup>.)  
 Line 3: Last day for *met\_yyyy\_yyyy.nc* file (best to end Dec. 31<sup>st</sup>, don't exceed 7 years for 2° x 2° grid)  
 Line 4: Name of CLM history file for the first year (netCDF format)  
 Line 5: Name of CLM surface data set (netCDF format)  
 Line 6: Name of CLM N deposition file (netCDF format)  
 Line 7: Name of text file with annual global mean CO<sub>2</sub> concentrations.

#### 2.1.4.2 Executing *netcdfTools*

NetCDFTools expects the CLM netCDF files to be in a specific format – it is looking for specific variable names, dimension names, and dimension orders. If the format of the input files is altered, then one will likely need to update the source code and recompile the program to accommodate the format change. Example NetCDF file headers generated with *ncdump* are included in CASACLM/NetCDFTools/NetCDF\_file\_headers.

Once the initialization file (*files.ini*) has been set up, type the following two commands at the command line prompt. The module load command needs only to be run once for each Linux session.

```
module load tool/netcdf/4.3.2/gcc
./netcdfTools
```

An error similar to the following will occur if the module load command is not executed before running *netcdfTools*:

```
./netcdfTools: error while loading shared libraries: libnetcdf.so.6: cannot open shared object file:
No such file or directory
```

The netcdf module version may change with time. To determine the NetCDF version available, type “module avail” at the command line to see available modules.

To create more than one *met.nc*, one could use a script to create met.nc files in batch. The perl script run-netcdfTools.pl is an example of how to do this. To run this script, update the file paths in the script to match your directory structure then type the following at the command line:

```
perl run-netcdfTools.pl
```

## 2.2 CASA-CNP Input Files

### 2.2.1 Input files generated by *netCDFTools* (see the section above for more information)

- *met\_yyyy\_yyyy.nc* file – daily meteorological inputs in netCDF format.
- *gridinfo\_igbpz.csv* – for each grid cell in the CLM grid, this file contains a grid cell id, latitude, longitude, PFT, land area, and some other information.
- *gridinfo\_soil.csv* – soil properties for each grid cell derived from the CLM surface data set.

CLM history file output has been reformatted for input to CASA-CNP using NetCDFTools. The lists below summarize the files that contain information from CLM, and their former source before CASA-CNP was updated to accommodate CLM inputs.

### 2.2.2 Daily Meteorological Forcings: *met\*.nc* files

The ***met\*.nc*** files contain daily meteorological inputs, LAI, and GPP. Usually the file is named *met\_yyyy\_yyyy.nc* where the first and last calendar years are incorporated in the name. Transient simulations require a series of *met\*.nc* files with only one year of data, whereas spinup runs use files with one or more years of data (6 years of data reaches the file size limit). Formerly CASA-CNP read this information from a single text file (*met.txt*), but I decided to store it in NetCDF files to allow for more efficient use of disk space for large amounts of data. Data for the entire time series is read all at once and assigned to CASA-CNP variables each day.

- *xlai(npt,day)* – daily LAI ( $\text{m}^2 \text{m}^{-2}$ ) read from *met.nc* file. Not used in latest version of CASA-CNP. LAI is calculated from the leaf carbon pool.
- *xcnpp(npt,day)* – daily NPP ( $\text{g C m}^{-2} \text{d}^{-1}$ ) is no longer used by latest version of CASA-CNP. The value of *casaflex%Cnpp(npt)* is computed in **subroutine casa\_rplant** called in **subroutine biogeochem**.
- *xcgpp(npt,day)* – daily GPP ( $\text{g C m}^{-2} \text{d}^{-1}$ ) read from *met.nc* file. Assigned to *casaflex%Cgpp(npt)* each day.
- *xtairk(npt,day)* – mean daily air temperature (K) read from *met.nc* file. Assigned to *casamet%tairk(npt)* each day.

- *xtsoil(npt,lyr,day)* – mean soil temperature by layer for each day (K) read from met.nc file. This is CLM soil temperature mapped to the 6 CASA-CNP soil layers. Assigned to *casamet%xtsoil(npt,mlyr)* each day. The weighted average soil temperature in these 6 soil layers (*casamet%tsoilavg(npt)*, K) is computed from *casamet%tsoil(\*,\*)* and the fraction of roots in each soil layer (SUBROUTINE avgsoil).
- *xmoist(npt,lyr,day)* – mean soil volumetric liquid soil moisture content by layer for each day (0.0 – 1.0) read from met.nc file. Assigned to *casamet%moist(npt,mlyr)* each day. This is CLM soil moisture mapped to the 6 CASA-CNP soil layers. The weighted average volumetric soil water content in these 6 soil layers (*casamet%moistavg(npt)*, 0.0 – 1.0) is computed from *casamet%moist(npt,mlyr)* and the fraction of roots in each soil layer (SUBROUTINE avgsoil).
- *xfrznmoist(npt,lyr,day)* – mean soil volumetric frozen soil moisture content by layer for each day (0.0 – 1.0) read from met.nc file. Assigned to *casamet%frznmoist(npt,mlyr)* each day. This is CLM frozen soil moisture mapped to the 6 CASA-CNP soil layers. The weighted average volumetric soil water content in these 6 soil layers (*casamet%frznmoistavg(npt)*, 0.0 – 1.0) is computed from *casamet%frznmoist(npt,mlyr)* and the fraction of roots in each soil layer (SUBROUTINE avgsoil).
- *xndepDay(time, lat, lon)* – daily N deposition ( $\text{g N m}^{-2} \text{d}^{-1}$ ) read from met.nc file. Assigned to *casafux%Nmindep(npt)* each day.

CASA computes nutrient-limited NPP from GPP; therefore, NPP in the met.nc file is just a place holder and equals GPP/2. Older versions of CASA-CNP required NPP instead of GPP as an input. The format of the met.nc files can be determined using ncdump.

#### **ncdump -h met\_1901\_1901.nc**

```
netcdf met_1901_1901 {
dimensions:
    lon = 144 ;
    lat = 96 ;
    time = 365 ;
    nsoilyrs = 6 ;
    myear = 1 ;
variables:
    float lon(lon) ;
        lon:long_name = "coordinate longitude" ;
        lon:units = "degrees_east" ;
        lon:_FillValue = 1.e+36f ;
        lon:missing_value = 1.e+36f ;
    float lat(lat) ;
        lat:long_name = "coordinate latitude" ;
        lat:units = "degrees_north" ;
        lat:_FillValue = 1.e+36f ;
        lat:missing_value = 1.e+36f ;
    int year(myear) ;
        year:long_name = "calendar years" ;
    float landfrac(lat, lon) ;
        landfrac:long_name = "land fraction from pft dataset" ;
```

```

landfrac:units = "unitless" ;
landfrac:_FillValue = 1.e+36f ;
landfrac:missing_value = 1.e+36f ;
int cellMissing(lat, lon) ;
    cellMissing:long_name = "Missing Data Mask" ;
    cellMissing:units = "0=no missing data, 1=missing data" ;
int cellid(lat, lon) ;
    cellid:long_name = "Grid Cell ID" ;
    cellid:units = "1..nlat*nlon" ;
float xtairk(time, lat, lon) ;
    xtairk:long_name = "average daily air temperature" ;
    xtairk:units = "K" ;
    xtairk:_FillValue = 1.e+36f ;
    xtairk:missing_value = 1.e+36f ;
float ndep(time, lat, lon) ;
    ndep:long_name = "daily N deposition derived from annual N deposition" ;
    ndep:units = "gN/m2/day" ;
    ndep:_FillValue = 1.e+36f ;
    ndep:missing_value = 1.e+36f ;
float xlai(time, lat, lon) ;
    xlai:long_name = "Leaf Area Index" ;
    xlai:units = "m2/m2" ;
    xlai:_FillValue = 1.e+36f ;
    xlai:missing_value = 1.e+36f ;
float xcnpp(time, lat, lon) ;
    xcnpp:long_name = "net primary production" ;
    xcnpp:units = "gC m-2 day-1" ;
    xcnpp:_FillValue = 1.e+36f ;
    xcnpp:missing_value = 1.e+36f ;
float xcgpp(time, lat, lon) ;
    xcgpp:long_name = "gross primary production" ;
    xcgpp:units = "gC m-2 day-1" ;
    xcgpp:_FillValue = 1.e+36f ;
    xcgpp:missing_value = 1.e+36f ;
float xtsoil(time, nsoilyrs, lat, lon) ;
    xtsoil:long_name = "average daily soil temperature by layer" ;
    xtsoil:units = "K" ;
    xtsoil:_FillValue = 1.e+36f ;
    xtsoil:missing_value = 1.e+36f ;
float xmoist(time, nsoilyrs, lat, lon) ;
    xmoist:long_name = "volumetric soil liquid water content by layer" ;
    xmoist:units = "m3/m3" ;
    xmoist:_FillValue = 1.e+36f ;
    xmoist:missing_value = 1.e+36f ;
float xfrznmoist(time, nsoilyrs, lat, lon) ;
    xfrznmoist:long_name = "volumetric soil frozen water content by layer" ;
    xfrznmoist:units = "m3/m3" ;
    xfrznmoist:_FillValue = 1.e+36f ;

```

```
xfrznmoist:missing_value = 1.e+36f ;
```

```
// global attributes:
```

```
:title = "CLM History file information for CASA-CNP model" ;
:comment = "NOTE: None of the variables are weighted by land fraction!" ;
:history = "created on 03/13/2017 15:28:21" ;
:source = "CLM Model" ;
```

### 2.2.3 Grid Cell Soil and Vegetation Properties

**gridinfo\_soil.csv** – this is a new file that was created in order to read soils data from CLM. There is one line for each grid cell simulated (the first 3 columns are identical to the first 3 columns in

**gridinfo\_igbpz.csv**):

- *ijcam* – index of the grid cell
- *lat* – latitude of the grid cell centroid (decimal degrees)
- *lon* – longitude of the grid cell centroid (decimal degrees)
- *soil%sand(npt)* – sand content from CLM surface data
- *soil%clay(npt)* – clay content from CLM surface data
- *soil%silt(npt)* – silt content from CLM surface data
- *soil%swilt(npt)* – volumetric soil water content at wilting point. Calculated from sand, clay, and silt by **subroutine hydraulicProperties** in **NetCDFTools**.
- *soil%sfc(npt)* – volumetric soil water content at field capacity. Calculated from sand, clay, and silt by **subroutine hydraulicProperties** in **NetCDFTools**.
- *soil%ssat(npt)* – volumetric soil water content at saturation. Calculated from sand, clay, and silt by **subroutine hydraulicProperties** in **NetCDFTools**.

Formerly values *soil%sand(\*)*, *soil%clay(\*)*, *soil%silt(\*)*, *soil%swilt(\*)*, *soil%sfc(\*)*, *soil%ssat(\*)* were assigned from hard-coded values based on soil type (1-7), where soil type was specified in

**gridinfo\_igbpz.csv**.

**gridinfo\_igbpz.csv** – this was a file that came with the original CASA-CNP code. There is one line for each grid cell simulated. The first 3 columns are identical to the first 3 columns in **gridinfo\_soil.csv**.

- I added columns *ilat* and *ilon*, the indices for the latitude and longitude on the grid (base 1), as the rightmost columns of this file. It is necessary to have *casamet%ilat(\*)* and *casamet%ilon(\*)* so that CASA-CNP output can be remapped to a 2D grid in NetCDF output file.
- Column *ist* (soil type) is no longer used. Soil properties come from **grid\_soil.csv** now and are not assigned according to soil type.
- Columns *doyP1*, *doyP2*, *doyP3*, *doyP4*, and *Phase(1)* are not used either. They are replaced with data from **modis\_phenology.txt** even before CLM was used.
- Column *annNfix*, annual N fixation, is ignored (set to zero).
- Column *annNdep* ( $\text{g N m}^{-2} \text{ yr}^{-1}$ ) is set from CLM values. This value is no longer used because N deposition is read daily from the met.nc file. (If there is a column named *Ndep(2001)* at the very right side of the file it is for reference only and is not read by CASA-CNP).

Complete list of **gridinfo\_igbpz.csv** columns:



- *ijcam* – index of the grid cell
- *lat* – latitude of the grid cell centroid (decimal degrees)
- *lon* – longitude of the grid cell centroid (decimal degrees)
- *ivt\_igbp* – IGBP vegetation type (1-18)
- *ist* – soil type (not used with CLM). Soil properties come from **grid\_soil.csv** now and are not assigned according to soil type.
- *iso* – soil order (1-12) used only when P is simulated (icycle = 3)
- *landarea* – land area in the grid cell (km<sup>2</sup>)
- *Ndep* – annual atmospheric N deposition (g N m<sup>-2</sup> yr<sup>-1</sup>) (not used, see above)
- *Nfix* – annual N fixation (g N m<sup>-2</sup> yr<sup>-1</sup>) (not used, see above)
- *Pwea* – annual P inputs from weathering (g P m<sup>-2</sup> yr<sup>-1</sup>) used only when P is simulated (icycle = 3)
- *Pdust* – annual P inputs from weathering (g P m<sup>-2</sup> yr<sup>-1</sup>) used only when P is simulated (icycle = 3)
- *doyP1* – not used (see above)
- *doyP2* – not used (see above)
- *doyP3* – not used (see above)
- *doyP4* – not used (see above)
- *Phase(1)* – not used (see above)
- *ivcasa* – never used with CLM. Only *ivt\_igbp* is used.
- *ilat* – latitude index for cell (base 1)
- *ilon* – longitude index for cell (base 1)

***laimonth\_mod.csv*** – monthly LAI by gridcell. No longer used by CASA-CNP.

## 2.2.4 Running the CASA testbed and setting run-time options

This “list” file *fCASA-CNP\_clm\_testbed.lst* contains run-time options and indicates the names of files to read and output during a testbed simulation. This is an expansion of the original fCASA-CNP.lst file that came with the original CASA-CNP code (June 2014). Documentation is included in the file itself.

### 2.2.4.1 Specifying parameter files

The following files may have different names than shown below. Actual names are specified in *fCASA-CNP\_clm\_testbed.lst*.

- Files required regardless of SOM model chosen
  - *pftlookup\_igbp.csv* – contains PFT-specific parameters.
  - *modis\_phenology\_wtundra.txt* – tabulated MODIS-derived leaf phenology data for each PFT type. The file is organized in rows by ½ degree latitudes from +79.75, +79.25, ..., -55.25). For each PFT across the columns, this file specifies the day of year that GREENUP and FALL occur. The PHENODAY1 columns specify the phenology stage at the beginning of the simulation (0=min LAI, after FALL but before GREENUP, mostly northern latitudes; 2=max LAI, after GREENUP but before FALL, mostly southern latitudes). Not all PFTs have phenology so only 11 of 18 of them are listed in this file.
  - *co2delta\_control.txt* – contains options for run-time perturbations.
- Additional files required when running MIMICS
  - *pftlookup\_mimics\*.csv* - contains MIMICS-specific parameters. The actual name of this file may vary and is specified in the .lst file.
- Additional files required when running CORPSE

- *corpse\_params.nml* – contains CORPSE specific parameters in a FORTRAN name-list format. The actual name of this file may vary and is specified in the .lst file.

#### 2.2.4.2 Example *fcasacnp\_clm\_testbed.lst* file

Example *fCASA-CNP\_clm\_testbed.lst* file

Comments are preceded with *!!*. Documentation is also located in the bottom half of the file.

```

4299      !! mp, number of points to simulate (formerly 3864)
18        !! mvt, number of vegetation types, =13 for CASA, =18 for IGBP+tundra
100       !! mloop, number of times to cycle through met file
0         !! mdaily, =1 output daily and annual fluxes, =0 output annual fluxes only
3         !! initcasa, =0 spin; =1 restart file; =2 transient (mloop=1); 3= repeated transient (mloop>1)
1901 1920 !! Transient years, contents of this line are ignored if initcasa < 2
3         !! isomModel, SOM model: 1=CASA-CNP, 2=MIMICS, 3=CORPSE
1         !! icycle, =1 for C only, =2 for C+N; =3 for C+N+P
./gridinfo_igbpz.csv                !! 9) Input file with grid info
./pftlookup_igbp_updated4.csv       !! 10) Input file with CASA PFT parameters
./modis_phenology_wtundra.txt       !! 11) Input file with CASA phenology
./gridinfo_soil_clm2.csv            !! 12) Input file with soil properties for each grid cell
../INPUT_MET_GRID/met_1901_1901.nc  !! 13) Input File for met data
./cnppool_end_prespin_1901_x100.csv !! 14) CASA initial conditions (initcasa > 0 only)
./cnppool_end_1901_1920_spin_x500.csv !! 15) CASA end-of-simulation output file (pools)
./cnpflux_end_1901_1920_spin_x500.csv !! 16) CASA end-of-simulation output file (fluxes)
../OUTPUT_GRID/CORPSE_SPIN/casacnm_pool_yyyy.nc !! 17) CASA annual/daily netcdf output file
./pftlookup_mimics.csv              !! 18) MIMICS input parameter file
./mimicspool_init.csv               !! 19) MIMICS initial conditions (initcasa > 0 only)
./mimicspool_end_1901_1920_spin_x500.csv !! 20) MIMICS end-of-simulation output file (pools)
../OUTPUT_GRID/MIMICS_SPIN/mimics_pool_yyyy.nc !! 21) MIMICS annual/daily netcdf output file
./corpsepool_init.csv               !! 22) CORPSE initial conditions (initcasa > 0 only)
./corpsepool_end_1901_1920_spin_x500.csv !! 23) CORPSE end-of-simulation output file (pools)
./corpse_params_new.nml             !! 24) CORPSE input parameter file
../OUTPUT_GRID/CORPSE_SPIN/corpse_pool_yyyy.nc !! 25) CORPSE annual/daily netcdf output file
./co2delta_control.txt              !! 26) Input file for perturbations (Tair, Tsoil, NPP)
-1                                  !! 27) Save daily output for this point. Set to -1 if no daily point file is to be generated.
/project/bgc01/melannie/PointSimulations/ !! 28) Location to write point files (if applicable)

```

!-----

!NOTES: text below line 28 is not read by casacnm\_mimics\_corpse

!Any text following a ' ' or '!' on Lines 9-28 is considered a comment and is not part of the filename

Line 9: Input File. Location of gridinfo file that assigns PFT and area to

each grid cell. Includes annual N fixation. N deposition amount in this file is ignored  
(N deposition is read from met.nc files now).

Internally named filename\_cnppoint.

Line 10: Input File. Contains CASA-CNP parameters for each PFT.

Internally named filename\_cnpbiome.

Line 11: Input File. Describes phenological stages for each grid cell.

Internally named filename\_phen.

- Line 12: Input File. Contains soil properties for each grid cell.  
Internally named filename\_soilprop.
- Line 13: Input File. The name of the met file that drives CASA-CNP.  
For transient runs (initcasa=2 or 3), the year in the filename is replaced by the transient year so N deposition can change over time.  
Internally named filename\_cnpmet.
- Line 14: Input (startup) file. Contains initial values for the CASA-CNP pools when initcasa > 0.  
Internally named filename\_cnpipool.
- Line 15: Output file. End-of-simulation pool values for CASA-CNP.  
Can be used to initialize subsequent runs.  
Internally named filename\_cnpepool.
- Line 16: Output file. Average annual CASA-CNP fluxes during the last "myear" years of the simulation, where myear is the number of years in the met.nc file. Can be used to initialize subsequent runs.  
Internally named filename\_cnpflux.
- Line 17: Output file. NetCDF file that contains the average daily CASA-CNP pools during the last "myear" years plus average annual CASA-CNP fluxes during the last "myear" years of the simulation, where myear is the number of years in the met.nc file. Each year of the transient run will have an output file with 1901 replaced by the transient year, 1901 ... 2100 in this case. Note: for transient simulations, myear = 1.  
Internally named filename\_ncOut.
- Line 18: Input File. Contains MIMICS parameters, some are PFT-specific.  
Internally named filename\_mimicsbiome.
- Line 19: Input (startup) file. Initial values for MIMICS pools when initcasa > 0.  
Internally named filename\_mimicsipool.
- Line 20: Output file. End-of-simulation pool values for MIMICS.  
Can be used to initialize subsequent runs.  
Internally named filename\_mimicsepool.
- Line 21: Output file. NetCDF file that contains the average daily MIMICS pools during the last "myear" years plus average annual MIMICS fluxes during the last "myear" years of the simulation, where myear is the number of years in the met.nc file. Each year of the transient run will have an output file with 1901 replaced by the transient year, 1901 ... 2100 in this case. Note: for transient simulations, myear = 1.  
Internally named filename\_ncOut\_mimics.
- Line 22: Input File. Initial CORPSE pool values. Contains initial values for the CORPSE pools when initcasa > 0. When initcasa=0 use initial\_C values (LABILE,RECALCITRANT,PROTECTED) in corpse\_param.nml (filename\_corpsenamelist) file.  
Internally named filename\_corpseipool.
- Line 23: Output file. End-of-simulation pool values for CASA-CNP.  
Internally named filename\_corpseepool.
- Line 24: Input file. Namelist parameters for CORPSE.  
Internally named filename\_corpsenamelist.
- Line 25: Output file. NetCDF file that contains end-of-simulation CORPSE pools and fluxes.  
Internally named filename\_ncOut\_corpse.

Line 26: Input file. Controls changes in air/soil temperature and NPP during the simulation (formerly co2delta.tx)

Line 27: Save daily output for this point. Set to -1 if no daily point file is to be generated.

TEST\_daily\_casa\_pt.csv and (TEST\_daily\_mimics\_pt.csv or TEST\_daily\_corpse\_pt.csv)

Line 28: Directory for point file.

#### 2.2.4.3 Specifying simulation type: *spinup*, *transient*, *transient repeat* and *using restart files*

If the *initcasa* parameter is set to 1, 2, or 3, the model will require a restart file from a previous simulation to initialize the model (or a file that you have set up with initial conditions). Restart files contain the state of the model at the very end (Dec. 31<sup>st</sup>) of the previous simulation. Restart files do not perfectly reset the model so it is wise not interrupt runs are restart them frequently.

#### 2.2.4.4 Annual vs. Daily Output files

If the *mdaily* parameter is set to 0, the model will create netcdf output for each simulation year. Each variable contains one value per grid cell. For pools, annual values are the MEAN of all daily; for fluxes they are the annual sum. If the *mdaily* parameter is set to 1, the model will create netcdf output for each simulation year. Each variable contains 365 daily values per grid cell. For pools, daily values are the state of the model at the end of the day, and fluxes are the total daily flux.

#### 2.2.5 Compiling the *casacm\_mimics\_corpse* executable

If the *casacm\_mimics\_corpse* executable does not exist or needs to be recompiled for any reason, change to the CASACLM/SOURCE\_CODE directory, remove any object files (to be safe), and type the following “make” command:

```
cd CASACLM/SOURCE_CODE
rm *.o *.mod
make -f Makefile.txt casacm_mimics_corpse
```

If the code fails to compile, the makefile, Makefile.txt, may need to be updated with the specifics (compiler and pathnames) for your system. Next, copy the *casacm\_mimics\_corpse* executable to the location where it will be run. The Linux *chmod* command will make it executable in case the file permissions get changed when it is copied. For example

```
cp casacm_mimics_corpse ../GRID/EXAMPLE_GRID
cd casacm_mimics_corpse ../GRID/EXAMPLE_GRID
chmod 755 netcdfTools
```

#### 2.2.6 Executing the program

Once the list file (*fCASA-CNP\_clm\_testbed.lst*) has been set up, type the following two commands at the command line prompt. The module load command needs only to be run once for each Linux session. It is best to run the model in the background

```
module load tool/netcdf/4.3.2/gcc
./casacm_mimics_corpse &
```

An error similar to the following will occur if the module load command is not executed before running *casacm\_mimics\_corpse*:

*./casacm\_mimics\_corpse: error while loading shared libraries: libnetcdf.so.6: cannot open shared object file: No such file or directory*

The netcdf module version may change with time. To determine the NetCDF version available, type “module avail” at the command line to see available modules.

## 2.3 FAQ

### 2.3.1 How are meteorological and other inputs that to into the in the met.nc files aggregated from CLM? How are soil properties aggregated?

CLM defines multiple PFTs for each 2° x 2° gridcell, whereas CASA-CNP defines only one (IGBP) PFT classification per each grid cell. Since CASA-CNP was already parameterized for IGBP vegetation classifications, and because there was not a good mapping of CLM PFTs to IGBP PFTs, we determined the dominant IGBP classification for each CLM grid cell. We used the mode from a finer resolution IGBP PFT coverage and has 18-vegetation types, including tundra.

CASA-CNP requires GPP as an input, and it calculates NPP by accounting for autotrophic respiration losses and nutrient limitation. Nutrient limitation not relevant when CASA-CNP is run in Carbon-only mode. The GPP values written to the met\*.nc files are total GPP that CLM reported for the grid cell even though CLM’s results are the aggregate of multiple PFT. The NPP written to the met\*.nc as a place holder was calculated as GPP/2, but CASA-CNP does not use this NPP estimate.

The soil water content and soil temperature in the met\*.nc files are the depth-weighted average of soil temperature and volumetric soil water content from CLM for the top 50 cm of soil. The soil texture data in *gridinfo\_soil.csv*, including sand, silt, and clay, are also depth-weighted averages in the top 50 cm of soil. Other soil properties in the *gridinfo\_soil.csv*, including soil water contents at wilting point, field capacity, and saturation (wwilt, wfiel, and wsat, respectively), were determine from soil texture by the hydraulicProperties subroutine in netCDFTools (see file CASACLM/NetCDFTools/SOURCE/clm\_common.F90).

### 2.3.2 What needs to be done to change the PFTs on the existing grid?

- netCDFTools:
  - Optional: Update the IGBP column in *clmGrid\_IGBP.csv* are rerun netCDFTools to generate a new *gridinfo\_igbpz.csv* file. The name of this input and the output file are hardcoded in netCDFTools source code.
- casacm\_mimics\_corpse:
  - If you didn’t run netCDFTools to generate a new *gridinfo\_igbpz.csv* as described above, update the vegetation type code in the *ivt\_igbp* column of “*gridinfo\_igbpz.csv*” (the actual file name may be different).
  - Update the “*pftlookup\_igbp.csv*” file so the parameters for each vegtype correspond with the new PFTS.
  - Similarly, if running MIMICS the “*pftlookup\_mimics.csv*” file also need to be updated. Currently only soil depth is PFT-specific, but this may change.
  - Update the second line in the *fCASA-CNP\_testbed.lst* file to specify the number of PFTs.

### 2.3.3 What needs to be done to change the soil properties on the existing grid?

Update the “gridinfo\_soil.csv” file. However, the volumetric soil moisture in the met.nc files were determined from CLM simulations that used soil textures from CLM surface data.

### 2.3.4 What needs to be done to change the grid resolution and/or lat/lon of grid cells?

The grid resolution is determined by the CLM history files that were used to create the CASA testbed input file. One must also set up an input file with the new PFT classification at the new resolution and rerun netcdf tools. See clmGrid\_IGBP.csv for example. There is one header line in this file, plus one row for each cell defined in the global grid (currently 13,824 grid cells = 144 x 96). This file has 7 columns:

lsm lon – longitude index (1..144)

lsm lat – latitude index (1..96)

LANDFRAC\_P – binary field, 1 = cell with land, 0 = cell with no land.

LONGXY – longitude of grid cell centroid (decimal degrees)

LATIXY – latitude of grid cell centroid (decimal degrees)

IGBP – PFT classification

WRTCELL – binary field. 1 = simulate as stand-alone cell.

NetCDFTools has never been tested for an alternative grid. So if the grid changes and/or the format of the CLM or other model’s history files change, then one will likely need to make updates to the netCDFtools code.

### 2.3.5 What processes are affected when soil temperature is perturbed in the CASA-CNP testbed?

- Temperature effect on soil organic matter turnover rates and heterotrophic respiration (all SOM models)
- N mineralization and N leaching (CASA-CNP C+N only)
- Root maintenance and growth respiration (and therefore NPP and litterfall rates)

### 2.3.6 What processes are affected when air temperature is perturbed in the CASA-CNP testbed?

- Wood maintenance and growth respiration (and therefore NPP and litterfall rates)
- Labile C (carbohydrate) storage (and therefore NPP and litterfall rates)
- Cold effects on leaf litter fall

### 2.3.7 Are there any input/output file size restraints?

The maximum size of a netCDF file is 2GB. The met.nc files for the 2° x 2° CLM grid (4299 cells that had complete data) with 7 years of daily data are just under this 2GB limit. NetCDF tools will likely fail if one tries to create a gridded file with more than 7 years. The number of years in a met.nc file will be fewer for finer-scaled global grids. However, met.nc files for single points can probably contain thousands of years (although I have not tested this).

### 2.3.8 What are the output file options for casaclm\_mimics\_corpse?

The output timestep is either daily or annual. The testbed outputs at least one netcdf file per year.

Daily netcdf output is saved in annual files with 365 days of results. Annual netcdf output files contain

mean annual pool values and total annual fluxes. If the SOM model is CASA-CNP, then the testbed outputs netcdf file per year. If the SOM model is MIMICS or CORPSE, then the testbed will output 2 netcdf files per year, one that contains CASA-CNP pools and fluxes, and the other for the pools and fluxes for the selected SOM model. Note, when MIMICS or CORPSE is the SOM model, then the CASA-CNP output file will still contain variables for its own SOM model, although the associated fluxes will be zero and the pools will likely contain non-zero values from the initialization process, so in this case one must be careful not to use these SOM variables from the CASA-CNP model. The CASA-CNP netcdf files always contain vegetation pools and fluxes, regardless of the SOM model specified.

Similarly, when the testbed is run with the CASA-CNP SOM model, it will generate one .csv file end-of-simulation pool values. When the testbed is run with either MIMICS or CORPSE as the SOM model, the testbed will output two .csv files end-of-simulation pool values; again, in this case, one should ignore the SOM variables in the CASA-CNP end-of-simulation file.

### 2.3.9 What is the best way to do two or more simultaneous runs?

You should never run two simulations simultaneously in the same directory, there will be likely be file conflicts. For example, you should copy the EXAMPLE\_GRID folder and start the second simulation there. Also make sure you aren't sending netcdf file output to the same directory where file results from one simulation could overwrite those from another.

## 3 Model Descriptions

### 3.1 CASA-CNP Vegetation Model

The CASA-CNP terrestrial biosphere model calculated net primary production (NPP) and subsequent plant litter inputs to the soil. When run in carbon-only mode, NPP is not nutrient limited. Daily NPP was daily GPP minus the sum of plant maintenance and growth respiration.

Maintenance respiration for wood and fine roots was a function of their N content. These respiration rates were zero for air/soil temperatures  $\leq 250$  K and increased exponentially with temperature using a fixed biome-specific  $Q_{10}$  ( $\text{g C g N}^{-1} \text{d}^{-1}$ ) (Sitch, Smith et al. 2003). In carbon-only mode, CASA-CNP determines plant pool N content from fixed biome-specific C:N ratios. Additional maintenance respiration flux may occur when CASA-CNP is run with N or N+P and is a function of the size of the labile carbon storage pool; it increases exponentially with temperature using a fixed biome-specific  $Q_{10}$  ( $\text{g C d}^{-1}$ ) for the labile pool. Maintenance respiration for leaves was set to zero. Growth respiration was a fraction ( $1.0 - \text{growth efficiency}$ ) of the quantity GPP minus the sum of maintenance respiration fluxes. For C only or C+N only, growth efficiency ( $Y_{\text{grow}}$ ) = 0.65 in C+N+P mode it is less (Figure 19).

The fraction of NPP allocated to leaf, wood or fine roots depended on leaf phenology (Wang, Law et al. 2010). Global leaf phenology for all biomes was derived from the estimates of remote sensing observations (Zhang, Friedl et al. 2006). Leaf growth was divided into four phases. Phase 1 was from leaf budburst to the start of steady leaf growth and was 14 days long, phase 2 was from the start of steady leaf growth to the beginning of leaf senescence, phase 3 was the 14-day period of leaf senescence, and phase 4 was from the end of leaf senescence to the start of leaf bud burst. For evergreen biomes, leaf phenology remained at phase 2 throughout the year. During maximal leaf growth (phase 1), 80% of C was allocated to leaves, the remainder of C was allocated to wood and fine roots. During the steady

growth period (phase 2), C allocation to leaves, wood, and fine roots was determined by the fixed biome-specific fractions, but leaf allocation was adjusted (increased to 80% or reduced to 0%) if LAI was below or above the theoretical biome-specific minimum and maximum LAI. During leaf growth phase 3 (senescence) and 4 (minimum LAI), no carbon was allocated to leaves and all C is allocated to wood and fine roots.

Turnover of live leaves, wood, and fine roots occurred daily at biome-specific age-related death rates, except that age-related death rates for leaves during Phase 1 were zero. The leaf turnover rate increased with cold and drought stress, and was modeled following the approach of Arora and Boer (2005). Drought- and cold-induced leaf death could occur during any phenology phase.

CASA-CNP defines a single International IGBP per each grid cell, and has a set of biome-specific parameters that control plant growth and turnover, SOM turnover, plant and SOM stoichiometry, and other processes.

Non-woody plant litter is partitioned into Structural and Metabolic litter material as a function of the lignin:N ratio of the plant litter. Woody plant litter accumulates in the coarse woody debris (CWD) pool. CWD decomposes as a function of temperature and soil moisture, with CO<sub>2</sub> respiration loss. Metabolic litter, Structural litter, and decomposing CWD provide C inputs to all soil carbon models in the testbed.

### 3.1.1 Plant Functional Types

The 18 plant functional types (PFTs) currently used by the testbed are described in Table 1 below. Ice, water, and urban types are not simulated by the testbed.

*Table 1. IGBP\_CERES plant functional types (PFTs) used by the CASA-CNP testbed, from pftlookup\_casa.csv.*

PFT	(ice,water,urban:0)/ grass:1/shrub:2/woody:3	
1	3	Evergreen Needleleaf Forest
2	3	Evergreen Broadleaf Forest
3	3	Deciduous Needleleaf Forest
4	3	Deciduous Broadleaf Forest
5	3	Mixed forest
6	2	Close shrublands
7	2	Open shrublands
8	3	woody savannas
9	3	savannas
10	1	grasslands
11	0	permanent wetlands
12	1	croplands
13	0	urban and built-up
14	1	cropland mosaic (as 12)
15	0	permanent snow and ice



16	1	barren or sparsely vegetated
17	0	ice, water
18	1	tundra

Source: National Center for Atmospheric Research Staff (Eds). Last modified 10 Feb 2017. "The Climate Data Guide: CERES: IGBP Land Classification." Retrieved from <https://climatedataguide.ucar.edu/climate-data/ceres-igbp-land-classification>. The web pages explain the use of the International Geosphere/Biosphere Programme (IGBP) scene types in the CERES/SARB surface map. There are 18 surface types used by the SARB group to identify surface properties of a given region. Scene types were delineated by IGBP. This map is determined using a 1km IGBP scene types supplied by USGS. An 18th scene type (Tundra) is added to distinguish the rocky/barren scene of northern climes vs. that of other deserts.

### 3.2 CASA-CNP Soil Carbon Model

CASA-CNP soil carbon model has two litter pools (Metabolic and Structural) and three soil organic matter pools (Fast (a.k.a. Microbial), Slow, and Passive) (Figure 3). Live microbial biomass is not explicitly simulated by CASA-CNP therefore we refer to CASA-CNP's microbial pool as the Fast pool to avoid confusion with the live microbial pools of the microbial-explicit SOM models. Non-woody plant litter is partitioned into Structural and Metabolic litter pools as a function of the lignin:N ratio of the plant litter. Woody plant litter accumulates in the coarse woody debris (CWD) pool. The decomposition rates of all pools are controlled by first-order kinetics and modified by soil temperature and moisture controls. Plant litter pools decompose into Fast and Slow pools as a function leaf/wood lignin, with CO<sub>2</sub> respiration loss. The CWD pool decomposes to the Fast and Slow SOM pools, with CO<sub>2</sub> respiration loss, as a function of the wood lignin. Transfers of C from the Fast and Slow pools form the Passive Pool are a function of soil texture. The passive pool decomposes, with CO<sub>2</sub> respiration loss, without transfers of C to other pools.

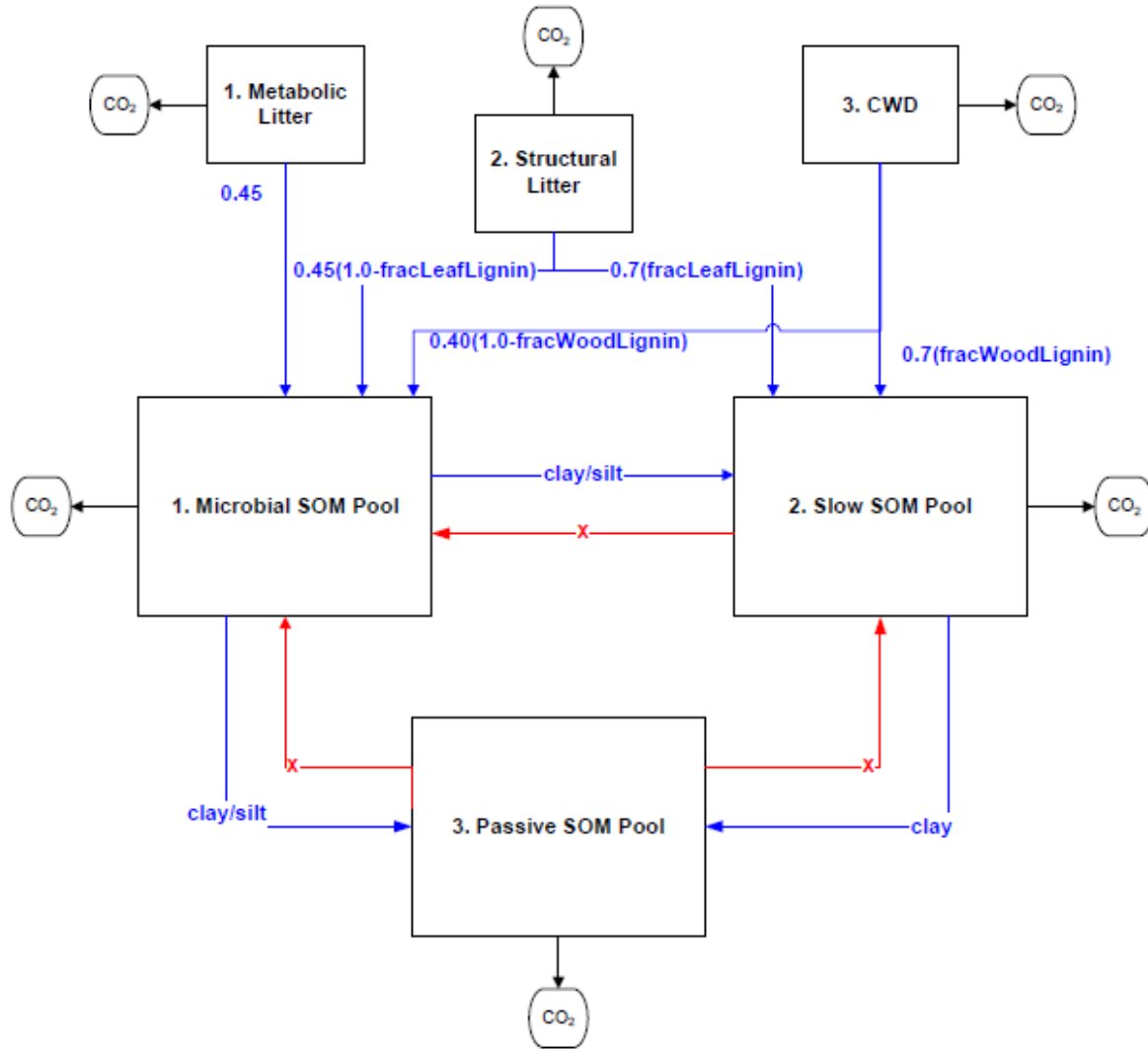


Figure 3. Litter and Soil Organic Matter Pools in the CASA-CNP model. All flows out of any litter or soil pool are controlled by  $f(T)$  and  $f(W)$  as well as the lignin/texture controls shown with the blue arrows. The blue text refers to the controls on the fraction of the total flow that is transferred from one pool to another; 1.0 minus these fractions is the portion of the total flow that goes to heterotrophic respiration. The red arrows indicate that there is no flow from the Passive SOM pool to the Fast (Microbial) or Slow SOM pools. See equations below.

### 3.2.1 Partitioning of plant litter inputs in CASA-CNP

The Lignin:N ratio (g lignin / g N) of plant biomass is used to partition leaf and fine root litter into structural and metabolic components. When running CASA-CNP in carbon-only mode, the initial C:N ratio parameters along with lignin fractions are used to compute lignin:N ratios (

Table 2). For plant part  $i$  = leaf, wood, and froot, the lignin:N ratios are the product of the lignin fraction and the C:N ratio:

$$\text{Lignin:N}_{i,pft} = \text{ligninFraction}_{i,pft} \times \text{C:N ratio}_{i,pft}$$

Table 2. Initial C:N ratios and lignin content of plant parts by PFT.

vegtype (PFT)	C:N leaf gC/gN	C:N wood gC/gN	C:N froot gC/gN	lignin leaf g lignin /gC	lignin CWD g lignin /gC	lignin froot g lignin /gC
1	50	250	78	0.25	0.4	0.25
2	25	150	68	0.2	0.4	0.2
3	60	250	41	0.2	0.4	0.2
4	50	175	41	0.2	0.4	0.2
5	50	175	41	0.22	0.4	0.22
6	45	150	41	0.2	0.4	0.2
7	40	150	41	0.2	0.4	0.2
8	25	150	41	0.15	0.4	0.15
9	25	150	41	0.15	0.4	0.15
10	50	150	41	0.1	0.4	0.1
11	30	150	41	0.15	0.4	0.15
12	50	125	41	0.2	0.4	0.2
13	40	150	41	0.15	0.4	0.15
14	30	125	41	0.1	0.4	0.1
15	40	150	41	0.1	0.4	0.1
16	40	150	41	0.15	0.4	0.15
17	40	135	41	0.25	0.4	0.25
18	47.6	150	41	0.166	0.4	0.166

The fraction of leaf and fine root litter allocation to metabolic litter ( $\text{fracC}$ , 0.0 – 0.85) increases with the ratio of lignin:N of the plant residue. The remaining fraction is allocated to structural litter (Figure 4). This partitioning is used by CASA-CNP and CORPSE SOM models. See also “Partitioning of plant litter inputs in MIMICS”.

$$\begin{aligned}
 \text{fracC}_{\text{leaf} \rightarrow \text{metb}} &= \max(0.001, 0.85 - 0.018 \cdot \text{ratioLignintoN}(\text{leaf})) \\
 \text{fracC}_{\text{froot} \rightarrow \text{metb}} &= \max(0.001, 0.85 - 0.018 \cdot \text{ratioLignintoN}(\text{froot})) \\
 \text{fracC}_{\text{leaf} \rightarrow \text{struc}} &= 1.0 - \text{fracC}_{\text{leaf} \rightarrow \text{metb}} \\
 \text{fracC}_{\text{froot} \rightarrow \text{struc}} &= 1.0 - \text{fracC}_{\text{froot} \rightarrow \text{metb}} \\
 \text{fracC}_{\text{wood} \rightarrow \text{cwd}} &= 1.0
 \end{aligned}$$

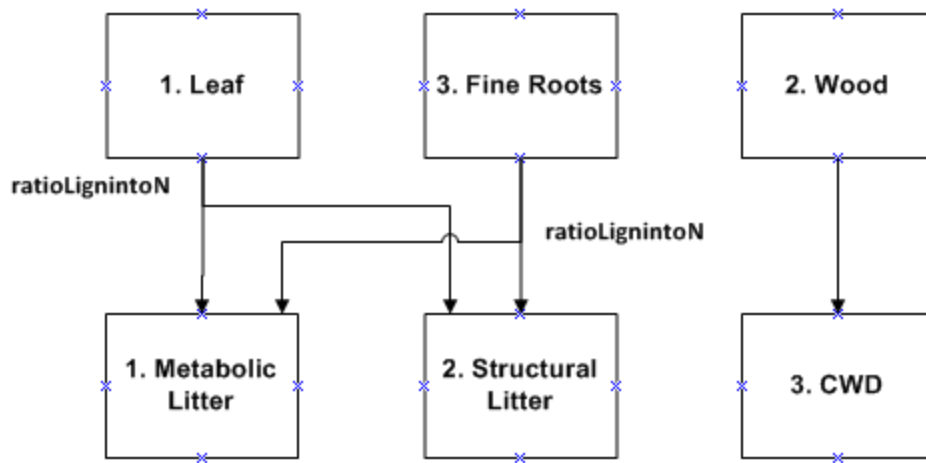


Figure 4. CASA-CNP plant litter transfers to the metabolic and structural litter pools

The lignin:N ratios are computed from plant C and N pools and biome-specific parameters. When CASA-CNP is run in carbon-only model, **plant N pools are determined from fixed biome-specific N:C ratios.**

$$\text{ratioLignintoN}(\text{leaf}) = \frac{\text{fracLigninplant}(PFT, \text{leaf})}{\text{ratioNCplant}(PFT, np)}$$

$$\text{ratioLignintoN}(\text{froot}) = \frac{\text{fracLigninplant}(PFT, \text{froot})}{\text{ratioNCplant}(PFT, \text{froot})}$$

Where:

$\text{fracLigninplant}(PFT, *)$  – biome-specific lignin:N ratio (g lignin / g N)

$\text{ratioNCplant}(PFT, *)$  – biome-specific fraction of N:C ratios

**Metabolic litter → Fast SOM**

$$C_{mic,metbc} = (0.45) \left( xkoptlitter(PFT) \cdot xktemp \cdot xkwater \right) \cdot \frac{1}{365 \cdot metbc_{age}(PFT)} \cdot METBC$$

$$CO_2Resp_{mic,metbc} = (1.0 - 0.45) \left( xkoptlitter(PFT) \cdot xktemp \cdot xkwater \right) \cdot \frac{1}{365 \cdot metbc_{age}(PFT)} \cdot METBC$$

### Structural litter → Fast SOM

$$C_{mic,struc} = 0.45 \left( 1.0 - fracLigninplant(PFT, leaf) \right) \cdot \left( xkoptlitter(PFT) \cdot xktemp \cdot xkwater \right) \cdot \frac{1}{365 \cdot struc_{age}(PFT)} \cdot STRUC$$

$$CO_2Resp_{mic,struc} = \left[ 1.0 - 0.45 \left( 1.0 - fracLigninplant(PFT, leaf) \right) \right] \cdot \left( xkoptlitter(PFT) \cdot xktemp \cdot xkwater \right) \cdot \frac{1}{365 \cdot struc_{age}(PFT)} \cdot STRUC$$

### Structural litter → Slow SOM

$$C_{slow,struc} = 0.7 \cdot fracLigninplant(PFT, leaf) \cdot \left( xkoptlitter(PFT) \cdot xktemp \cdot xkwater \right) \cdot \frac{1}{365 \cdot struc_{age}(PFT)} \cdot STRUC$$

$$CO_2Resp_{slow,struc} = \left[ 1.0 - 0.7 \cdot fracLigninplant(PFT, leaf) \right] \cdot \left( xkoptlitter(PFT) \cdot xktemp \cdot xkwater \right) \cdot \frac{1}{365 \cdot struc_{age}(PFT)} \cdot STRUC$$

### Coarse Woody Debris → Fast SOM

$$C_{mic,cwd} = 0.40(1.0 - \text{fracLigninplant}(PFT, wood)) \\ \cdot (xkoptlitter(PFT) \cdot xktemp \cdot xkwater) \\ \cdot \frac{1}{365 \cdot CWD_{age}(PFT)} \cdot CWD$$

$$CO_2Resp_{mic,cwd} = [1.0 - 0.40(1.0 - \text{fracLigninplant}(PFT, wood))] \\ \cdot (xkoptlitter(PFT) \cdot xktemp \cdot xkwater) \\ \cdot \frac{1}{365 \cdot CWD_{age}(PFT)} \cdot CWD$$

### Coarse Woody Debris → Slow SOM

$$C_{slow,cwd} = 0.7 \text{fracLigninplant}(PFT, wood) \\ \cdot (xkoptlitter(PFT) \cdot xktemp \cdot xkwater) \\ \cdot \frac{1}{365 \cdot CWD_{age}(PFT)} \cdot CWD$$

$$CO_2Resp_{slow,cwd} = [1.0 - 0.7 \text{fracLigninplant}(PFT, wood)] \\ \cdot (xkoptlitter(PFT) \cdot xktemp \cdot xkwater) \\ \cdot \frac{1}{365 \cdot CWD_{age}(PFT)} * CWD$$

### Fast SOM → Slow SOM

$$C_{slow,mic} = (0.85 - 0.68(clay + silt)) \cdot (0.997 - 0.032clay) \\ \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \cdot \frac{1}{365 \cdot MIC_{age}(PFT)} \cdot MIC$$

$$CO_2Resp_{slow,mic} = \left[ 1.0 - (0.85 - 0.68(clay + silt)) \cdot (0.997 - 0.032clay) \right] \\ \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \cdot \frac{1}{365 \cdot MIC_{age}(PFT)} \cdot MIC$$

**Fast SOM → Passive SOM**

$$C_{pass,mic} = (0.85 - 0.68(clay + silt)) \cdot (0.003 + 0.032clay) \\ \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \cdot \frac{1}{365 \cdot MIC_{age}(PFT)} \cdot MIC$$

$$CO_2Resp_{pass,mic} = \left[ 1.0 - (0.85 - 0.68(clay + silt)) \cdot (0.003 + 0.032clay) \right] \\ \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \cdot \frac{1}{365 \cdot MIC_{age}(PFT)} \cdot MIC$$

**Slow SOM → Passive SOM**

$$C_{pass,slow} = 0.45(0.003 + 0.009clay) \\ \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \\ \cdot \frac{1}{365 \cdot SLOW_{age}(PFT)} \cdot SLOW$$

$$CO_2Resp_{pass,slow} = \left[ 1.0 - 0.45(0.003 + 0.009clay) \right] \\ \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \\ \cdot \frac{1}{365 \cdot SLOW_{age}(PFT)} \cdot SLOW$$

**Passive Pool Decomposition**

$$CO_2Resp_{pass} = (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \cdot \frac{1}{365 \cdot PASS_{age}(PFT)} \cdot PASS$$

### 3.2.2 CASA-CNP Temperature and Moisture Controls on Decomposition of Litter and SOM

The decomposition of litter or SOM pools is a first order equation. The maximum decomposition rate is multiplied by temperature and moisture functions.

$$xklitter = xkoptlitter(PFT) \cdot xktemp \cdot xkwater$$

$$xksoil = xkoptsoil(PFT) \cdot xktemp \cdot xkwater$$

Where  $xkoptlitter(PFT)$  and  $xkoptsoil(PFT)$  are the biome-specific maximum decomposition rates (1/day) for litter and soil, respectively;  $xktemp$  is the soil temperature effect on decomposition (0.0-2.0), and  $xkwater$  is the effect of soil moisture (0.0-1.0). In CASA-CNP croplands PFTs have no moisture limitation on soil organic matter decomposition ( $xkwater=1.0$ ) and daily turnover rates for the fast, slow, and passive pools are multiplied by 1.25, 1.5, and 1.5 respectively.

#### 3.2.2.1 CASA-CNP Temperature Controls on Decomposition

The  $Q_{10}$  of the soil temperature function is a biome-specific input, set to 1.72 for all biomes. The value  $tsavg$  is the average soil temperature in the rooting zone (50 – 150 cm) (K) (Figure 5).

$$xktemp = Q_{10,soil}(PFT)^{0.1(tsavg - TK_{zeroC} - 35.0)}$$



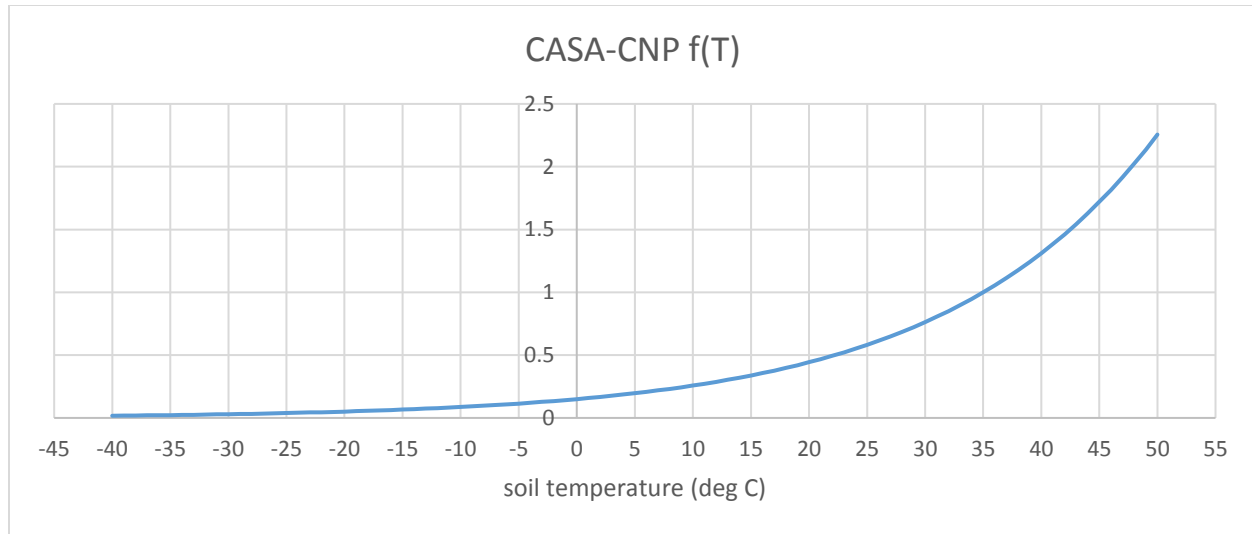


Figure 5. CASA-CNP soil temperature effect on Soil Organic Matter decomposition.

### 3.2.2.2 CASA-CNP Soil Moisture Controls on Decomposition

wfpscoefa = 0.55 ! Kelly et al. (2000) JGR, Figure 2b), optimal wfps

wfpscoefb = 1.70 ! Kelly et al. (2000) JGR, Figure 2b)

wfpscoefc = -0.007 ! Kelly et al. (2000) JGR, Figure 2b)

wfpscoefd = 3.22 ! Kelly et al. (2000) JGR, Figure 2b)

wfpscoefe = 6.6481 ! =wfpscoefd\*(wfpscoefb-wfpscoefa)/(wfpscoefa-wfpscoefc)

*fwps* is soil moisture expressed as the fraction of water filled pore space (0.0 – 1.0) (Figure 6).

$$fwps = \frac{moistavg}{ssat}$$

$$xkwater = \begin{cases} \left( \frac{fwps - wfpscoefb}{wfpscoefa - wfpscoefb} \right)^{wfpscoefe} \cdot \left( \frac{fwps - wfpscoefc}{wfpscoefa - wfpscoefc} \right)^{wfpscoefd}, & \text{non-cropland} \\ 1.0, & \text{cropland} \end{cases}$$

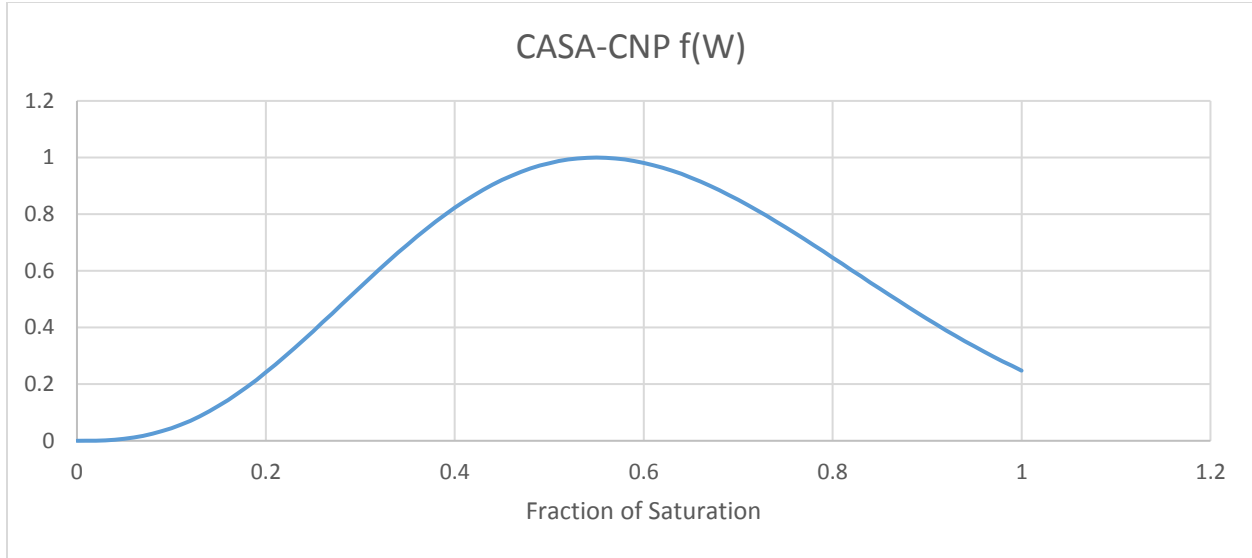


Figure 6. CASA-CNP soil moisture effect on SOM decomposition.

### 3.2.3 Carbon Stabilization and Destabilization in CASA-CNP

Protected C resides in the Passive SOM pool. The flow of C from the Fast and Slow pools to the Passive pool is a function of silt and clay (Figure 7).

$$C_{mic \rightarrow pass} = (0.85 - 0.68(clay + silt)) \cdot (0.003 + 0.032clay) \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \cdot \frac{1}{365 \cdot MIC_{age}(PFT)} \cdot MIC$$

$$C_{slow \rightarrow pass} = 0.45(0.003 + 0.009clay) \cdot (xkoptsoil(PFT) \cdot xktemp \cdot xkwater) \cdot \frac{1}{365 \cdot SLOW_{age}(PFT)} * SLOW$$

All carbon from the decomposition of the Passive SOM pool is lost as CO<sub>2</sub>. The intrinsic rate of decomposition of the passive pool is a biome-specific constant.

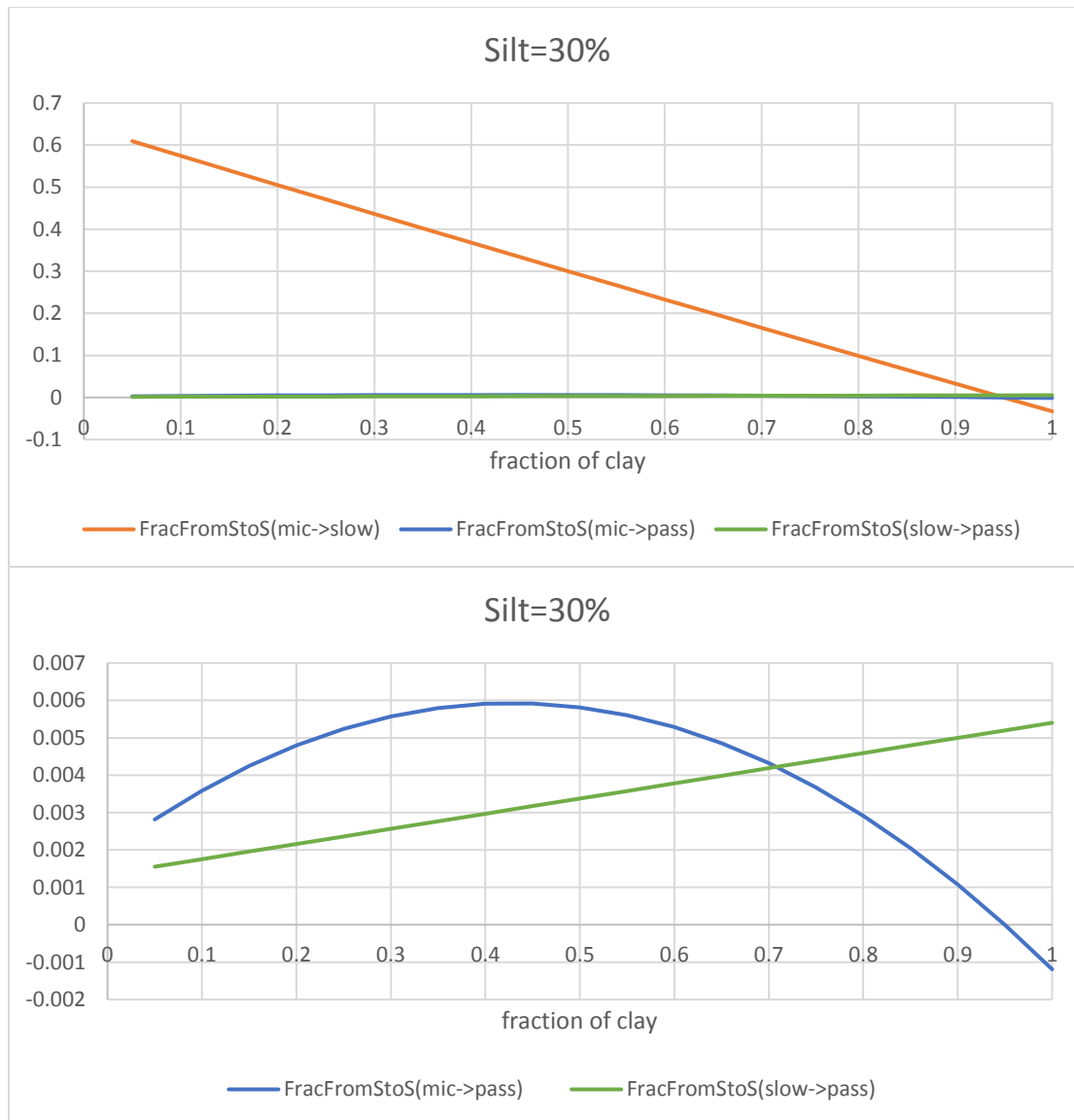


Figure 7. The effect of soil clay content (% weight) on the fraction of flows between soil organic matter pools. The silt fraction was held at a constant 30%. The lower figure is a zoomed in version of the top figure.

### 3.3 CASA-CNP Soil Layer Structure

CASA-CNP defines six soil layers with increasing thicknesses with depth (Table 3). These layer thicknesses are defined internally and cannot be reset outside of the code.

Table 3. *CASA-CNP Soil Layer Structure*

Layer Number	1	2	3	4	5	6
--------------	---	---	---	---	---	---

Layer Thickness (m)	0.022	0.058	0.154	0.409	1.085	2.872
depthsoila (m)	0.000	0.022	0.080	0.234	0.643	1.728
depthsoilb (m)	0.022	0.080	0.234	0.643	1.728	4.600

### 3.3.1 Mapping of CLM soil layers to CASA-CNP soil layers

In order to compute soil moisture and soil temperature for each of the six CASA-CNP soil layers, the six CASA-CNP soil layers were mapped to ten CLM soil layers as shown in the tables below, based on the maximum depth of each soil layer. Soil moisture and soil temperature of CASA-CNP were the weighted average of the corresponding values in the CLM layers:

CASA-CNP layer 1 to CLM layer 1

CASA-CNP layer 2 to CLM layers 2 and 3

CASA-CNP layer 3 to CLM layers 4 and 5

CASA-CNP layer 4 to CLM layers 6 and 7

CASA-CNP layer 5 to CLM layers 8 and 9

CASA-CNP layer 6 to CLM layers 10

CLM layer #	z (center of layer, m)	$\Delta z$ (m)	$\Delta z$ (cm)	upper depth (cm)	lower depth (cm)
1	0.0071	0.0175	1.75	0	1.75
2	0.0279	0.0276	2.76	1.75	4.51
3	0.0623	0.0455	4.55	4.51	9.06
4	0.1189	0.075	7.5	9.06	16.56
5	0.2122	0.1236	12.36	16.56	28.92
6	0.3661	0.2038	20.38	28.92	49.3
7	0.6198	0.336	33.6	49.3	82.9
8	1.038	0.5539	55.39	82.9	138.29
9	1.7276	0.9133	91.33	138.29	229.62
10	2.8646	1.137	113.7	229.62	343.32

CASA-CNP layer #	$\Delta z$ (m)	$\Delta z$ (cm)	upper depth (cm)	lower depth (cm)	z (center of layer, cm)
1	0.022	2.2	0	2.2	1.1
2	0.058	5.8	2.2	8	5.1
3	0.154	15.4	8	23.4	15.7
4	0.409	40.9	23.4	64.3	43.85
5	1.085	108.5	64.3	172.8	118.55
6	2.872	287.2	172.8	460	316.4

### 3.3.2 Fraction of root biomass in each CASA-CNP soil layer

The fraction of root biomass in each of six soil layers (ns=1..6) is determined from three biome-specific parameters and the following equations (Table 4, Table 5).

$$totroot(pft) = 1.0 - \exp(-casabiome\%kroot(pft) * casabiome\%rootdepth(pft))$$

$$fracroot(pft, ns) = \frac{\left( \exp(-casabiome\%kroot(pft) * \min(casabiome\%rootdepth(pft), depthsoila(ns))) - \exp(-casabiome\%kroot(pft) * \min(casabiome\%rootdepth(pft), depthsoilb(ns))) \right)}{totroot(pft)}$$

Table 4. CASA-CNP parameters used to calculate fraction of root in each soil layer

vegtype (PFT)	Kroot (1/m)	rootdepth (m)	Krootlen (m/g C)
1	5.5	1.5	14.87805
2	3.9	1.5	14.38596
3	5.5	1.5	14.02597
4	3.9	1.5	18.94737
5	2	1.5	16.71642
6	2	0.5	0
7	2	0.5	32.30769
8	2	1.5	120.8
9	2	1.5	120.8
10	5.5	0.5	84
11	5.5	0.5	0
12	5.5	0.5	120.5
13	2	0.5	0
14	5.5	0.5	0
15	5.5	0.5	0
16	2	0.5	30.76923
17	5.5	1.5	0
18	5.5	0.5	84

Table 5. Fraction of roots in each soil layer by PFT

Vegtype (PFT)	fracroot(1)	fracroot(2)	fracroot(3)	fracroot(4)	fracroot(5)	fracroot(6)
1	0.11	0.24	0.37	0.25	0.03	0.0
2	0.08	0.19	0.33	0.32	0.08	0.0

Vegtype (PFT)	fracroot(1)	fracroot(2)	fracroot(3)	fracroot(4)	fracroot(5)	fracroot(6)
3	0.11	0.24	0.37	0.25	0.03	0.0
4	0.08	0.19	0.33	0.32	0.08	0.0
5	0.05	0.11	0.24	0.37	0.24	0.0
6	0.07	0.17	0.36	0.41	0.0	0.0
7	0.07	0.17	0.36	0.41	0.0	0.0
8	0.05	0.11	0.24	0.37	0.24	0.0
9	0.05	0.11	0.24	0.37	0.24	0.0
10	0.12	0.26	0.39	0.23	0.0	0.0
11	0.12	0.26	0.39	0.23	0.0	0.0
12	0.12	0.26	0.39	0.23	0.0	0.0
13	0.07	0.17	0.36	0.41	0.0	0.0
14	0.12	0.26	0.39	0.23	0.0	0.0
15	0.12	0.26	0.39	0.23	0.0	0.0
16	0.07	0.17	0.36	0.41	0.0	0.0
17	0.11	0.24	0.37	0.25	0.03	0.0
18	0.12	0.26	0.39	0.23	0.0	0.0

### 3.4 MIMICS

MIMICS has two litter pools (Metabolic and Structural), two live microbial biomass pools (R-selected and K-selected), and three soil organic matter pools (Available, Chemically Protected, and Physically Protected) (Figure 8). Non-woody plant litter is partitioned into Structural and Metabolic litter pools as a function of the lignin:N ratio of the plant litter, using a slightly different function than the CASA-CNP model's. Decomposing CWD carbon is transferred to the structural litter pool as a function of soil moisture and temperature, with CO<sub>2</sub> respiration loss. The decomposition rates of Metabolic and Structural litter and Available SOM pools are controlled by reverse Michaelis-Menton kinetics (substrate limited) and modified by soil temperature controls. The Structural and Metabolic litter pools are consumed by R-selected and K-selected live microbial pools, with CO<sub>2</sub> respiration loss. Microbial turnover, which is proportional to annual NPP, transfers C to Physically Protected, Chemically Protected, and Available SOM pools, without CO<sub>2</sub> respiration loss. Desorption of the Physically Protected pool, a function of soil clay content, and oxidation of the Chemically Protected pool, transfer C to the Available pool, without CO<sub>2</sub> loss. Carbon in the Available pool is consumed by the two microbial pools, with CO<sub>2</sub> respiration loss.

Decomposition of carbon pool (C<sub>i</sub>) by microbe pool (MIC<sub>r/k</sub>)

$$D_i = Vmax_{r/K}(T) \cdot C_i \frac{MIC_{r/K}}{Km_{r/K}(T) + MIC_{r/K}}$$

where Vmax(T) is the temperature-sensitive Vmax(T)– temperature sensitive maximum reaction velocity, Km(T) is the temperature-sensitive half-saturation constant.

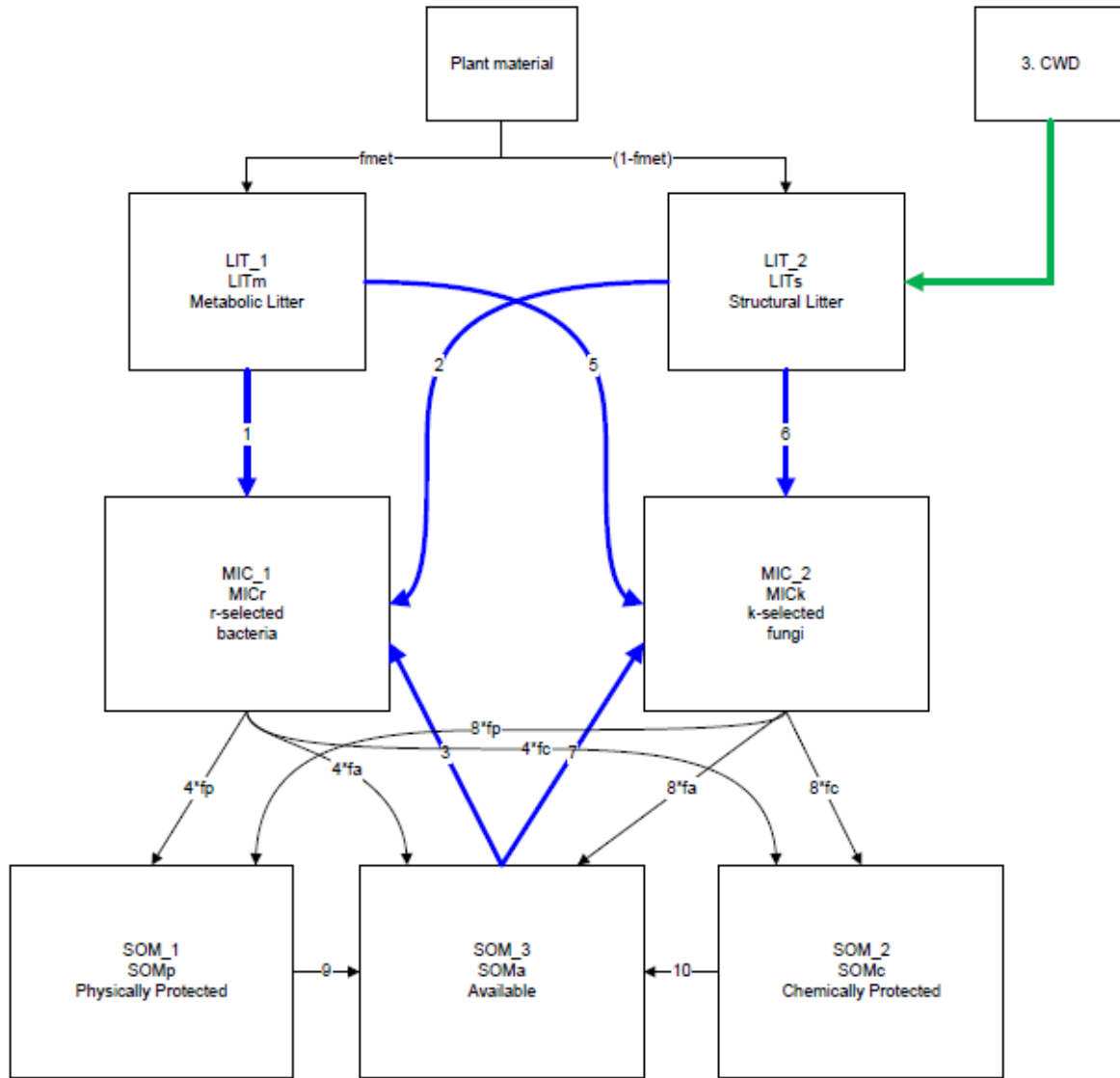


Figure 8. Litter and Soil Organic Matter pools in the MIMICS model. Heterotrophic respiration losses occur with consumption of litter and available pools by the microbes, and with the decomposition of the CWD pool.

### 3.4.1 Partitioning plant litter in MIMICS

The fraction of plant litter partitioned to metabolic litter ( $f_{met}$ ) is a function the weighted average lignin:N ratio of all litter inputs ( $nP$ =leaf, froot).

$$f_{met}(nP) = f_{metP}(1) * \left( f_{metP}(2) - f_{metP}(3) * \frac{\text{ligninNratio}(npt, nP) * \text{litterInput}(npt, nP)}{\sum_{nP} \text{litterInput}(npt, nP)} \right)$$

where:

$fmetP(1) = 0.75$  (or as defined in pftlookup\_mimics.csv)

$fmetP(2) = 0.85$  (or as defined in pftlookup\_mimics.csv)

$fmetP(3) = 0.013$  (or as defined in pftlookup\_mimics.csv)

Hourly changes in MIMICS Litter and SOM pools and heterotrophic respiration losses are summarized as follows:

$$dLITm / dt = litInput[metb] \cdot (1.0 - Fi[metb]) - LITmin[1] - LITmin[3]$$

$$dMICr / dt = MGE[1] \cdot (LITmin[1] + SOMmin[1]) + MGE[2] \cdot (LITmin[2]) - \sum_{i=1}^3 MICtrn[i]$$

$$dSOMp / dt = litInput[metb] \cdot Fi[metb] + MICtrn[1] + MICtrn[4] - DEsorb$$

$$dLITs / dt = litInput[struct] \cdot (1.0 - Fi[struct]) - LITmin[2] - LITmin[4]$$

$$dMICK / dt = MGE[3] \cdot (LITmin[3] + SOMmin[2]) + MGE[4] \cdot (LITmin[4]) - \sum_{i=4}^6 MICtrn[i]$$

$$dSOMc / dt = litInput[struct] \cdot Fi[struct] + MICtrn[2] + MICtrn[5] - OXIDAT$$

$$dSOMa / dt = MICtrn[3] + MICtrn[6] + DEsorb + OXIDAT - SOMmin[1] - SOMmin[2]$$

$$hResp = (1.0 - MGE[1]) \cdot (LITmin[1] + SOMmin[1]) + (1.0 - MGE[2]) \cdot (LITmin[2]) \\ + (1.0 - MGE[3]) \cdot (LITmin[3] + SOMmin[2]) + (1.0 - MGE[4]) \cdot (LITmin[4])$$

where:

$LITmin[1..4]$  = litter decomposition

$MICtrn[1..3]$  = microbial turnover

$SOMmin[1..2]$  = SOM decomposition

$litInput[metb]$  – litter inputs to metabolic litter ( $\text{mg C cm}^{-3} \text{ hr}^{-1}$ )

$litInout[struct]$  – litter inputs to structural litter ( $\text{mg C cm}^{-3} \text{ hr}^{-1}$ )

$Fi[metb]$  – fraction of metabolic litter inputs transferred to SOMp (0.05), the remainder goes to the metabolic litter pool.

$Fi[struct]$  – fraction of structural litter inputs transferred to SOMc (0.05), the remainder goes to the structural litter pool.

$MGE[1]$  – microbial growth efficiency for C fluxes from LITm or SOMa into MICr (0.55,  $\text{mg mg}^{-1}$ )

$MGE[2]$  – microbial growth efficiency for C fluxes from LITs into MICr (0.25,  $\text{mg mg}^{-1}$ )

$MGE[3]$  – microbial growth efficiency for C fluxes from LITm or SOMa into MICK (0.75,  $\text{mg mg}^{-1}$ )

$MGE[4]$  – microbial growth efficiency for C fluxes from LITs into MICK (0.35,  $\text{mg mg}^{-1}$ )



$hResp$  – total heterotrophic respiration ( $\text{mg C cm}^{-3} \text{ hr}^{-1}$ ). Multiple by depth (cm) to get respiration per unit area.

The individual flows from pool to pool are summarized below. Variables  $F_1 \dots F_{10}$  below refer to equations in Wieder, Grandy et al. (2015).

#### 3.4.1.1 Flows to and from MICr

##### MICr decomposition of metabolic litter (f1. LITm-->MICr)

$$F_1 = LITmin[1] = \frac{MICr \cdot Vmax[r1] \cdot LITm}{Km[r1] + MICr}$$

##### MICr decomposition of structural litter (f2. LITs-->MICr)

$$F_2 = LITmin[2] = \frac{MICr \cdot Vmax[r2] \cdot LITs}{Km[r2] + MICr}$$

##### MICr turnover to physically protected SOM (f41. MICr-->SOMp)

$$F_{4.1} = MICtrn[1] = MICr \cdot \tau_r \cdot fPHYS[1]$$

where:

$fPHYS[1]$  – fraction of  $\tau_r$  partitioned into  $SOMp$  as a function of  $fclay$  (0.0 – 1.0)

##### MICr turnover to chemically protected SOM (f42. MICr-->SOMc)

$$F_{4.2} = MICtrn[2] = MICr \cdot \tau_r \cdot fCHEM[1]$$

where:

$fCHEM[1]$  – fraction of  $\tau_r$  partitioned into  $SOMc$  as a function of  $fmet$  (0.0 – 1.0)

##### MICr turnover to available SOM (f43. MICr-->SOMa)

$$F_{4.3} = MICtrn[3] = MICr \cdot \tau_r \cdot fAVAL[1]$$

where:

$fAVAL[1]$  — fraction of  $\tau_r$  partitioned into  $SOMa$  (0.0 – 1.0)

##### Decomposition of SOMa by MICr (f3. SOMa-->MICr)

$$F_3 = SOMmin[1] = \frac{MICr \cdot Vmax[r3] \cdot SOMa}{Km[r3] + MICr}$$

### 3.4.1.2 Flows to and from MICK

#### MICK decomposition of metabolic litter (f5. LITm -->MICK)

$$F_5 = LITmin[3] = \frac{MICK \cdot Vmax[k1] \cdot LITm}{Km[k1] + MICK}$$

#### MICK decomposition of structural litter (f6. LITs-->MICK)

$$F_6 = LITmin[4] = \frac{MICK \cdot Vmax[k2] \cdot LITs}{Km[k2] + MICK}$$

#### MICK turnover to physically protected SOM (f81. MICK-->SOMp)

$$F_{8.1} = MICtrn[4] = MICK \cdot \tau_k \cdot fPHYS[2]$$

where:

$fPHYS[2]$  – fraction of  $\tau_k$  partitioned into  $SOMp$  as a function of  $fclay$  (0.0 – 1.0)

#### MICK turnover to chemically protected SOM (f82. MICK-->SOMc)

$$F_{8.2} = MICtrn[5] = MICK \cdot \tau_k \cdot fCHEM[2]$$

where:

$fCHEM[2]$  – fraction of  $\tau_k$  partitioned into  $SOMc$  as a function of  $fmet$  (0.0 – 1.0)

#### MICK turnover to available SOM (f83. MICK->SOMa)

$$F_{8.3} = MICtrn[6] = MICK \cdot \tau_k \cdot fAVAL[2]$$

where:

$fAVAL[2]$  — fraction of  $\tau_k$  partitioned into  $SOMa$  (0.0 – 1.0)

#### Decomposition of SOMa by MICK (f7. SOMa-->MICK)

$$F_7 = SOMmin[2] = \frac{MICK \cdot Vmax[k3] \cdot SOMa}{Km[k3] + MICK}$$

### 3.4.1.3 Desorption of physically protected SOM to available SOM

$$F_9 = DEsorb = SOMp \cdot 1.5 \cdot 10^{-5} \cdot \exp(-1.5 fclay)$$

### 3.4.1.4 Oxidation of SOMc to SOMa

$$F_{10} = OXIDAT = \left( \frac{MICr \cdot Vmax[r2] \cdot SOMc}{KO[1] \cdot KM[r2] + MICr} \right) + \left( \frac{MICK \cdot Vmax[k2] \cdot SOMc}{KO[2] \cdot KM[k2] + MICK} \right)$$

where:

$KO[1]$  – Further modifies  $Km[r2]$  for oxidation of  $SOMc$  (6.0)

$KO[2]$  – Further modifies  $Km[k2]$  for oxidation of  $SOMc$  (6.0)

### 3.4.2 MIMICS Temperature Controls on Decomposition of Litter and SOM

In MIMICS, maximum reaction velocities ( $Vmax$ ) and the Michaelis-Menton half saturation values ( $Km$ ) are temperature sensitive. MIMICS has no soil moisture effect on decomposition.

Decomposition is substrate limited (Reverse Michaelis-Menton Kinetics):

$$\text{Decomposition of litter pool by microbial pool} = \frac{MIC_{r/k} \cdot Vmax_{[rk]}(T) \cdot LIT_{met/struc}}{Km_{[rk]}(T) + MIC_{r/k}}$$

$$\text{Decomposition of } SOM_a \text{ pool by microbial pool} = \frac{MIC_{r/k} \cdot Vmax_{[rk]}(T) \cdot SOM_a}{Km_{[rk]}(T) + MIC_{r/k}}$$

Where  $[rk]$ =

- r1: LITm to MICr flows
- r2: LITs to MICr flows
- r3: SOMa to MICr flows
- k1: LITm to MICK flows
- k2: LITs to MICK flows

#### 3.4.2.1 $Vmax(T)$ – temperature sensitive maximum reaction velocities

The MIMICS microbe-specific maximum reaction velocities ( $Vmax_{[rk]}(T)$ ,  $mg\ C\ (mg\ MIC)^{-1}\ h^{-1}$ ) (Figure 9), are computed as

$$Vmax_{[rk]}(T) = \exp(Vslope_{[rk]} \cdot T_{soil} + Vint_{[rk]}) \cdot av_{[rk]} \cdot Vmod_{[rk]}$$

where:

$T_{soil}$  – soil temperature ( $^{\circ}C$ )

$Vslope[r1]..Vslope[k3]$  – 0.063 or as defined in pftlookup\_mimics.csv

$Vint[r1]..Vint[k3]$  – 5.47 or as defined in pftlookup\_mimics.csv

$av[r1]..av[k3]$  – tuning coefficient ( $1.25 \cdot 10^{-8}$ ) or as defined in pftlookup\_mimics.csv

$Vmod[r1]..Vmod[k3]$  – [10, 2, 10, 3, 3, 2] or as defined in pftlookup\_mimics.csv

### 3.4.2.1.1 $Km(T)$ – temperature sensitive half saturation constants

The MIMIMCS microbe-specific half saturation constants ( $Km_{[rk]}(T)$ , mg C cm<sup>-3</sup>) (Figure 10) are computed as

$$Km_{[rk]}(T) = \exp(Kslope_{[rk]} * T_{soil} + Kint_{[rk]}) * ak_{[rk]} / Kmod_{[rk]}$$

$$Km_{[r3]}(T) = \exp(Kslope_{[r3]} * T_{soil} + Kint_{[r3]}) * ak_{[r3]} / (Kmod_{[r3]} * Pscalar)$$

$$Km_{[k3]}(T) = \exp(Kslope_{[k3]} * T_{soil} + Kint_{[k3]}) * ak_{[k3]} / (Kmod_{[k3]} * Pscalar)$$

where:

$T_{soil}$  – soil temperature (°C)

$Kslope[r1]..Kslope[k3]$  – 0.02 or as defined in pftlookup\_mimics.csv

$Kint[r1]..Kint[k3]$  – 3.19 or as defined in pftlookup\_mimics.csv

$ak[r1]..av[k3]$  – tuning coefficients (0.015625) or as defined in pftlookup\_mimics.csv

$Kmod[r1]..Kmod[k3]$  – [8, 2, 4, 2, 4, 6] or as defined in pftlookup\_mimics.csv.

$Kmod[r3]$  and  $Kmod[k3]$  are multiplied by physical protection scalar (Pscalar, see below).

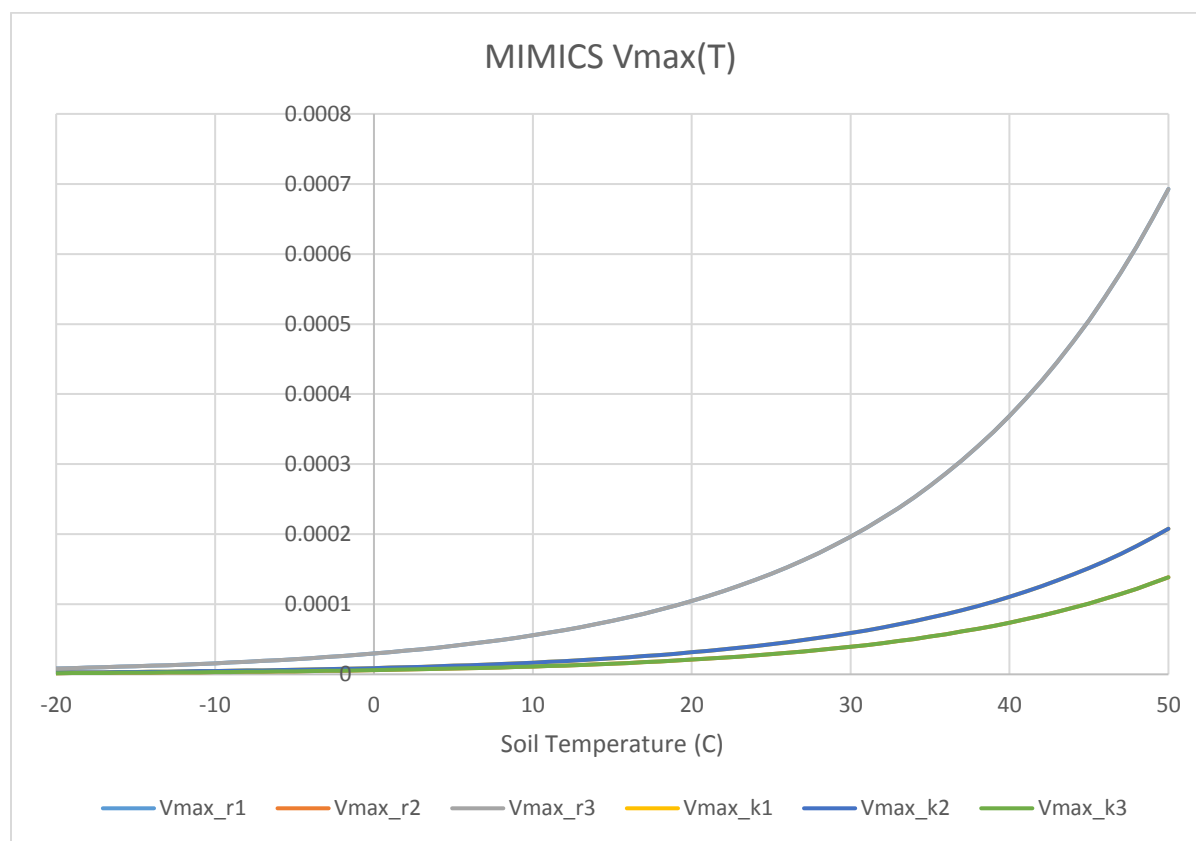


Figure 9. Temperature sensitive maximum reaction velocities,  $V_{\max}(T)$ , for the MIMICS model..

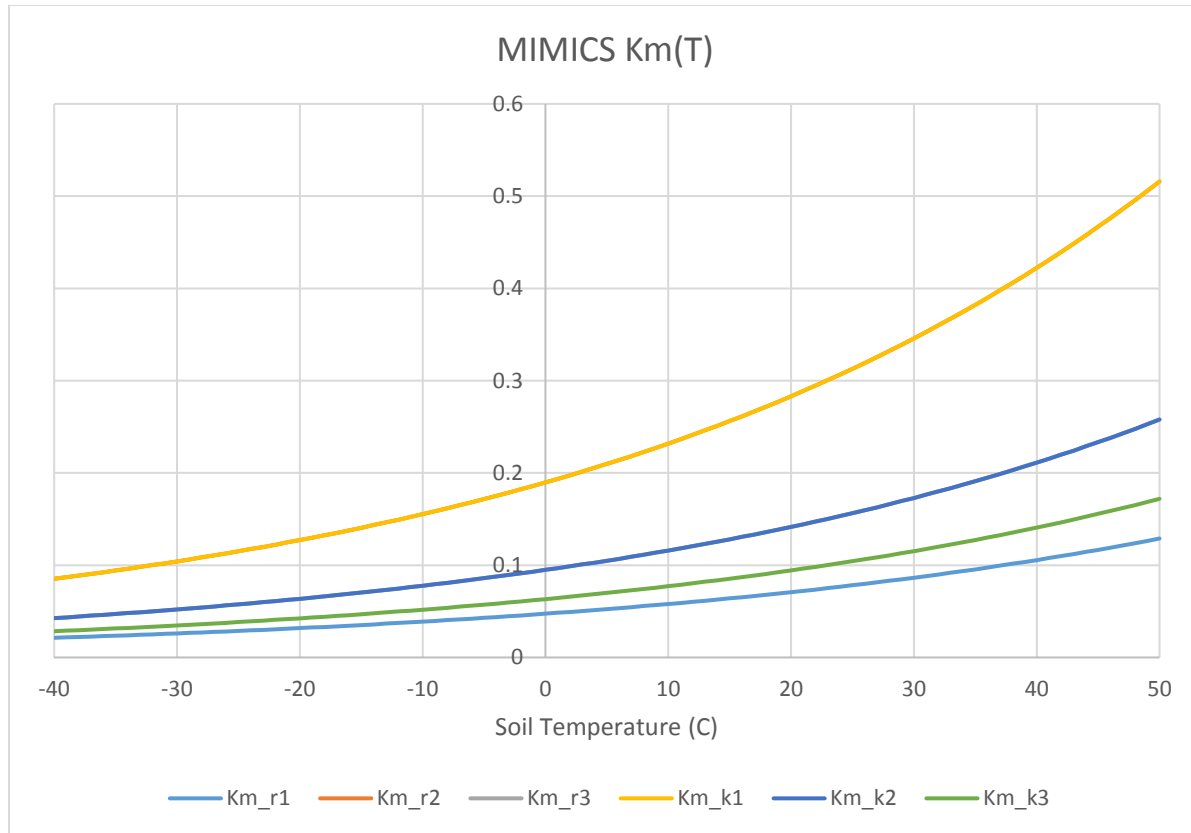


Figure 10. Temperature sensitive half saturation constants,  $K_m(T)$ , for the MIMICS model.

### 3.4.3 Microbial Turnover in MIMICS

Microbial biomass turnover rates increase with annual net primary production (ANPP).

$\tau_r = \text{mimicsbiome\%tauR}(npt, nP)$  – microbial biomass turnover rate for *MICr* ( $\text{hr}^{-1}$ )

$\tau_k = \text{mimicsbiome\%tauK}(npt, nP)$  – microbial biomass turnover rate for *MICK* ( $\text{hr}^{-1}$ )

$\tau_{\text{mod}} = \text{mimicsbiome\%tauMod}(npt)$  – modifies microbial turnover rate,  $0.8 < \tau_{\text{mod}} < 1.2$

$$\tau_r = \text{tau\_r}(1) * \exp(\text{tau\_r}(2) * f_{\text{met}}) * \tau_{\text{mod}}$$

$$\tau_k = \text{tau\_k}(1) * \exp(\text{tau\_k}(2) * f_{\text{met}}) * \tau_{\text{mod}}$$

where:

$\text{tau\_r}(1) = 5.2 * 10^{-4}$  (or as defined in pftlookup\_mimics.csv)

$\text{tau\_r}(2) = 0.3$  (or as defined in pftlookup\_mimics.csv)

$\text{tau\_k}(1) = 2.4 * 10^{-4}$  (or as defined in pftlookup\_mimics.csv)

$\text{tau\_k}(2) = 0.1$  (or as defined in pftlookup\_mimics.csv)

$\tau_{\text{mod}}$  values changes annually with NPP.

$$\tau_{mod} = \sqrt{NPP/100}$$

where:

NPP – net primary production from the previous growing season ( $\text{gC m}^{-2} \text{yr}^{-1}$ )

#### 3.4.4 Carbon Stabilization and Destabilization in MIMICS:

Carbon stabilization in the MIMICS model is controlled by clay content and a microbe-specific fPHYS factor (Figure 11):

$\tau_r$  = microbial biomass turnover rate for *MICr* ( $\text{hr}^{-1}$ )

$\tau_k$  = microbial biomass turnover rate for *MICk* ( $\text{hr}^{-1}$ )

$fPHYS(1)$  – fraction of  $\tau_r$  partitioned into *SOMp* (0.0 – 1.0)

$fPHYS(2)$  – fraction of  $\tau_k$  partitioned into *SOMp* (0.0 – 1.0)

$$fPHYS[1] = fPHYSr(1) \cdot \exp(fPHYSr(2) \cdot fclay)$$

$$fPHYS[2] = fPHYSk(1) \cdot \exp(fPHYSk(2) \cdot fclay)$$

where:

$fPHYSr(1) = 0.15$  (or as defined in pftlookup\_mimics.csv)

$fPHYSr(2) = 1.3$  (or as defined in pftlookup\_mimics.csv)

$fPHYSk(1) = 0.1$  (or as defined in pftlookup\_mimics.csv)

$fPHYSk(2) = 0.8$  (or as defined in pftlookup\_mimics.csv)

$fclay$  = fraction of clay in soil (0.0 – 1.0)

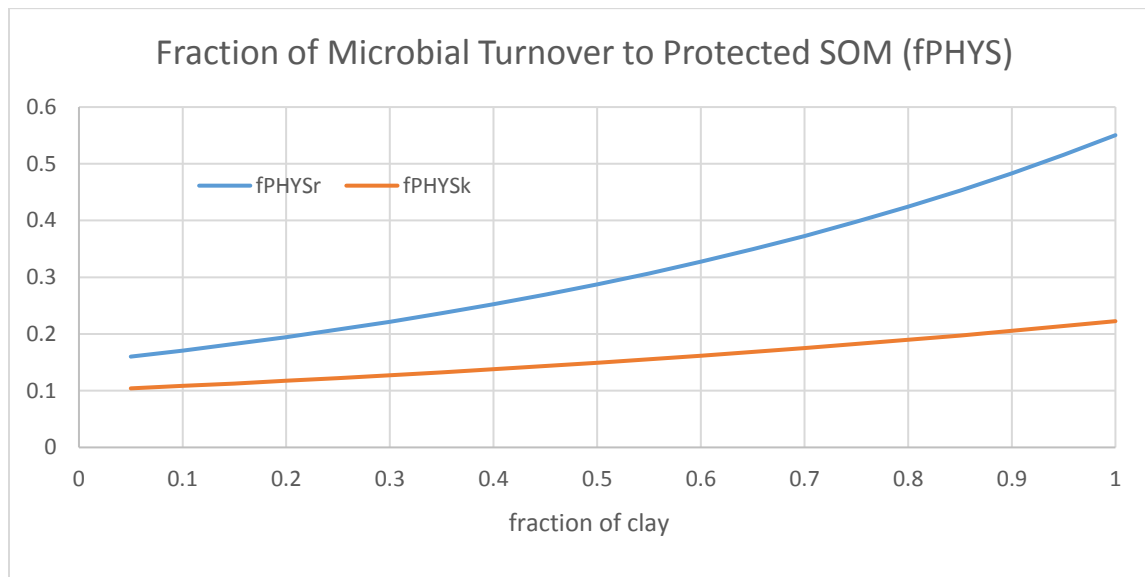


Figure 11. Fraction of Microbial Turnover to the protected Soil Organic Matter pool in the MIMICS model (fPHYS).

$f_{CHEM}(1)$  – fraction of  $\tau_r$  partitioned into  $SOM_c$  (0.0 – 1.0)

$f_{CHEM}(2)$  – fraction of  $\tau_k$  partitioned into  $SOM_c$  (0.0 – 1.0)

$$f_{CHEM}[1] = f_{CHEMr}(1) \cdot \exp(f_{CHEMr}(2) \cdot f_{met}) \cdot f_{CHEMr}(3)$$

$$f_{CHEM}[2] = f_{CHEMk}(1) \cdot \exp(f_{CHEMk}(2) \cdot f_{met}) \cdot f_{CHEMk}(3)$$

where:

$f_{CHEMr}(1) = 0.1$  (or as defined in pftlookup\_mimics.csv)

$f_{CHEMr}(2) = -3.0$  (or as defined in pftlookup\_mimics.csv)

$f_{CHEMr}(3) = 4.0$  (or as defined in pftlookup\_mimics.csv)

$f_{CHEMk}(1) = 0.3$  (or as defined in pftlookup\_mimics.csv)

$f_{CHEMk}(2) = -3.0$  (or as defined in pftlookup\_mimics.csv)

$f_{CHEMk}(3) = 4.0$  (or as defined in pftlookup\_mimics.csv)

$f_{met}$  = fraction of plant residue transferred to metabolic litter (0.0 – 1.0)

$f_{AVAL}(1)$  – fraction of  $\tau_r$  partitioned into  $SOM_a$  (0.0 – 1.0)

$f_{AVAL}(2)$  – fraction of  $\tau_k$  partitioned into  $SOM_a$  (0.0 – 1.0)

$$f_{AVAL}[1] = 1.0 - (f_{PHYS}[1] + f_{CHEM}[1])$$

$$f_{AVAL}[2] = 1.0 - (f_{PHYS}[2] + f_{CHEM}[2])$$

As  $f_{met}$  increases,  $f_{CHEM}[]$  decreases and  $f_{AVAL}[]$  increases.

### Desorption of physically protected SOM to available SOM ( $hr^{-1}$ )

$$DE_{sorb} = SOM_p \cdot 1.5 \times 10^{-5} \cdot \exp(-1.5 f_{clay})$$

### Oxidation of $SOM_c$ to $SOM_a$

$$OXIDAT = \left( \frac{MIC_r \cdot V_{max}[r2] \cdot SOM_c}{KO[1] \cdot KM[r2] + MIC_r} \right) + \left( \frac{MIC_k \cdot V_{max}[k2] \cdot SOM_c}{KO[2] \cdot KM[k2] + MIC_k} \right)$$

where:

$KO[1]$  – Further modifies  $Km[r2]$  for oxidation of  $SOM_c$  (6.0)

$KO[2]$  – Further modifies  $Km[k2]$  for oxidation of  $SOM_c$  (6.0)

### Microbial consumption of $SOM_a$



Microbial consumption of the available SOM pool is reduced with the soil clay fraction (Figure 12):

$K_{mod}[r3]$  – modifies  $K_{m[r3]}$  for fluxes from SOMa to MICr (\*Pscalar)

$K_{mod}[k3]$  – modifies  $K_{m[k3]}$  for fluxes from SOMa to MICk (\*Pscalar)

$P_{scalar}(npt)$  – physical protection scalar used in  $K_{mod}[r3]$  and  $K_{mod}[k3]$ .

$$P_{scalar} = physScalar[1] \cdot \exp\left(physScalar[2] \cdot \sqrt{f_{clay}}\right)$$

where:

$f_{clay} = soil\%clay(npt)$  – fraction of clay in soil (0.0 – 1.0)

$physScalar[1] = 3.0$  (or as defined in pftlookup\_mimics.csv)

$physScalar[2] = -2.0$  (or as defined in pftlookup\_mimics.csv)

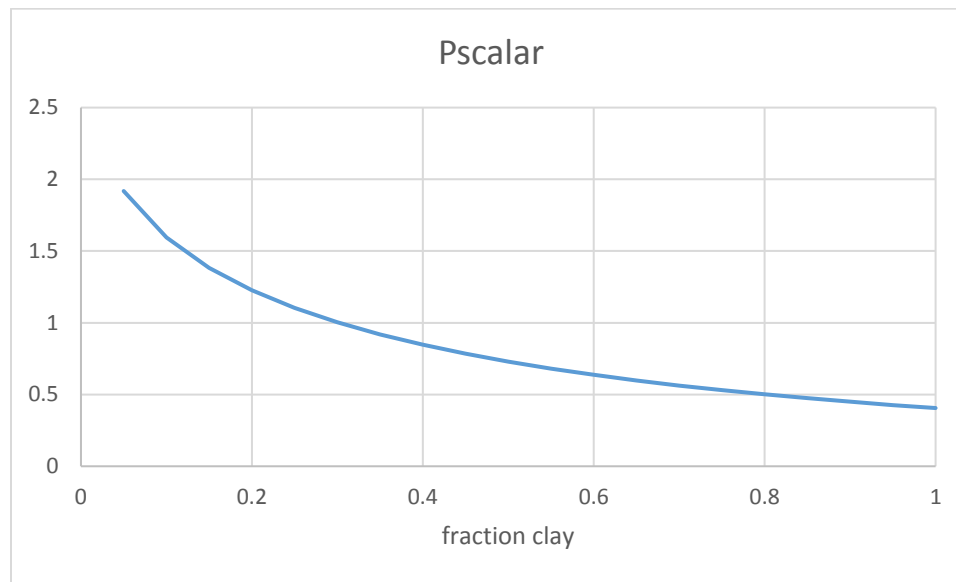
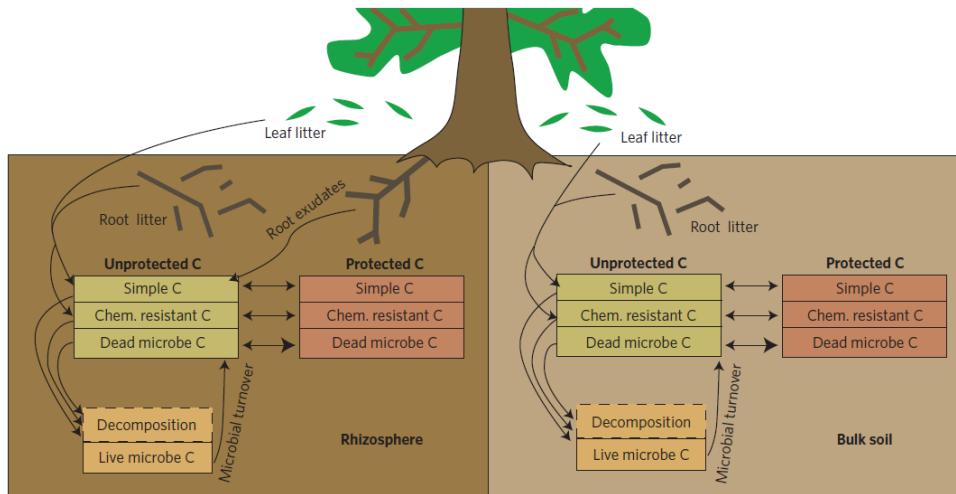


Figure 12. MIMICS physical protection scalar (Pscalar). The scalar modifies fluxes from available SOM to microbial pools.

### 3.5 CORPSE

CORPSE has separate surface litter layer pools and soil layer pools, each with three carbon species (labile, recalcitrant, and dead microbes) and a live microbial biomass pool (Figure 13). The surface litter pools are unprotected while the soil carbon pools have unprotected and protected counterparts. Leaf litter is partitioned into Structural and Metabolic material as a function of the lignin:N ratio of the leaf litter. Metabolic leaf litter is transferred to the Labile surface litter pool and structural leaf litter is transferred to the Recalcitrant surface litter pool. Similarly, root litter is partitioned into Structural and Metabolic material as a function of its lignin:N ratio. Metabolic root litter is transferred to the Labile soil pool and Structural root litter is transferred to the Recalcitrant soil pool. Root exudates also contribute to the Labile soil pool. Carbon from the decomposing CWD pool is transferred to the Recalcitrant litter pool, with CO<sub>2</sub> respiration loss. The decomposition of unprotected labile, recalcitrant, and dead microbe litter and SOM pools are controlled by microbial biomass and modified by soil temperature and moisture controls. The model assumes that the microbial biomass limitation on decomposition is related to the microbial biomass as a fraction of total carbon. When microbial biomass is much larger than 1% of total

carbon microbes decompose the substrate at their maximum rate, similar to a first-order model. If microbial biomass is very low, then decomposition rate at any temperature will also be very low. Microbial turnover, which is proportional to a fixed turnover rate, transfers C to the unprotected dead microbes pool, with CO<sub>2</sub> respiration loss. Microbial death transfers C to the unprotected dead microbes pool, also with CO<sub>2</sub> respiration loss. Carbon transfers from the unprotected soil pools to their protected counterparts is a function of clay and soil porosity (Q<sub>max</sub>) and the base protection rate, without CO<sub>2</sub> respiration losses. Loss of protected carbon is proportional to a fixed turnover rate. No carbon is transferred from the surface litter layer to the soil layer.



**Figure 1 | Diagram of model structure.** Soil carbon is divided into three chemical classes, which can be protected or unprotected. Decomposition is mediated by microbial biomass, which takes up a portion of decomposed carbon and loses carbon to CO<sub>2</sub> and the dead microbial C pool over time. Soil is separated into the rhizosphere, which receives root exudate inputs, and bulk soil, which does not.

Figure 13. CORPSE model litter and soil organic matter pools (from Sulman et al. 2014).

Decomposition (heterotrophic respiration flux) ( $D_i$ ) of unprotected carbon pool ( $C_i$ ) by microbe pool ( $M$ )

$$D_i = V_{max,i}(T) \cdot \left( \frac{\theta}{\theta_{sat}} \right)^3 \cdot \left( 1 - \frac{\theta}{\theta_{sat}} \right)^{gas\_diffusion} \cdot C_i \cdot \frac{M}{kC \cdot \sum_{j=1}^3 C_j + M}$$

where  $V_{max,i}(T)$  is the temperature-dependent maximum enzymatic conversion rate,  $\theta$  is volumetric soil water content,  $\theta_{sat}$  is the volumetric soil moisture at saturation,  $gas\_diffusion = 2.5$ , and  $kC$  is 1%. The rate of change in the unprotected carbon pool is defined as

$$\frac{dC_i}{dt} = I_i - D_i - \frac{dP_i}{dt}$$

where  $I_i$  is the carbon input rate to the pool and  $P_i$  is the protected carbon pool for each species.

### 3.5.1 CORPSE Temperature and Moisture Controls on Decomposition of Litter and SOM

#### 3.5.1.1 CORPSE Temperature Controls on Decomposition of Litter and SOM

The decomposition rate in CORPSE is determined by a temperature-dependent maximum enzymatic conversion rate  $V_{max,i}(T)$  ( $\text{yr}^{-1}$ ) (Figure 14), where  $T$  is the soil temperature (K),  $T_{ref}$  is the reference soil temperature (293.7 K),  $V_{max,ref,i}$  is the reference  $V_{max}$  for the species (4500e0, 25e0, 600e0,  $\text{yr}^{-1}$ ),  $R_{gas}$  is the ideal gas constant (8.314472  $\text{J}\cdot\text{K}^{-1}\cdot\text{mol}^{-1}$ ),  $Ea_i$  is the activation energy for the species (37e3, 54e3, 50e3,  $\text{kJ}\cdot\text{mol}^{-1}$ )

$$\alpha_i = \frac{V_{max,ref,i}}{\exp\left(\frac{-Ea_i}{R_{gas} \cdot T_{ref}}\right)}$$

$$V_{max,i}(T) = \alpha_i \cdot \exp\left(\frac{-Ea_i}{R_{gas} \cdot T}\right)$$

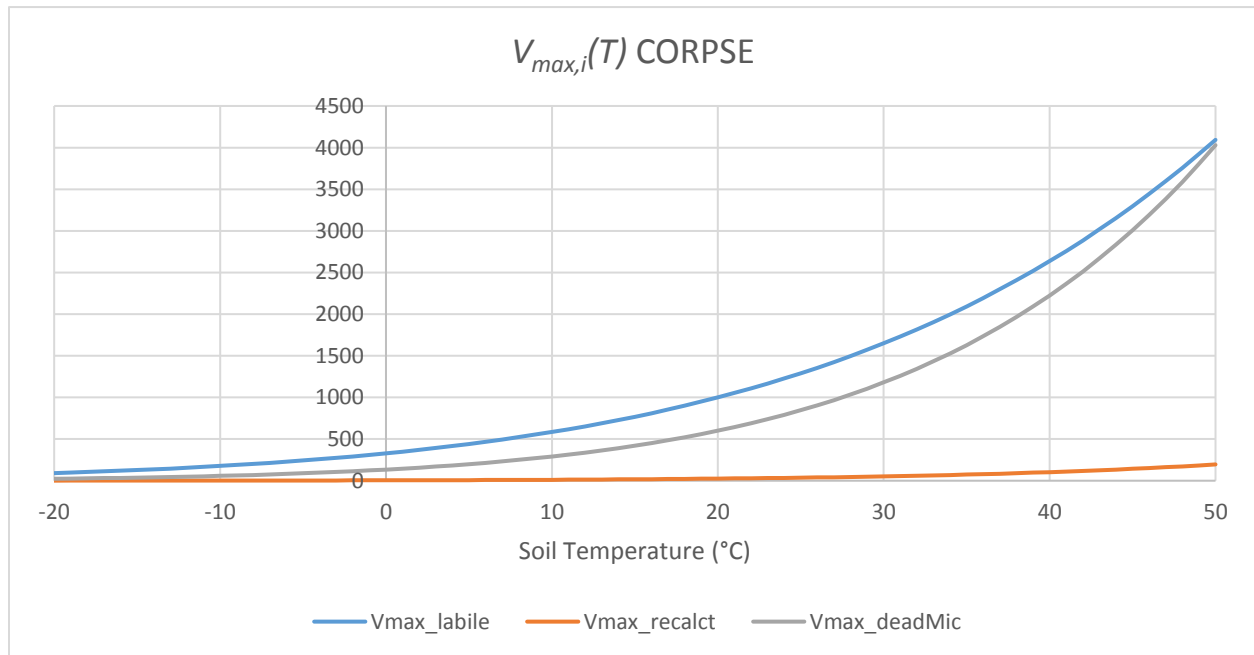


Figure 14. The temperature-dependent maximum enzymatic conversion rate  $V_{max,i}(T)$  ( $\text{yr}^{-1}$ ) in the CORPSE model.

### 3.5.1.2 CORPSE Soil Moisture Controls on Decomposition of Litter and SOM

The soil moisture effect on decomposition of soil organic matter in the CORPSE model (Figure 15) is defined as:

$f(W) = \left( \frac{\theta}{\theta_{sat}} \right)^3 \left( 1.0 - \frac{\theta}{\theta_{sat}} \right)^{2.5}$ , where  $\theta$  is volumetric soil water content and  $\theta_{sat}$  is the volumetric soil moisture at saturation.

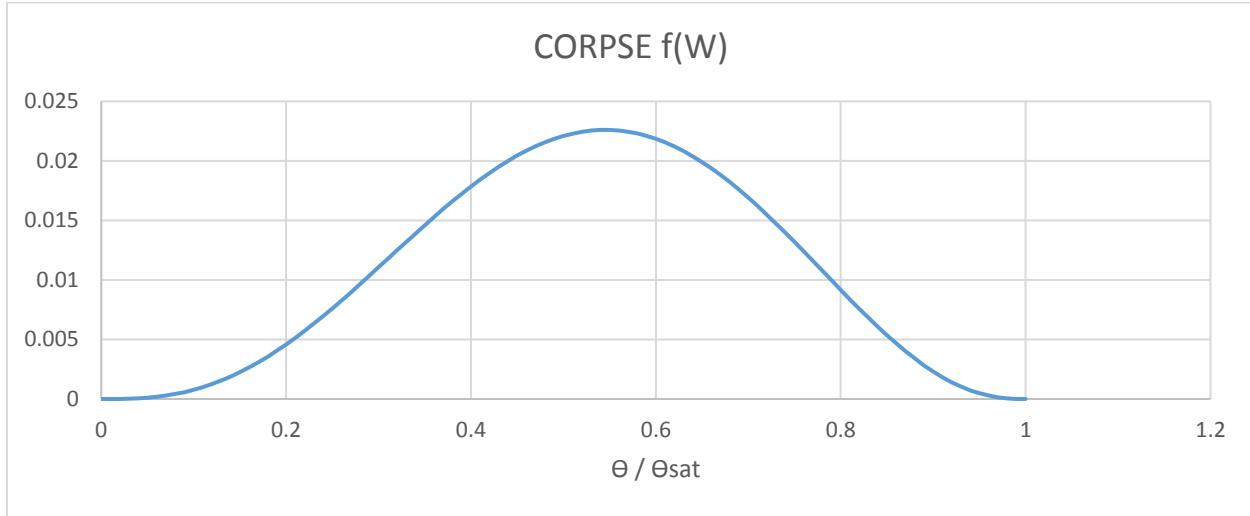


Figure 15. The soil moisture effect on soil organic matter decomposition in the CORPSE model.

### 3.5.2 Microbial growth and turnover in CORPSE

The change in microbial biomass ( $M$ ) is a balance between uptake of decomposed substrate carbon ( $D_i$ ) and the loss of biomass through the combination of cell death and maintenance respiration,

$$\frac{dM}{dt} = \sum_i \varepsilon_i D_i - \frac{M}{\tau_{mic}}$$

where  $\varepsilon_i$  is the microbial uptake efficiency for each and  $\tau_{mic}$  is the average turnover rate ( $0.25 \text{ yr}^{-1}$ ) for the microbial community and represents a combination of microbial death and maintenance respiration.

### 3.5.3 Carbon Stabilization and Destabilization in CORPSE:

Carbon transfers from the unprotected soil pools ( $C_i$ ) to their protected counterparts ( $P_i$ ) is a function of clay and soil porosity ( $Q_{max}$ ) (Figure 16). Loss of protected carbon is proportional to a fixed turnover rate ( $1/\tau_p$ ).

$$\frac{dP_i}{dt} = C_i \cdot Q_{max} \cdot \gamma - \frac{P_i}{\tau_p}$$

$T_p$ =residence time of the protected pool (45 years)

$\chi$  (protection rate) = 1.5

$$Q_{max} = \max\left(0.0, 10^{**}\left(0.4833 \cdot \log_{10}(\text{clay}) + 2.3282\right)(1.0 - \text{porosity}) \cdot 2650 \cdot 1e-6\right)$$

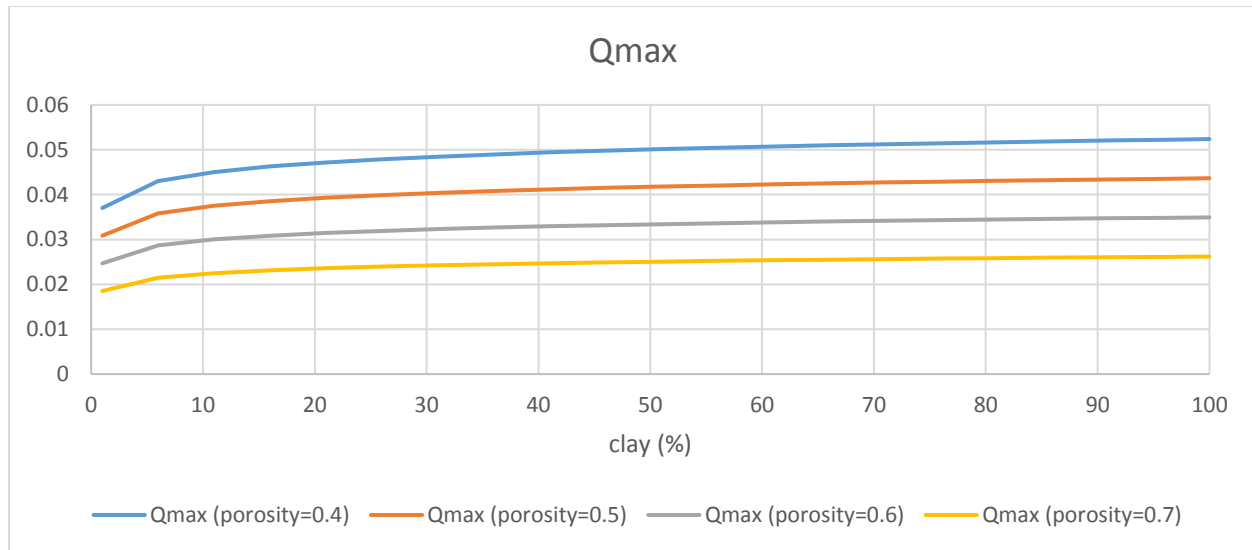


Figure 16. The effect of soil clay fraction on transfers of C to the protected pools in the CORPSE model.

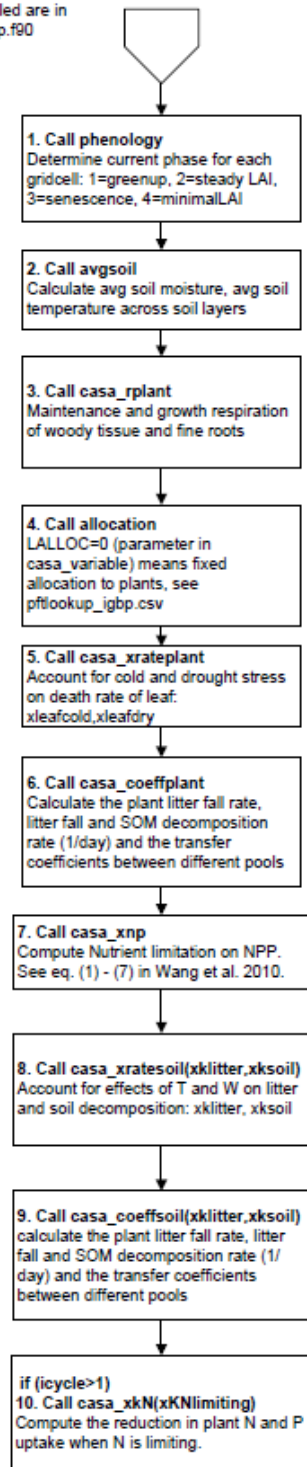
## 4 Detailed Summary of CASA-CNP Subroutines and Biogeochemical Equations

### 4.1 Daily biogeochemistry: SUBROUTINE biogeochem

Subroutine biogeochem, called once each day, controls daily biogeochemical calculations. The numbers in front of subroutines indicate their calling position in **subroutine** biogeochem. These subroutines are found in file *casa\_cnp.f90* (Figure 17).

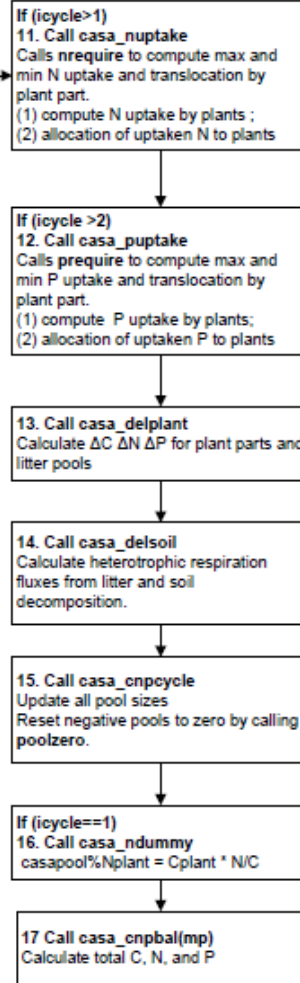
1. **phenology** – Determine current phase for each gridcell: 0=minimalLAI, 1=greenup, 2=steady LAI, 3=senescence
2. **avgsoil** – Calculate average soil moisture, average soil temperature across soil layers
3. **casa\_rplant** – Calculate maintenance respiration of woody tissue and fine roots, plant growth respiration, and nutrient unlimited NPP.
4. **casa\_allocation** – Calculate fraction of new C allocated to each plant part.
5. **casa\_xrateplant** – Calculate cold and drought effects on death rate of leaves: *xkleafcold*, *xkleafdry*
6. **casa\_coeffplant** – Calculate plant litter fall rates (1/day) and the transfer coefficients between plant and litter pools
7. **casa\_xnp** – Calculate nutrient limitation on NPP.
8. **casa\_xratesoil** – Calculate for effects of temperature and water on litter and soil decomposition: *xklitter*, *xksoil*
9. **casa\_coeffsoil** – Calculate the litter and SOM decomposition rates (1/day), respiration rates (fraction of flow), and the transfer coefficients between litter and soil pools, and between soil pools.
10. **casa\_xkN** – Calls Nrequire to compute max and min N uptake and translocation by plant part. Computes the reduction in plant N and P uptake when N is limiting.
11. **casa\_nuptake** – Calls Nrequire to compute max and min N uptake and translocation by plant part. (1) compute N uptake by plants; (2) allocation of uptaken N to plant pools.
12. **casa\_puptake** – Calls Prequire to compute max and min P uptake and translocation by plant part. (1) compute P uptake by plants; (2) allocation of uptaken P to plants
13. **casa\_delplant** – Calculate  $\Delta C$ ,  $\Delta N$ , and  $\Delta P$  for plant parts and litter pools
14. **casa\_delsoil** – Calculate heterotrophic respiration fluxes from litter and soil decomposition. Calculate gross and net mineralization.
15. **casa\_cnpcycle** – Update all pool sizes. Reset negative pools to zero by calling **poolzero**.

Functions called are in  
casa\_cnp.f90



## Subroutine biogeochem

called once each day  
(casa\_inout.f90)



**Casa\_delplant**  
! For plant C this includes gains from NPP  
and losses from senescence  
! For plant N,P this includes gains from  
retranslocation and uptake, and losses  
from senescence  
! For litter C this includes gains from plant  
senescence  
! For litter N, P this includes N and P  
losses from plants (prior to uptake  
calculation  
! casapool%Nsoilmin and  
casapool%Nsoilmin are reduced by the  
amount of N and P uptake

Return to casa\_cnp\_driver

Figure 17. Order of calculations in subroutine biogeochem in the CASA-CNP model. Subroutine biogeochem is called once each day and controls daily biogeochemical calculations in CASA-CNP.

## 4.2 CASA-CNP Dimensions, Constants, and Pointers

mp = number of grid cells simulated

mplant = number of plant pools (3)

msoil = number of soil pools (3)

mlitter = number of litter pools (3)

ms = number of mineral soil layers (6)

! mineral soil layer thickness (m) defined in SUBROUTINE readbiome

data dzsoil/.022, .058, .154, .409, 1.085, 2.872/

### Plant Pools

integer, parameter :: leaf = 1

integer, parameter:: wood = 2

integer, parameter:: froot = 3

### Litter Pools

integer, parameter:: metb = 1

integer, parameter:: str = 2

integer, parameter:: cwd = 3

### Soil Organic Matter (SOM) pools

integer, parameter:: mic = 1

integer, parameter:: slow = 2

integer, parameter:: pass = 3

Equation documentation shorthand : index (1-18) for biome-specific values

pft = *veg%iveg(npt)*

The convention in this documentation is that *npt* iterates through all points (grid cells), *nP* iterates through all plant pools, *nL* iterates through all litter pools, *nS* and *nSS* iterate through all soil organic



matter pools, and *nLyr* iterates through all soil mineral layers. The indices used in the actual code vary from this convention.

DO *npt*=1, *mp* (iterate through all grid cells)

DO *nP*=1, *mplant* (iterate through all 3 plant pools)

DO *nL*=1, *mlitter* (iterate through all 3 litter pools)

DO *nS*=1, *msoil* (iterate through all 3 soil organic matter pools)

DO *nSS*=1, *msoil* (iterate through all 3 soil organic matter pools)

DO *nLyr*=1, *ms* (iterate through all 6 mineral soil layers)

*pft* is the PFT for grid cell *npt*.

*casabiome%* is a pointer to PFT specific parameters

*casamet%* is a pointer to meteorological drivers and soil conditions from the CLM model (read from *met\*.nc* files).

*casaflex%* is a pointer to C and N fluxes

*casapool%* is a pointer to plant, litter, and soil C and N pools. For example:

*casapool%cplant(npt,nP)* – C content of plant pool *nP* (g C m<sup>-2</sup>)

*casapool%nplant(npt,nP)* – N content of plant pool *nP* (g N m<sup>-2</sup>)

*casapool%clitter(npt,nL)* – C content of litter pool *nL* (g C m<sup>-2</sup>)

*casapool%nlitter(npt,nL)* – N content of litter pool *nL* (g N m<sup>-2</sup>)

*casapool%csoil(npt,nS)* – C content of soil organic matter pool *nS* (g C m<sup>-2</sup>)

*casapool%nsoil(npt,nS)* – N content of soil organic matter pool *nS* (g N m<sup>-2</sup>)

If running CASA-CNP as a spinup, C pools are initialized from biome-specific parameters. N pools are initialized with biome-specific N:C ratios. If extending CASA-CNP from a previous simulation, C and N pools are initialized from an output file from the previous simulation.

#### 4.3 Soil and Litter Decomposition and Heterotrophic Respiration Variables

*casaflex%Crsoil(npt)* = *casaflex%fluxCtoCO2(npt)* (Heterotrophic Respiration)

*fromLtoS(npt,nL,nS)*: fraction of decomposed litter pool *nL* that is transferred to soil pool *nS*

*fromStoS(npt,nSS,nS)*: fraction of decomposed soil C pool *nS* that is transferred to soil pool *nSS*

*fromLtoCO2(npt,nL)*: fraction of decomposed litter pool *nL* emitted as CO<sub>2</sub>

*fromStoCO2(npt,nS)*: fraction of decomposed soil C pool *nS* emitted as CO<sub>2</sub>

*casaflex%klitter(npt,nL)*: decomposition rate of litter pool *nL* (1/day)

*casaflex%ksoil(npt,nS)*: decomposition rate of soil pool *nS* (1/day)

## 4.4 CASA-CNP Documentation by Subroutine

### 4.4.1 Phenology: (1) SUBROUTINE phenology

This subroutine determines the current phase for each gridcell: 0=minimalLAI, 1=greenup, 2=steady LAI, 3=senescence

CASA-CNP implements a fixed phenology each year, in latitude bands by PFT type, based on MODIS data that came with the CASA-CNP code (data in ***modis\_phenology.txt***).

Phase 0 – minimal LAI

Phase 1 – green up, maximum leaf growth (14 days)

Phase 2 – steady LAI

Phase 3 – senescence (14 days)

- During leaf growth phase 0 (minimum LAI) or 3 (senescence), no carbon is allocated to leaves and all C is allocated to wood and fine roots.
- During maximal leaf growth phase, 80% of C is allocated to leaves, the remainder of C is allocated to wood and fine roots.
- During the steady growth period, C allocation to leaves, wood, and fine roots is determined by the fixed biome-specific fractions, but leaf allocation can be adjusted (increased to 80% or reduced to 0%) if LAI is below or above the theoretical biome-specific minimum and maximum LAI.

### 4.4.2 Average Soil Conditions: (2) SUBROUTINE avgsoil

This subroutine computes average soil temperature and soil moisture conditions in the soil. The values *casamet%tsoilavg(npt)* and *casamet%moistavg(npt)* are used to compute soil and temperature effects on soil organic matter decomposition rates in **subroutine casa\_xratesoil**. The value *casamet%tsoilavg(npt)* is also used to calculate fine root maintenance respiration in **subroutine casa\_rplant**.

$$casamet\%tsoilavg(npt) = \sum_{nLyr} veg\%froot(npt, nLyr) * casamet\%tsoil(npt, nLyr)$$

$$casamet\%moistavg(npt) = \sum_{nLyr} veg\%froot(npt, nLyr) * \min(soil\%sfc(npt), casamet\%moist(npt, nLyr))$$

Where  $froot(npt, nLyr)$  is the fraction of root biomass in soil layer  $nLyr$ ,  $casamet\%tsoil(npt, nLyr)$  is the soil temperature (K) for layer  $nLyr$  (from CLM),  $soil\%sfc(npt)$  is the volumetric field capacity, and  $casamet\%moist(npt, nLyr)$  is the volumetric soil moisture content of soil layer  $nLyr$  (from CLM).

The value  $casamet\%btran(npt)$  is the relative water content of the soil used to calculate plant death due to dryness in **subroutine casa\_xrateplant**.

$$casamet\%btran(npt) = \sum_{nLyr} \frac{veg\%froot(npt, nLyr) * (\min(soil\%sfc(npt), casamet\%moist(npt, nLyr)) - soil\%swilt(npt))}{soil\%sfc(npt) - soil\%swilt(npt)}$$

Where  $froot(npt, nLyr)$  is the fraction of root biomass in soil layer  $nLyr$ ,  $soil\%fwilt(npt)$  is the volumetric wilting point,  $soil\%sfc(npt)$  is the volumetric field capacity, and  $casamet\%moist(npt, nLyr)$  is the volumetric soil moisture content of soil layer  $nLyr$  (from CLM).

**End SUBROUTINE avgsoil**

#### 4.4.3 NPP and Autotrophic Respiration: (3) SUBROUTINE casa\_rplant

This subroutine calculates the maintenance respiration of woody tissue and fine roots, the growth efficiency of the plant, and the total plant growth respiration. It also calculates C losses from the labile pool.

**Plant maintenance respiration:**  $casaf\%crmp\%plant(npt, wood) + casaf\%crmp\%plant(npt, froot)$   
(maintenance respiration is not calculated for leaves - the code for this calculation was commented out).

**Plant growth respiration:**  $casaf\%crg\%plant(npt)$

Maintenance respiration for wood and fine roots increases exponentially with air or soil temperature using a fixed  $Q_{10}$  that is specific to the PFT (Sitch, Smith et al. 2003).

**Maintenance respiration for wood ( $gC\ m^{-2}\ d^{-1}$ ) (Figure 18):**

$$casaf\%crmp\%plant(npt, wood) = \begin{cases} 0, & tairk(npt) \leq 250 \\ casabiome\%rmplant(pft, wood) \\ *casapool\%nplant(npt, wood) \\ * \exp\left(308.56 * \left(\frac{1.0}{56.02} - \frac{1.0}{casamet\%tairk(npt) + 46.02 - tkzeroc}\right)\right) \end{cases}$$

where  $\text{casabiome}\% \text{rmplant}(npt, \text{wood})$  is the daily maintenance respiration rate for wood (PFT-specific parameter) ( $\text{g C g N}^{-1} \text{d}^{-1}$ ) on a  $10^\circ\text{C}$  base,  $\text{casapool}\% \text{nplant}(npt, \text{wood})$  is the N content of wood ( $\text{g N m}^{-2}$ ),  $\text{tair}(npt)$  is the average air temperature (K), and  $\text{tkzeroc}$  is 273.15 K.

**Maintenance respiration for fine roots ( $\text{gC m}^{-2} \text{d}^{-1}$ ) (Figure 18):**

$$\text{casaflux}\% \text{crmplant}(npt, \text{froot}) = \begin{cases} 0, & \text{tsoilavg}(npt) \leq 250 \\ \text{casabiome}\% \text{rmplant}(pft, \text{froot}) \\ * \text{casapool}\% \text{nplant}(npt, \text{froot}) \\ * \exp\left(308.56 * \left(\frac{1.0}{56.02} - \frac{1.0}{\text{casamet}\% \text{tsoilavg}(npt) + 46.02 - \text{tkzeroc}}\right)\right) \end{cases}$$

where  $\text{casabiome}\% \text{rmplant}(npt, \text{froot})$  is the daily maintenance respiration rate for fine roots (PFT-specific parameter) ( $\text{g C g N}^{-1} \text{d}^{-1}$ ) on a  $10^\circ\text{C}$  base,  $\text{casapool}\% \text{nplant}(npt, \text{froot})$  is the N content of fine roots ( $\text{g N m}^{-2}$ ),  $\text{tsoilavg}(npt)$  is the average soil temperature (K), and  $\text{tkzeroc}$  is 273.15 K.

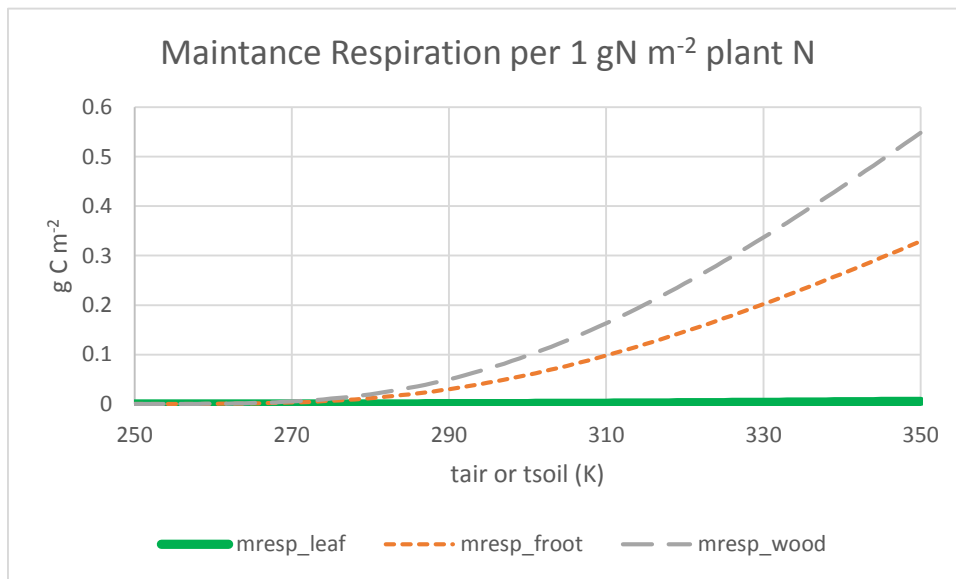


Figure 18. Maintenance respiration assuming  $\text{rmplant}(pft, \text{leaf}) = 0.1/365$ ,  $\text{rmplant}(pft, \text{froot}) = 6.0/365$ ,  $\text{rmplant}(pft, \text{wood}) = 10.0/365$ .

**Respiration losses from the labile C pool,  $\text{casaflux}\% \text{clabloss}(npt)$  ( $\text{g C m}^{-2} \text{d}^{-1}$ )...not sure what this pool is exactly, plant carbohydrate storage?**

$$casaf\text{lux}\%clabloss(npt) = \begin{cases} 0, & tairk(npt) \leq 250 \\ casabiome\%kclabrate(veg\%iveg(npt)) \\ * \max(0.0, casapool\%Clabile(npt)) \\ * \exp\left(308.56 * \left(\frac{1.0}{56.02} - \frac{1.0}{casamet\%tairk(npt) + 46.02 - tkzeroc}\right)\right) \end{cases}$$

where  $casabiome\%kclabrate(n)$  is the biome-specific respiration rate for the labile C pool (1/day),  $casapool\%Clabile(n)$  is the C content of labile pool (g C m<sup>-2</sup>),  $tairk(npt)$  is the average air temperature (K), and  $tkzeroc$  is 273.15 K.

### Growth Efficiency

Growth efficiency correlated to leaf N:P ratio. Q.Zhang @ 22/02/2011

Plant growth efficiency ( $Y_{grow}$ , 0.0 – 1.0) increases with the P/N ratio of leaves,  $ratioPNplant(npt, leaf)$ . For C only or C+N only,  $Y_{grow} = 0.65$  (Figure 19).

$$ratioPNplant(npt, leaf) = \frac{casapool\%Pplant(npt, leaf)}{casapool\%Nplant(npt, leaf)}$$

$$Y_{grow}(npt) = 0.65 + 0.2 * \frac{ratioPNplant(npt, leaf)}{ratioPNplant(npt, leaf) + \frac{1.0}{15.0}}$$

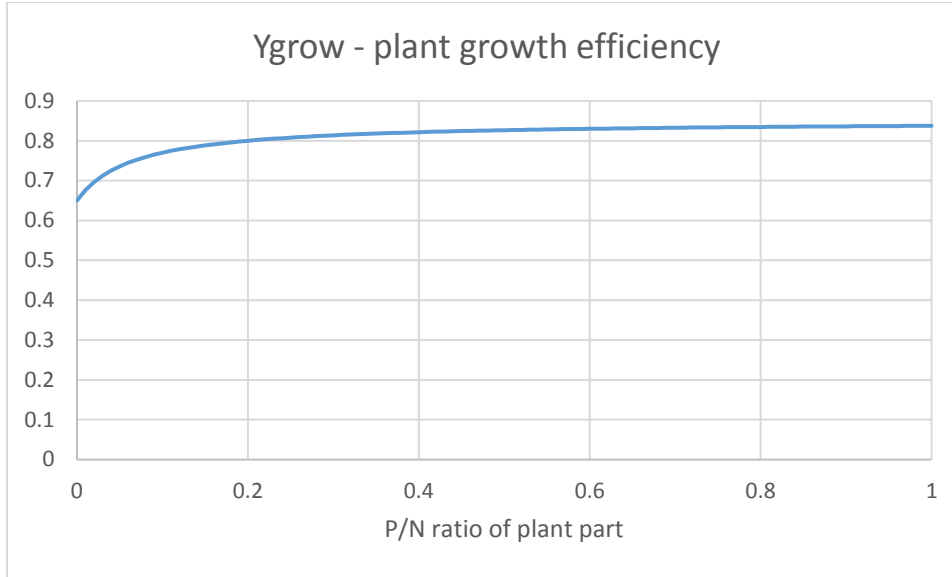


Figure 19. The plant growth efficiency ( $Y_{grow}$ ). For C only or C+N only,  $Y_{grow} = 0.65$ .

**Total growth respiration for the plant,  $casaf\%crgplant(npt)$  ( $g\ C\ m^{-2}\ d^{-1}$ )**

$$casaf\%crgplant(npt) = (1.0 - Y_{grow}(npt)) \\ * MAX \left( 0.0, casaf\%Cgpp(npt) - \sum_{nP} casaf\%crmplant(npt, nP) \right)$$

**Total autotrophic respiration (maintenance + growth),  $casaf\%crgplant(npt)$  ( $g\ C\ m^{-2}\ d^{-1}$ )**

$$casaf\%Crp(npt) = \sum_{nP} casaf\%crmplant(npt, nP) + casaf\%crgplant(npt)$$

**Nutrient-unlimited Net Primary Production (GPP minus autotrophic respiration),  $casaf\%Cnpp(npt)$  ( $g\ C\ m^{-2}\ d^{-1}$ )**

$$casaf\%Cnpp(npt) = casaf\%Cgpp(npt) \\ - \sum_{nP} casaf\%crmplant(npt, nP) \\ - casaf\%crgplant(npt)$$

Note:  $casaf\%Cnpp(npt)$  will be reduced in **subroutine casa\_xnp** if there is a nutrient limitation.

**End SUBROUTINE casa\_rplant**

#### 4.4.4 Carbon Allocation: (4) SUBROUTINE casa\_allocation

This subroutine computes the fraction of net photosynthate allocated to leaf, wood and froot.

Inputs:

*moistavg(mp)* – average soil moisture (volumetric fraction) in the rooting zone, calculated in **subroutine avgsoil**.

*tsoilavg(mp)* – average temperature in the rooting zone (K), calculated in **subroutine avgsoil**.

*btran(mp)* – relative water content in the rooting zone (0.0 – 1.0), calculated in **subroutine avgsoil**.

Outputs:

*fracCalloc(npt,nP)* – fraction of NPP allocated to each plant pool (*nP*) (0.0 – 1.0).

#### Fixed allocation fractions based on biome-specific parameters

$$casaflux\%fracCalloc(npt,nP) = casabiome\%fracnpptop(pft,nP)$$

WHERE (*phen%phase(npt)==0*), Minimum LAI

$$casaflux\%fracCalloc(npt,leaf) = 0.0$$

$$casaflux\%fracCalloc(npt,froot) = \frac{casaflux\%fracCalloc(npt,froot)}{casaflux\%fracCalloc(npt,froot) + casaflux\%fracCalloc(npt,wood)}$$

$$casaflux\%fracCalloc(npt,wood) = 1.0 - casaflux\%fracCalloc(npt,froot)$$

END WHERE

WHERE (*phen%phase==1*), Greenup

$$casaflux\%fracCalloc(npt,leaf) = 0.8$$

For woodland or forest

$$casaflux\%fracCalloc(npt,froot) = 0.5 * (1.0 - casaflux\%fracCalloc(npt,leaf))$$

$$casaflux\%fracCalloc(npt,wood) = 0.5 * (1.0 - casaflux\%fracCalloc(npt,leaf))$$

For grassland, cropland:

$$casaflux\%fracCalloc(npt,froot) = 1.0 - casaflux\%fracCalloc(npt,leaf)$$

$$casaflux\%fracCalloc(npt,wood) = 0.0$$

END WHERE

WHERE (*phen%phase==3*), Maximum LAI

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{wood}) = \text{casabiome}\% \text{fracnpptop}(\text{pft}, \text{wood})$   
 $\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot}) = 1.0 - \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{wood})$   
 $\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf}) = 0.0$

ENDWHERE

If prognostic LAI reached *glaimax*, no C is allocated to leaf. Q.Zhang 17/03/2011

WHERE( $\text{casamet}\% \text{glai}(\text{npt}) \geq \text{casabiome}\% \text{glaimax}(\text{pft})$ )

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf}) = 0.0$

$$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot}) = \frac{\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot})}{\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot}) + \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{wood})}$$

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{wood}) = 1.0 - \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot})$

ENDWHERE

**If prognostic LAI < *glaimin*, increase allocation to leaves**

WHERE( $\text{casamet}\% \text{glai}(\text{npt}) < \text{casabiome}\% \text{glaimin}(\text{pft})$ )

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf}) = 0.8$

For woodland or forest

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot}) = 0.5 * (1.0 - \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf}))$

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{wood}) = 0.5 * (1.0 - \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf}))$

For grassland or cropland

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot}) = 1.0 - \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf})$

ENDWHERE

**Normalization the allocation fraction to ensure they sum up to 1.0**

$\text{totfracCalloc}(\text{npt}) = \text{sum}(\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{nP}))$

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf}) = \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{leaf}) / \text{totfracCalloc}(\text{npt})$

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{wood}) = \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{wood}) / \text{totfracCalloc}(\text{npt})$

$\text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot}) = \text{casaflux}\% \text{fracCalloc}(\text{npt}, \text{froot}) / \text{totfracCalloc}(\text{npt})$



**END SUBROUTINE casa\_allocation****4.4.5 Plant Turnover Rates: (5) SUBROUTINE casa\_xrateplant**

This subroutine calculates *xkleafcold* and *xkleafdry*, the effect of cold and drought stress on death rate of leaves (0.0 – 1.0). These values are 0.0 when there is no death due to cold or drought, and 1.0 when there is maximum death.

Inputs:

*iveg(npt)* : biome type (PFT)  
*phase(npt)*: leaf growth stage  
*tairk(npt)* : air temperature in K

Outputs:

*xkleafcold(npt)*: cold stress induced leaf senescence rate (1/day)  
*xkleafdry(npt)*: drought-induced leaf senescence rate (1/day)  
*xkleaf(npt)*: set to 0.0 during maximal leaf growth phase to turn off leaf death due to aging, 1.0 otherwise.

Following the formulation of Arora (2005) on the effect of cold or drought stress on leaf litter fall calculate cold stress (eqn (18), Arora 2005, GCB 11:39-59):

**Leaf Death Rates Due to Cold** (Figure 20, Figure 21).

$$x_{coldleaf}(npt) = \begin{cases} 1.0, & casamet\%tairk(npt) \geq phen\%TKshed(pft) \\ 0.0, & casamet\%tairk(npt) \leq phen\%TKshed(pft) - 5.0 \\ \frac{casamet\%tairk(npt) - phen\%TKshed(pft) - 5.0}{5.0}, & otherwise \end{cases}$$

$$x_{coldleaf}(npt) = \min(1.0, \max(0.0, x_{coldleaf}(npt)))$$

$$xkleafcold(npt) = casabiome\%xkleafcoldmax(pft) \\ * (1.0 - x_{coldleaf}(npt))^{casabiome\%xkleafcoldexp(pft)}$$

where *phen%TKshed* is the air temperature (K) at our below where plants shed their leaves. The value of *xkleafcold(npt)* is added to *casafux%kplant(npt,leaf)* in **subroutine casa\_coeffplant** to compute total turnover rate.

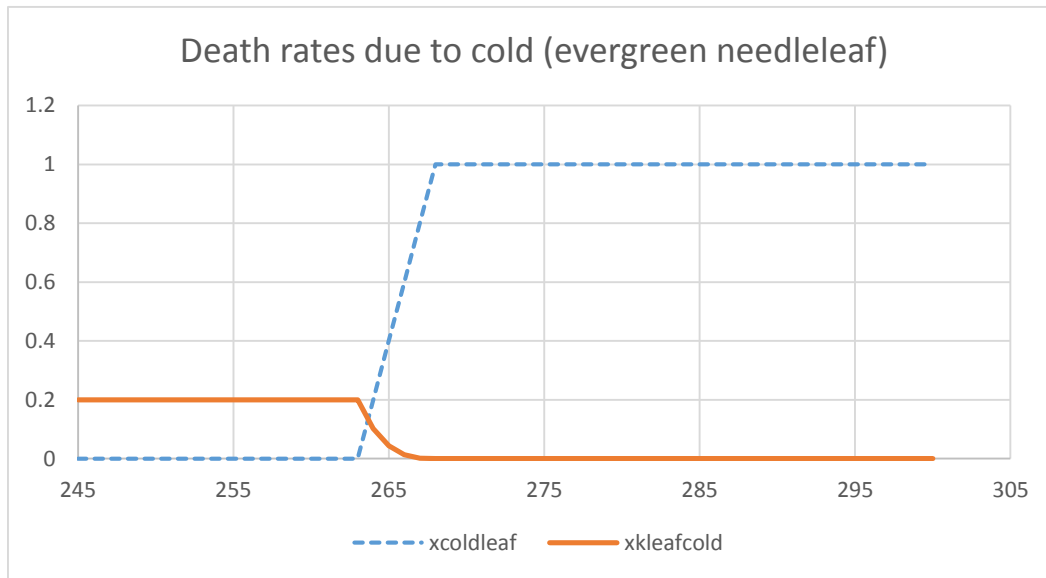


Figure 20. Effect of cold on evergreen leaf tree death rates. In this example for evergreen needle leaves,  $x_{\text{kleafcoldmax}} = 0.20$ ,  $x_{\text{kleafcoldexp}} = 3.0$ ,  $TK_{\text{shed}} = 268$ . When  $x_{\text{kleafcold}} = 0.0$  (orange line) there is no death due to cold. Note that the death rate for evergreen needle leaves is lower than the death rate for deciduous leaves at low temperatures (Figure 21).

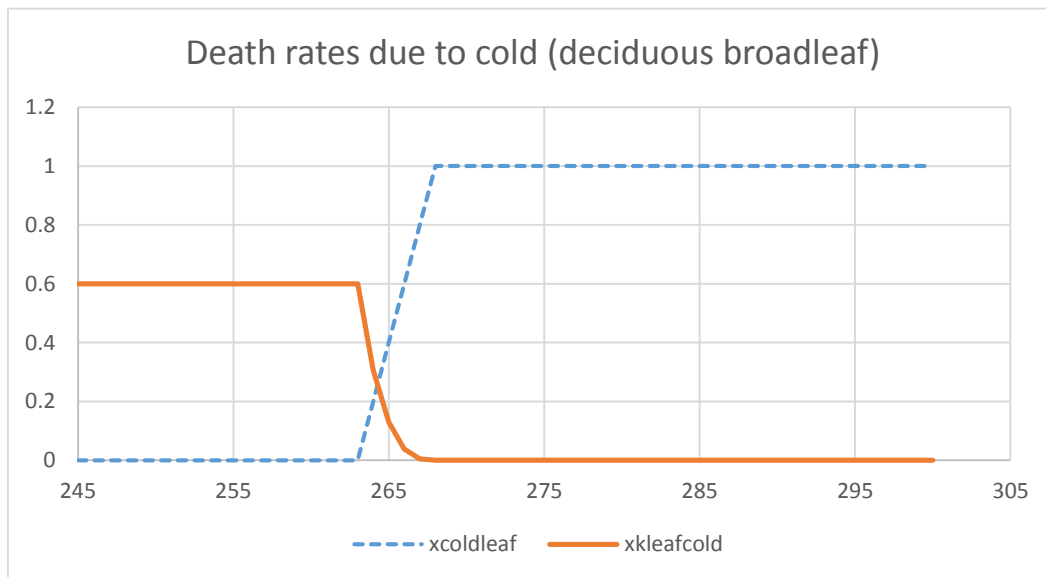


Figure 21. Effect of cold on deciduous leaf death rates. In this example for deciduous leaves,  $x_{\text{kleafcoldmax}} = 0.60$ ,  $x_{\text{kleafcoldexp}} = 3.0$ ,  $TK_{\text{shed}} = 268$ . When  $x_{\text{kleafcold}} = 0.0$  (orange line) there is no death due to cold. Note that the death rate for deciduous leaves is greater than the death rate for evergreen needle leaves at low temperatures (Figure 20).

**Leaf Death Rates Due to dryness (Figure 22, Figure 23).**

$$xkleafdry(npt) = casabiome\% xkleafdrymax(pft) \\ * (1.0 - casamet\% btran(npt))^{casabiome\% xkleafdryexp(pft)}$$

where  $casamet\% btran(npt)$  is the relative water content of the soil ( $1.0 \geq$  field capacity), calculated in **subroutine avgsoil**. The value of  $xkleafdry(npt)$  is added to  $casaflex\% kplant(npt, leaf)$  in **subroutine casa\_coeffplant** to compute total turnover rate.

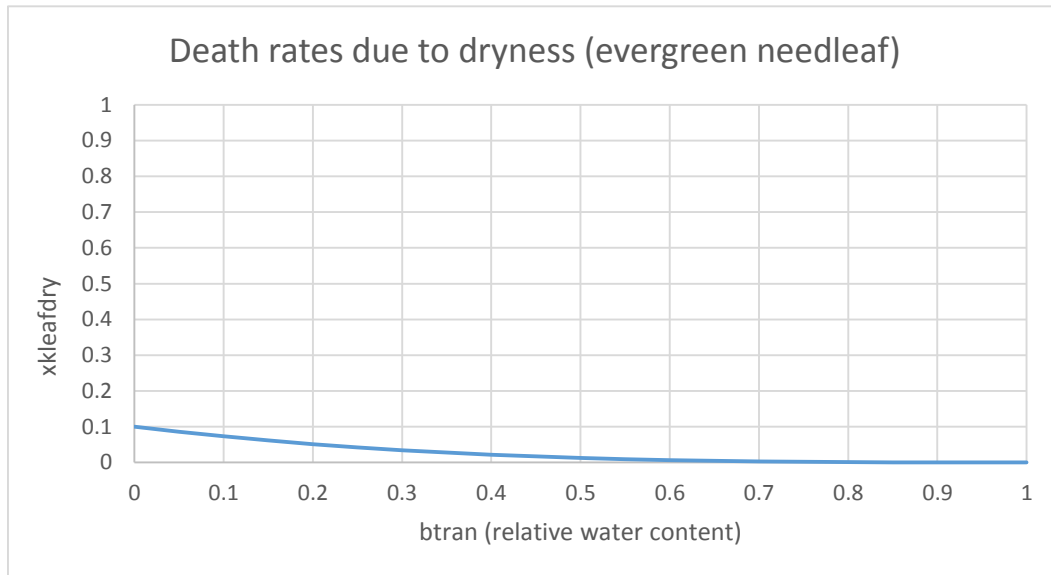


Figure 22. Effect of soil dryness on evergreen leaf death rates. In this example for evergreen needle leaves,  $xkleafdrymax = 0.1$ ,  $xkleafdryexp = 3.0$ . When  $xkleafdry = 0.0$  there is no death due to drought.

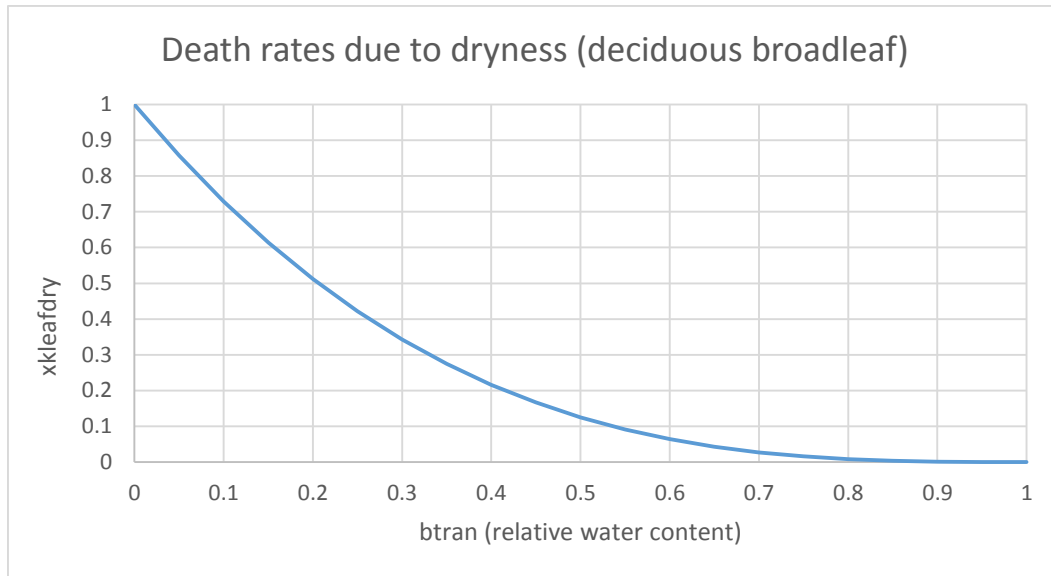


Figure 23. Effect of soil dryness on deciduous leaf death rates. In this example for deciduous leaves,  $xkleafdry_{max} = 1.0$ ,  $xkleafdry_{exp} = 3.0$ . When  $xkleafdry = 0.0$  there is no death due to drought.

The binary value  $xkleaf(npt)$  is 1 except during maximal leaf growth phase (greenup). This value is used to calculate the total turnover rate of leaves,  $casaflux\%kplant(npt, leaf)$  (see **subroutine casa\_coeffplant**).

$$xkleaf(npt) = \begin{cases} 0.0, & phen\%phase(npt) = 1 \\ 1.0, & otherwise \end{cases}$$

**END SUBROUTINE casa\_xrateplant**

#### 4.4.6 Plant Litterfall rate: (6) SUBROUTINE casa\_coeffplant

This subroutine calculates the plant litter fall rate (1/day) and the transfer coefficients between plant and litter pools.

Inputs:

$xkleafcold(npt)$ : cold stress induced leaf senescence rate (1/day)

$xkleafdry(npt)$ : drought-induced leaf senescence rate (1/day)

$xkleaf(npt)$ : set to 0.0 during maximal leaf growth phase to turn off leaf death due to aging, 1.0 otherwise.

*casabiome%fracNPtoL(pft,nP)*: fraction of N or P in plant part *nP* that is transferred to litter (0.0 – 1.0). The PFT lookup files shows this is about 0.5 for leaves, 0.95 for wood, and 0.90 for fine roots.

Outputs:

*casaflex%kplant(npt,nP)*: senescence rate of plant pool *nP* (1/day)

*casabiome%fromPtoL(npt,nL,nP)*: fraction of senesced plant biomass from plant pool *nP* transferred to litter pool *nL*

### Partitioning of plant residue to litter pools

The Lignin:N ratio (g lignin / g N) of plant biomass is used to partition litter into structural and metabolic pools.

$$ratioLignintoN(npt, leaf) = \frac{casapool\%Cplant(npt, leaf) * casabiome\%fracLigninplant(pft, leaf)}{casapool\%Nplant(npt, leaf) * casabiome\%ftransNPtoL(pft, leaf)}$$

$$ratioLignintoN(npt, froot) = \frac{casapool\%Cplant(npt, froot) * casabiome\%fracLigninplant(pft, froot)}{casapool\%Nplant(npt, froot) * casabiome\%ftransNPtoL(pft, froot)}$$

Where:

*casabiome%fracLigninplant(\*,nP)* – biome-specific lignin:N ratio (g lignin / g N)

*casabiome%ftransNPtoL(\*,nP)* – biome-specific fraction of plant N transferred to litter (fraction).

The fraction of leaf and fine root litter allocation to metabolic litter (0.0 – 0.85) increases with the ratio of lignin:N of the plant residue (similar to DayCent). The remaining fraction is allocated to structural litter (Figure 24).

$$casaflex\%fromPtoL(npt, metb, leaf) = \max(0.001, 0.85 - 0.018 * ratioLignintoN(npt, leaf))$$

$$casaflex\%fromPtoL(npt, metb, froot) = \max(0.001, 0.85 - 0.018 * ratioLignintoN(npt, froot))$$

$$casaflex\%fromPtoL(npt, str, leaf) = 1.0 - casaflex\%fromPtoL(npt, metb, leaf)$$

$$casaflex\%fromPtoL(npt, str, froot) = 1.0 - casaflex\%fromPtoL(npt, metb, froot)$$

$$casaflex\%fromPtoL(npt, cwd, wood) = 1.0$$

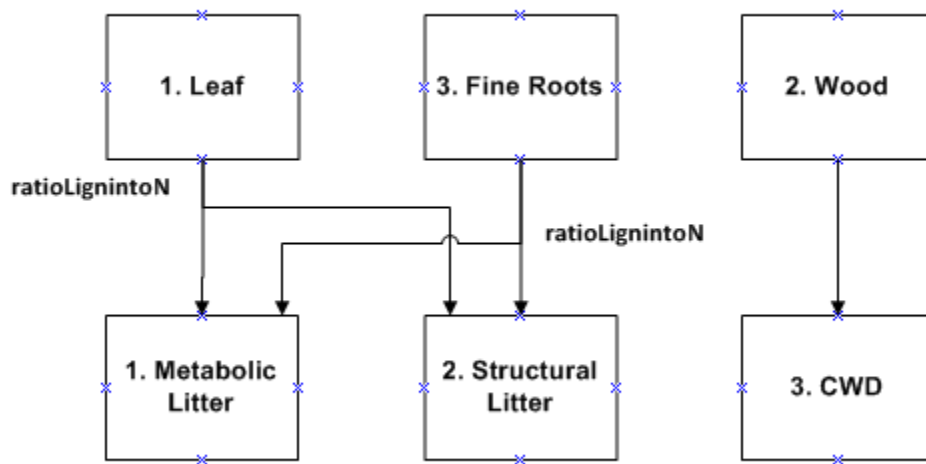


Figure 24. Carbon fluxes from plant pools to litter pools in the CASA-CNP model.

#### Plant senescence rates (*casaflex%kplant(npt,\*)*)

$$\begin{aligned} \text{casaflex\%kplant}(npt, \text{leaf}) &= \text{casabiome\%plantrate}(pft, \text{leaf}) * xkleaf(:) \\ &\quad + xkleafcold(npt) + xkleafdry(npt) \end{aligned}$$

$$\text{casaflex\%kplant}(npt, \text{wood}) = \text{casabiome\%plantrate}(pft, \text{wood})$$

$$\text{casaflex\%kplant}(npt, \text{froot}) = \text{casabiome\%plantrate}(pft, \text{froot})$$

where *casabiome%plantrate(pft,nP)* is the biome-specific age-related death rate of the plant parts (1/day), *xkleafcold(npt)* and *xkleafdry(npt)* are the leaf death rates due to cold and drought (0.0 – 1.0, calculated in **subroutine casa\_xrateplant**), and *xkleaf(npt)* which equals 0 during greenup and 1 otherwise, is calculated in **subroutine casa\_xrateplant**

**When glai<glaimin, leaf biomass will not decrease anymore (Q.Zhang 10/03/2011).**

$$\text{If } (\text{casamet\%glai}(npt) \leq \text{casabiome\%glaimin}(pft)) \text{ casaflex\%kplant}(npt, \text{leaf}) = 0.0$$

**END SUBROUTINE casa\_coeffplant**

#### 4.4.7 Nutrient Limitation on Production: (7) SUBROUTINE casa\_xnp

This subroutine calculates the effect of soil nutrient limitation on NPP. Note: CASA-CNP is no longer using N concentration restriction on production as is described in Wang, Law et al. (2010).

If simulating C-only (*icycle*=1), set nutrient-limiting variables to 1.0:

$$\begin{aligned} xnlimit &= 1.0 \\ xplimit &= 1.0 \\ xnplimit &= 1.0 \\ xNuptake &= 1.0 \\ xPuuptake &= 1.0 \end{aligned}$$

In addition, all but the final two equations listed below are skipped, and there is no soil nutrient limitation on NPP: *casaflex%fracClabile(npt)* = 0.0 and *casaflex%Cnpp(npt)* is not updated by this subroutine. See calculations at the end of the subroutine.

This subroutine calls **subroutine Nrequire** to compute the minimum and maximum plant N requirements, *Nreqmin(npt,\*)* and *Nreqmax(npt,\*)* (g N m<sup>-2</sup> d<sup>-1</sup>), based on nutrient-unlimited NPP and minimum and maximum N:C ratios of plant pools, *ncplantmin(npt,\*)* and *ncplantmax(npt,\*)*. Minimum and maximum N:C ratios are a function of biome-specific limits, *casabiome%ratioNCplantmin(pft,\*)* and *casabiome%ratioNCplantmax(pft,\*)*, and the amount of soil mineral N available, *casapool%Nsoilmin(npt)* (g N m<sup>-2</sup>).

If *casapool%Nsoilmin(npt)* < 2.0 then *ncplantmax(npt,\*)* is less than *ratioNCplantmax(\*,\*)* according to the following relationship (Figure 25):

$$\begin{aligned} ncplantmax(npt, leaf) &= casabiome\%ratioNCplantmin(pft, leaf) \\ &\quad + \left( casabiome\%ratioNCplantmax(pft, leaf) - casabiome\%ratioNCplantmin(pft, leaf) \right) \\ &\quad * \left( 2.0^{0.5 * casapool\%Nsoilmin(npt)} - 1.0 \right) \\ ncplantmax(npt, wood) &= casabiome\%ratioNCplantmin(pft, wood) \\ &\quad + \left( casabiome\%ratioNCplantmax(pft, wood) - casabiome\%ratioNCplantmin(pft, wood) \right) \\ &\quad * \left( 2.0^{0.5 * casapool\%Nsoilmin(npt)} - 1.0 \right) \\ ncplantmax(npt, froot) &= casabiome\%ratioNCplantmin(pft, froot) \\ &\quad + \left( casabiome\%ratioNCplantmax(pft, froot) - casabiome\%ratioNCplantmin(pft, froot) \right) \\ &\quad * \left( 2.0^{0.5 * casapool\%Nsoilmin(npt)} - 1.0 \right) \end{aligned}$$

Else ( $\text{casapool}\%N_{\text{soilmin}}(npt) \geq 2.0$ )

$\text{ncplantmax}(npt, \text{leaf}) = \text{casabiome}\%ratioNC_{\text{plantmax}}(pft, \text{leaf})$   
 $\text{ncplantmax}(npt, \text{wood}) = \text{casabiome}\%ratioNC_{\text{plantmax}}(pft, \text{wood})$   
 $\text{ncplantmax}(npt, \text{froot}) = \text{casabiome}\%ratioNC_{\text{plantmax}}(pft, \text{froot})$

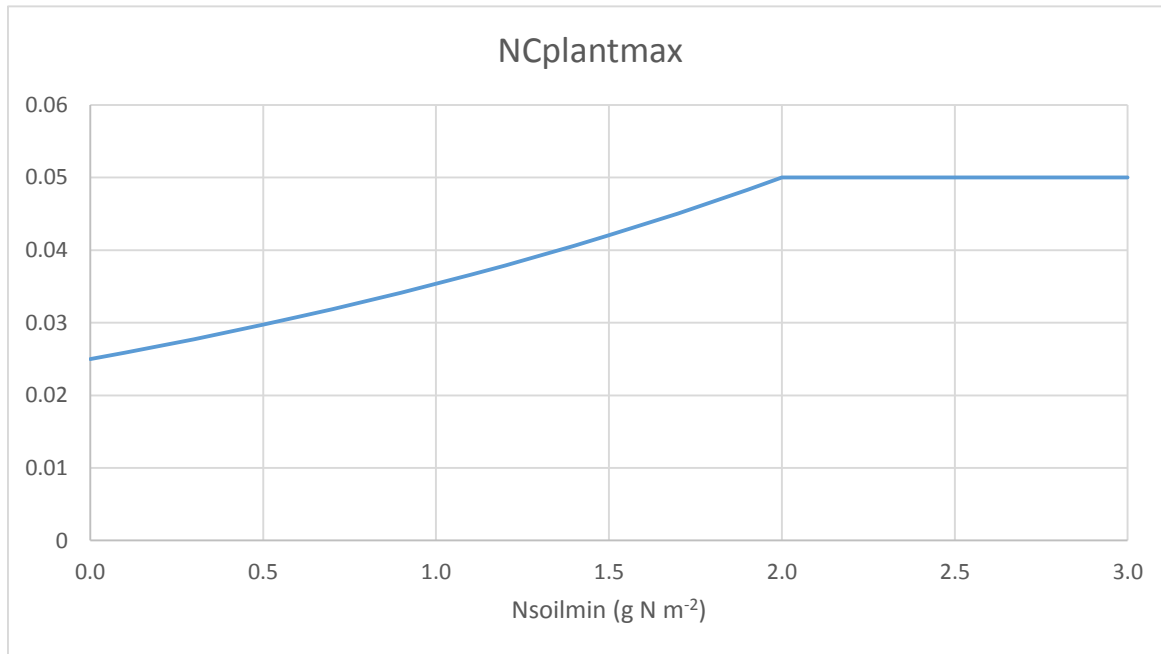


Figure 25. The N:C ratio of plant parts is bounded by biome-specific parameters  $\text{ratioNC}_{\text{plantmin}}$  and  $\text{ratioNC}_{\text{plantmax}}$ , and is a function of  $N_{\text{soilmin}}$ , the amount of mineral soil N available ( $\text{g N m}^{-2}$ ). Here  $\text{ratioNC}_{\text{plantmin}} = 0.25$  and  $\text{ratioNC}_{\text{plantmax}} = 0.5$ .

The maximum N demand by plants ( $N_{\text{reqmax}}(npt, *)$ ,  $\text{g N m}^{-2} \text{d}^{-1}$ ) is a product of the nutrient-unlimited NPP, the fraction of carbon allocation to each plant part (calculated in **subroutine casa\_allocation**), and the maximum N:C ratio calculated above.

$N_{\text{reqmax}}(npt, \text{leaf}) = x_{\text{Cnpp}}(npt) * \text{casaflux}\%frac_{\text{Calloc}}(npt, \text{leaf}) * \text{ncplantmax}(npt, \text{leaf})$   
 $N_{\text{reqmax}}(npt, \text{wood}) = x_{\text{Cnpp}}(npt) * \text{casaflux}\%frac_{\text{Calloc}}(npt, \text{wood}) * \text{ncplantmax}(npt, \text{wood})$   
 $N_{\text{reqmax}}(npt, \text{froot}) = x_{\text{Cnpp}}(npt) * \text{casaflux}\%frac_{\text{Calloc}}(npt, \text{froot}) * \text{ncplantmax}(npt, \text{froot})$

The minimum N demand by plants ( $N_{\text{reqmin}}(npt, *)$ ,  $\text{g N m}^{-2} \text{d}^{-1}$ ) is a product of the nutrient-unlimited NPP ( $x_{\text{Cnpp}}$ ,  $\text{g C m}^{-2} \text{d}^{-1}$ ), the fraction of carbon allocation to each plant part (calculated in **subroutine casa\_allocation**), and the minimum N:C ratio calculated above. **Note**, when **subroutine Nrequire** is later called by **subroutine nuptake**,  $x_{\text{Cnpp}}$  has been nutrient-limited.

$N_{\text{reqmin}}(npt, \text{leaf}) = x_{\text{Cnpp}}(npt) * \text{casaflux}\%frac_{\text{Calloc}}(npt, \text{leaf}) * \text{casabiome}\%ratioNC_{\text{plantmin}}(pft, \text{leaf})$   
 $N_{\text{reqmin}}(npt, \text{wood}) = x_{\text{Cnpp}}(npt) * \text{casaflux}\%frac_{\text{Calloc}}(npt, \text{wood}) * \text{casabiome}\%ratioNC_{\text{plantmin}}(pft, \text{wood})$



$$Nreqmin(npt, froot) = xnCnpp(npt) * casaflux \% fracCalloc(npt, froot) * casabiome \% ratioNCplantmin(pft, froot)$$

Retranslocation of N from dying plant material to live plant parts ( $NtransPtoP(npt, *)$ ) is the biome-specific fraction of N that is not transferred to the litter pools.

$$NtransPtoP(npt, leaf) = casaflux \% kplant(npt, leaf) * casapool \% Nplant(npt, leaf) * (1.0 - casabiome \% ftransNPtoL(pft, leaf))$$

$$NtransPtoP(npt, wood) = casaflux \% kplant(npt, wood) * casapool \% Nplant(npt, wood) * (1.0 - casabiome \% ftransNPtoL(pft, wood))$$

$$NtransPtoP(npt, froot) = casaflux \% kplant(npt, froot) * casapool \% Nplant(npt, froot) * (1.0 - casabiome \% ftransNPtoL(pft, froot))$$

Where:

$casabiome \% ftransNPtoL(npt, nP)$  – biome-specific fraction of N transferred from plant pool  $nP$  to litter pools

$casaflux \% kplant(npt, nP)$  – senescence rate of plant pool  $nP$  (1/day), calculated in **subroutine coeffplant**.

The maximum N requirement by each plant part is reduced by the amount of N translocation,  $NtransPtoP(npt, *)$  after plant death (calculated above).

$$\begin{aligned} Nreqmax(npt, leaf) &= \max(0.0, Nreqmax(npt, leaf) - NtransPtoP(npt, leaf)) \\ Nreqmax(npt, wood) &= \max(0.0, Nreqmax(npt, wood) - NtransPtoP(npt, wood)) \\ Nreqmax(npt, froot) &= \max(0.0, Nreqmax(npt, froot) - NtransPtoP(npt, froot)) \\ Nreqmin(npt, leaf) &= \max(0.0, Nreqmin(npt, leaf) - NtransPtoP(npt, leaf)) \\ Nreqmin(npt, wood) &= \max(0.0, Nreqmin(npt, wood) - NtransPtoP(npt, wood)) \\ Nreqmin(npt, froot) &= \max(0.0, Nreqmin(npt, froot) - NtransPtoP(npt, froot)) \end{aligned}$$

If the N:C ratios of live plant material is > the biome-specific maximum N:C ratio, don't allow plant N uptake.

if( $casapool \% nplant(npt, nP) / (casapool \% cplant(npt, nP) + 1.0e-10) > casabiome \% ratioNCplantmax(pft, nP)$ )  
then

$$Nreqmax(npt, nP) = 0.0$$

$$Nreqmin(npt, nP) = 0.0$$

endif

### Nutrient limitation on NPP

Sum total minimum and maximum N requirements by plants :

$$\begin{aligned}
totNreqmax(npt) &= Nreqmax(npt, leaf) + Nreqmax(npt, wood) + Nreqmax(npt, froot) \\
totNreqmin(npt) &= Nreqmin(npt, leaf) + Nreqmin(npt, wood) + Nreqmin(npt, froot) \\
xNuptake(npt) &= MAX \left( 0.0, MIN \left( 1.0, \frac{casapool\%Nsoilmin(npt)}{totNreqmin(npt) * deltpool} \right) \right)
\end{aligned}$$

Where *deltpool* is the time step (1 for daily), and *Nsoilmin(npt)* is available soil mineral N (g N m<sup>-2</sup>).

The value *xNPuptake(npt)* (0.0 – 1.0) is the N/P nutrient limitation on plant production, the minimum of the N limitation (*xNuptake(npt)*) and the P limitation (*xPuptake(npt)*) fractions. The value of *xPuptake(npt)* = 1.0 when P is not simulated.

$$xNPuptake(npt) = \min(xNuptake(npt), xPuptake(npt))$$

If there is a nutrient limitation on production (*xNPuptake(npt)* < 1.0), calculate the fraction of GPP that is diverted to the labile pool instead of NPP, *fracClabile(npt)* (0.0 – 1.0). This fraction is used again in **subroutine casa\_delplant**.

$$casaflux\%fracClabile(npt) = (1.0 - xNPuptake(npt)) * \frac{casaflux\%Cnpp(npt)}{casaflux\%Cgpp(npt)}$$

$$\begin{aligned}
casaflux\%Cnpp(npt) &= casaflux\%Cnpp(npt) - casaflux\%fracClabile(npt) * casaflux\%Cgpp(npt) \\
&= xNPuptake(npt) * Cnpp(npt)
\end{aligned}$$

As mentioned at the top of the subroutine, if *icycle*=1, there is no soil nutrient limitation on NPP: *xNPuptake* = 1.0, *casaflux%fracClabile(npt)* = 0.0, and *casaflux\%Cnpp(npt)* is not updated by this subroutine.

**END SUBROUTINE casa\_xnp**

#### 4.4.8 Soil Temperature and Moisture effects on SOM decomposition: (8) SUBROUTINE casa\_xratesoil

This subroutines calculates the effects of soil temperature and soil moisture on litter and soil decomposition rates: *xklitter*, *xksoil*

Inputs:

*iveg(npt)* : biome type (PFT)

*tsoilavg(npt)*: average soil temperature in the 6 soil layers (K)

*moistavg(npt)*: average volumetric soil moisture in the 6 soil layers (0.0 – 1.0)

Outputs:

*xklitter(npt)*: modifier of litter decomposition rate, similar to a climate decomposition index (dimensionless)

*xksoil(npt)*: modifier of soil decomposition rate, similar to climate decomposition index (dimensionless)

Constants:

REAL(r\_2), parameter :: wfpscoefa=0.55 ! Kelly et al. (2000) JGR, Figure 2b), optimal wfps

REAL(r\_2), parameter :: wfpscoefb=1.70 ! Kelly et al. (2000) JGR, Figure 2b)

REAL(r\_2), parameter :: wfpscoefc=-0.007 ! Kelly et al. (2000) JGR, Figure 2b)

REAL(r\_2), parameter :: wfpscoefd=3.22 ! Kelly et al. (2000) JGR, Figure 2b)

REAL(r\_2), parameter :: wfpscoefe=6.6481 ! =wfpscoefd\*(wfpscoefb-wfpscoefa)/(wfpscoefa-wfpscoefc)

##### **Kirschbaum function parameters**

REAL(r\_2), parameter :: xkalpha=-3.764 ! Kirschbaum (1995, SBB)

REAL(r\_2), parameter :: xkbeta=0.204

REAL(r\_2), parameter :: xktoptc=36.9

##### **Soil temperature and moisture modifiers on decomposition rates**

$$fwps(npt) = \frac{casamet\%moistavg(npt)}{soil\%ssat(npt)}$$

$$tsavg(npt) = casamet\%tsoilavg(npt)$$

$$xktemp(npt) = casabiome \% q10soil(veg \% iveg(npt))^{0.1 * (tsavg(npt) - TKzeroC - 35.0)}$$

$$xkwater(npt) = \begin{cases} \left( \frac{fwps(npt) - wfpscoefb}{wfpscoefa - wfpscoefb} \right)^{wfpscoefe} * \left( \frac{fwps(npt) - wfpscoefc}{wfpscoefa - wfpscoefc} \right)^{wfpscoefd} & , \text{non-cropland} \\ 1.0, & \text{cropland or cropland2} \end{cases}$$

$$xklitter(npt) = casabiome \% xkoptlitter(pft) * xktemp(npt) * xkwater(npt)$$

$$xksoil(npt) = casabiome \% xkoptsoil(pft) * xktemp(npt) * xkwater(npt)$$

where *casabiome%xkoptlitter* and *casabiome%xkoptsoil* are the biome-specific maximum decomposition rates (1/day); *fwps(npt)* is soil moisture expressed as the fraction of water filled pore space (0.0 – 1.0); *tsavg(npt)* is the average soil temperature in the 6 soil layers (K).

#### END SUBROUTINE casa\_xratesoil

---

#### 4.4.9 Litter and SOM decomposition rates: (9) SUBROUTINE casa\_coeffsoil

This subroutine calculates the litter and SOM decomposition rates (1/day), respiration rates (fraction of flow), and the transfer coefficients between litter and soil pools, and between soil pools.

Inputs:

*xklitter* and *xksoil* are calculated in **subroutine casa\_xratesoil (above)**

*xklitter(npt)*: modifier of litter decomposition rate, similar to a climate decomposition index (dimensionless)

*xksoil(npt)*: modifier of soil decomposition rate, similar to climate decomposition index (dimensionless)

Outputs:

*klitter(npt,mL)*: decomposition rate of litter pool *mL* (1/day)

*ksoil(npt,mS)*: decomposition rate of soil pool *mS* (1/day)

*fromLtoS(npt,nL,nS)*: fraction of decomposed litter pool *nL* to soil pool *nS*

*fromStoS(npt,nSS,nS)*: fraction of decomposed soil pool *nS* to another soil pool *nSS*

*fromLtoCO2(npt,nL)*: fraction of decomposed litter C pool *nL* emitted as CO<sub>2</sub>

*fromStoCO2(npt,nL)*: fraction of decomposed soil C pool *nS* emitted as CO<sub>2</sub>

### Litter Decomposition Rates

$$casaflux\%klitter(npt,metb) = xklitter(npt) * casabiome\%litterrate(pft,metb)$$

$$casaflux\%klitter(npt,str) = xklitter(npt) * casabiome\%litterrate(pft,str) \\ * \exp(-3.0 * casabiome\%fracLigninplant(pft,leaf))$$

$$casaflux\%klitter(npt,cwd) = xklitter(npt) * casabiome\%litterrate(pft,cwd)$$

$$casaflux\%ksoil(npt,mic) = xksoil(npt) * casabiome\%soilrate(veg\%iveg(npt),mic) \\ * (1.0 - 0.75 * (soil\%silt(npt) + soil\%clay(npt)))$$

$$casaflux\%ksoil(npt,slow) = xksoil(npt) * casabiome\%soilrate(veg\%iveg(npt),slow)$$

$$casaflux\%ksoil(npt,pass) = xksoil(npt) * casabiome\%soilrate(veg\%iveg(npt),pass)$$

For cultivated land types, increase the rate of soil decomposition

WHERE (pft==cropland)

$$casaflux\%ksoil(npt,mic) = casaflux\%ksoil(npt,mic) * 1.25$$

$$casaflux\%ksoil(npt,slow) = casaflux\%ksoil(npt,slow) * 1.5$$

$$casaflux\%ksoil(npt,pass) = casaflux\%ksoil(npt,pass) * 1.5$$

### Litter and Soil Organic Matter Decomposition (Figure 26)

#### Metabolic litter → Fast SOM

$$casaflux\%fromLtoS(npt,mic,metb) = 0.45$$

#### Structural litter → Fast SOM

$$casaflux\%fromLtoS(npt,mic,str) = 0.45 * (1.0 - casabiome\%fracLigninplant(pft,leaf))$$

**Structural litter → Slow SOM**

$$casaflux\% \text{ fromLtoS}(npt, slow, str) = 0.7 * casabiome\% \text{ fracLigninplant}(pft, leaf)$$

**Coarse Woody Debris → Fast SOM**

$$casaflux\% \text{ fromLtoS}(npt, mic, cwd) = 0.40 * (1.0 - casabiome\% \text{ fracLigninplant}(pft, wood))$$

**Coarse Woody Debris → Slow SOM**

$$casaflux\% \text{ fromLtoS}(npt, slow, cwd) = 0.7 * casabiome\% \text{ fracLigninplant}(pft, wood)$$

**Fast SOM → Slow SOM**

$$casaflux\% \text{ fromStoS}(npt, slow, mic) = (0.85 - 0.68 * (soil\% \text{ clay}(npt) + soil\% \text{ silt}(npt))) \\ * (0.997 - 0.032 * soil\% \text{ clay}(npt))$$

**Fast SOM → Passive SOM**

$$casaflux\% \text{ fromStoS}(npt, pass, mic) = (0.85 - 0.68 * (soil\% \text{ clay}(npt) + soil\% \text{ silt}(npt))) \\ * (0.003 + 0.032 * soil\% \text{ clay}(:))$$

**Slow SOM → Passive SOM**

$$casaflux\% \text{ fromStoS}(npt, pass, slow) = 0.45 * (0.003 + 0.009 * soil\% \text{ clay}(npt))$$

**Fractions of Litter C pools released as CO<sub>2</sub>**

$$casaflux\% \text{ fromLtoCO2}(npt, nL) = \sum_{nL} \sum_{nS} casaflux\% \text{ fromLtoS}(npt, nS, nL)$$

$$casaflux\% \text{ fromLtoCO2}(npt, nL) = \sum_{nL} 1.0 - casaflux\% \text{ fromLtoCO2}(npt, nL)$$

### Fractions of Soil C pools released as CO<sub>2</sub>

$$casaflux\%fromStoCO2(npt, nS) = \sum_{nS} \sum_{nSS} casaflux\%fromStoS(npt, nSS, nS)$$

$$casaflux\%fromStoCO2(npt, nS) = -casaflux\%fromStoCO2(npt, nS)$$

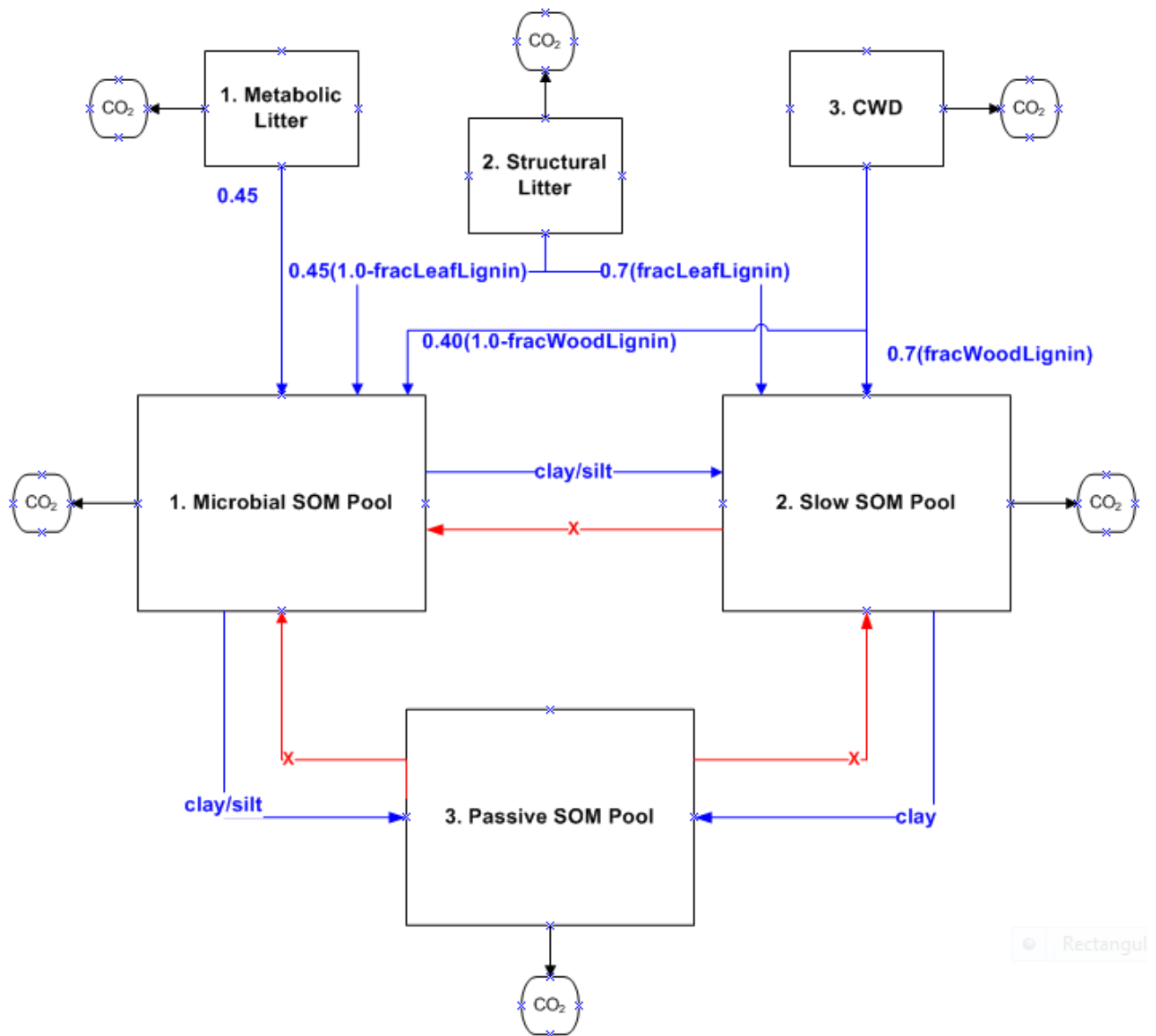


Figure 26. Carbon and CO<sub>2</sub> fluxes as litter and soil organic matter pools decompose in the CASA-CNP model.

**END SUBROUTINE casa\_coeffsoil****4.4.10 Mineralization, Immobilization, N limits on decomposition: (10) SUBROUTINE casa\_xkN**

This subroutine computes the mineralization, immobilization, and the reduction in litter and SOM decomposition when decomposition rate is N-limiting.

**Initialization**

*xkNlimiting(npt)* – multiplier on plant uptake and decomposition rates (0.0 – 1.0). It is < 1.0 when N is limiting to decomposition. Also defined as the reduction of N uptake by plants (0.0 – 1.0) due to competition from microbes (1.0 = no reduction). This factor will be used in **subroutine casa\_nuptake** to reduce N uptake by plants.

**Mineral N fluxes (Local Variables)**

*xFluxNlittermin(npt)* – gross mineralization from decomposition of litter pools (positive) (g N m<sup>-2</sup> d<sup>-1</sup>)

*xFluxNsoilmin(npt)* – gross mineralization from decomposition of soil pools (positive) (g N m<sup>-2</sup> d<sup>-1</sup>)

*xFluxNsoilimm(npt)* – immobilization from litter and soil C flows to destination soil pools (negative) (g N m<sup>-2</sup> d<sup>-1</sup>)

*xFluxNsoilminnet(npt)* – net mineralization (gross mineralization – immobilization), negative for net microbial uptake and positive for net release of mineral N.

**Calculate N:C ratio of newly formed SOM as function of soil mineral N pool (*casapool%Nsoilmin(npt)*, g N m<sup>-2</sup>)**

This calculation is like the variable C:N ratios in DayCent (Figure 27).

If *casapool%Nsoilmin(npt)* < 2.0

Limited soil mineral N forces the N:C ratio of new SOM to be below the maximum:

$$\begin{aligned} & \text{casapool\%ratioNCsoilnew}(npt, nS) \\ &= \text{casapool\%ratioNCsoilmin}(npt, nS) \\ &+ (\text{casapool\%ratioNCsoilmax}(npt, nS) - \text{casapool\%ratioNCsoilmin}(npt, nS)) \\ &\quad * \frac{\text{casapool\%Nsoilmin}(npt)}{2.0} \end{aligned}$$

If *casapool%Nsoilmin(npt)* ≥ 2.0

Mineral N unlimited, N:C ratio of new SOM equals the maximum:



$$casapool\%ratioNCsoilnew(npt, nS) = casapool\%ratioNCsoilmax(npt, nS)$$

where  $casapool\%ratioNCsoilmin(*, *)$  and  $casapool\%ratioNCsoilmax(*, *)$  are biome-specific parameters specifying the minimum and maximum N:C ratios of soil organic matter pools.

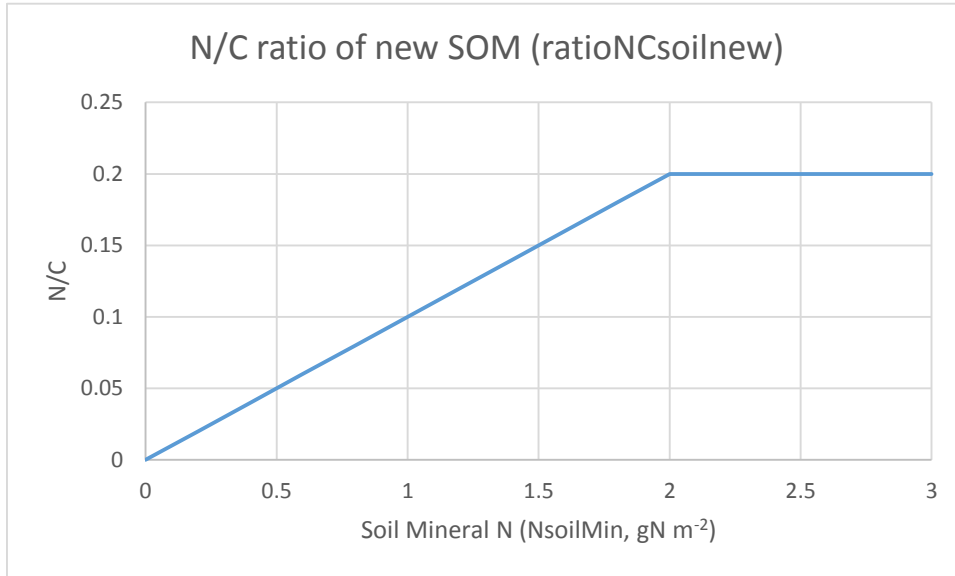


Figure 27. The N:C ratio required by the receiving SOM pool is a function of soil mineral N content. In this example,  $ratioNCsoilMin = 0.0$ ,  $ratioNCsoilMax = 0.2$

### Mineralization of litter and soil pools

$$xFluxNlittermin(npt) = \sum_{nL} casaflux\%klitter(npt, nL) * casapool\%Nlitter(npt, nL)$$

$$xFluxNsoilmin(npt) = \sum_{nS} casaflux\%ksoil(npt, nS) * casapool\%Nsoil(npt, nS)$$

### N immobilization from Litter to Soil

Immobilization from litter pool  $nL$  to soil pool  $nSS$  ( $xFluxnsoilimm(npt)$ ,  $gN\ m^{-2}\ d^{-1}$ ) is negative for microbial uptake.

$$xFluxNsoilimm(npt) = \sum_{nL} \sum_{nSS} \begin{pmatrix} - casaflux\% fromLtoS(npt, nSS, nL) \\ *casaflux\% klitter(npt, nL) \\ *casapool\% Clitter(npt, nL) \\ *casapool\% ratioNCsoilnew(npt, nSS) \end{pmatrix}$$

Where:

*casaflux%fromLtoS(npt, nSS, nL)* – fraction of decomposed litter pool *nL* that flows to soil pool *nSS* (0.0 – 1.0)

*casaflux%klitter(npt, nL)* - turnover rate of litter pool *nL* (1/day)

*casapool%Clitter(npt, nL)* – carbon in litter pool *nL* (g C m<sup>-2</sup>)

*casapool%ratioNCsoilnew(npt, nSS)* – the required N:C ratio of the receiving soil pool.

total C flow from litter pool *nL* to soil pool *nSS* assuming no N limitation:

$$casaflux\%fromLtoS(npt, nSS, nL) * casaflux\%klitter(npt, nL) * casapool\%Clitter(npt, nL)$$

total N flow from litter pool *nL* to soil pool *nSS* assuming no N limitation:

$$casaflux\%fromLtoS(npt, nSS, nL) * casaflux\%klitter(npt, nL) * casapool\%Clitter(npt, nL) * casapool\%ratioNCsoilnew(npt, nSS)$$

### N immobilization from Soil to Soil

Immobilization from soil pool *nS* to soil pool *nSS* (added to *xFluxnsoilimm(npt)*, gN m<sup>-2</sup> d<sup>-1</sup>) is negative for microbial uptake.

$$xFluxNsoilimm(npt) + = \sum_{nS} \sum_{nSS \neq nS} \begin{pmatrix} - casaflux\% fromStoS(npt, nSS, nS) \\ *casaflux\% ksoil(npt, nS) \\ *casapool\% Csoil(npt, nS) \\ *casapool\% ratioNCsoilnew(npt, nSS) \end{pmatrix}$$

Where:

*casaflux%fromStoS(npt, nSS, nS)* – fraction of decomposed SOM pool *nS* that flows to SOM pool *nSS* (0.0 – 1.0)

*casaflux%ksoil(npt, nS)* – turnover rate of SOM pool *nS* (1/day)

*casapool%Csoil(npt, nS)* – C in soil pool *nS* (g C m<sup>-2</sup>)

$casapool\%ratioNCsoilnew(npt,nSS)$  –required N:C ratio of the receiving soil pool.

total C flow from SOM pool  $nS$  to SOM pool  $nSS$ . assuming no N limitation:

$$casaf\%flux\%fromStoS(npt,nSS,nS)*casaf\%flux\%ksoil(npt,nS)*casapool\%Csoil(npt,nS)$$

total N flowing from SOM pool  $nS$  into SOM pool  $nSS$  assuming no N limitation:

$$casaf\%flux\%fromStoS(npt,nSS,nS)*casaf\%flux\%ksoil(npt,k)*casapool\%Csoil(npt,nS)*casapool\%ratioNCsoilnew(npt,nSS)$$

**Check if there is sufficient mineral N. Compute the limit on plant N,P uptake if there is not sufficient mineral N.**

$xFluxNsoilminnet$  (Net mineralization) = N mineralization from source litter pool flow + N mineralization from source soil pool flow + N immobilization by destination soil pool (negative).

$$xFluxNsoilminnet(npt) = xFluxNlittermin(npt) + xFluxNsoilmin(npt) + xFluxNsoilimm(npt)$$

If net mineralization is positive or if there is at least 2.0 g N m<sup>-2</sup> after accounting for the N demand by microbes,  $xkNlimiting = 1.0$ .

$xkNlimiting(npt)$  – reduction of N uptake by plants (0.0 – 1.0) due to competition from microbes (1.0 = no reduction).

if  $((xFluxNsoilminnet(npt)*delt\%pool + (casapool\%Nsoilmin(npt) - 2.0)) > 0.0$  OR  $xFluxNsoilminnet(npt) > 0.0$ )

$$xkNlimiting(npt) = 1.0$$

Otherwise,  $0.0 \leq xkNlimiting(npt) \leq 1.0$  and is equal to the ratio of available mineral N – 0.5 to the microbial demand for N

$$xkNlimiting(npt) = \max\left(0.0, -\frac{casapool\%Nsoilmin(npt) - 0.5}{delt\%pool * xFluxNsoilminnet(npt)}\right) \\ = \min(1.0, xkNlimiting(npt))$$

**If the amount of metabolic + structural litter is > the maximum fine litter + CWD then  $xkNlimiting = 1.0$ ?**

if  $(sum(casapool\%clitter,2) > casabiome\%maxfinelitter(pft) + casabiome\%maxc\%wd(pft))$

$$xkNlimiting(npt) = 1.0$$

**END SUBROUTINE casa\_xkN**

Note: after this subroutine returns to **SUBROUTINE biogeochem** (*casa\_inout.f90*), *casafux%klitter(npt, nL)* is multiplied by *xkNlimiting(npt)*, but *casafux%ksoil(npt, nS)* is not! Why? Then **subroutine casa\_nuptake** is called.

DO nL=1,mlitter

*casafux%klitter(npt,nL) = casafux%klitter(npt,nL)\* xkNlimiting(npt)*

ENDDO

call **casa\_nuptake**(veg, *xkNlimiting*, casabiome, casapool, casafux, casamet)

#### 4.4.11 Plant N uptake: (11) SUBROUTINE casa\_nuptake

This subroutine computes the total N uptake by plants (*casafux%Nminuptake(npt)*, g N m<sup>-2</sup> d<sup>-1</sup>) and the allocation of uptaken N to the 3 plant pools (*casafux%fracNalloc(npt,nP)*, 0.0 – 1.0).

This subroutine calls **subroutine Nrequire** to compute the minimum and maximum plant N requirements, *Nreqmin(npt,\*)* and *Nreqmax(npt,\*)* (g N m<sup>-2</sup> d<sup>-1</sup>), based on nutrient-limited NPP and minimum and maximum N:C ratios of plant pools, *ncplantmin(npt,\*)* and *ncplantmax(npt,\*)*. Minimum and maximum N:C ratios are a function of biome-specific limits, *casabiome%ratioNCplantmin(pft,\*)* and *casabiome%ratioNCplantmax(pft,\*)*, and the amount of soil mineral N available, *casapool%Nsoilmin(npt)* (g N m<sup>-2</sup>). Equations from **subroutine Nrequire** are found in documentation for **subroutine casa\_xnp**.

*xkNlimiting(npt)* – reduction of N uptake by plants (0.0 – 1.0) due to competition from microbes (1.0 = no reduction). Calculated in **subroutine casa\_xkN**.

Sum total minimum and maximum N requirements by plants (g N m<sup>-2</sup> d<sup>-1</sup>):

$$totNreqmax(npt) = Nreqmax(npt, leaf) + Nreqmax(npt, wood) + Nreqmax(npt, froot)$$

$$totNreqmin(npt) = Nreqmin(npt, leaf) + Nreqmin(npt, wood) + Nreqmin(npt, froot)$$

Note: These are local variables and I don't think these sums are used anywhere.

**N uptake from each plant pool *nP*, *xnuptake(npt,nP)* (g N m<sup>-2</sup> d<sup>-1</sup>).**

$$\begin{aligned}
 xnuptake(npt, nP) = & Nreqmin(npt, nP) \\
 & + xkNlimiting(npt) * (Nreqmax(npt, nP) - Nreqmin(npt, nP)) \\
 & * \frac{casapool\%Nsoilmin(npt)}{casapool\%Nsoilmin(npt) + casabiome\%kminN(pft)}
 \end{aligned}$$

Where  $xkNlimiting$  (0.0 – 1.0) is set in **subroutine casa\_xkN**,  $casabiome\%kminN(pft)$  ( $\text{g N m}^{-2}$ ) is a biome-specific parameter, the amount of soil mineral N to reach  $\frac{1}{2}$  the maximum N uptake (Figure 28).

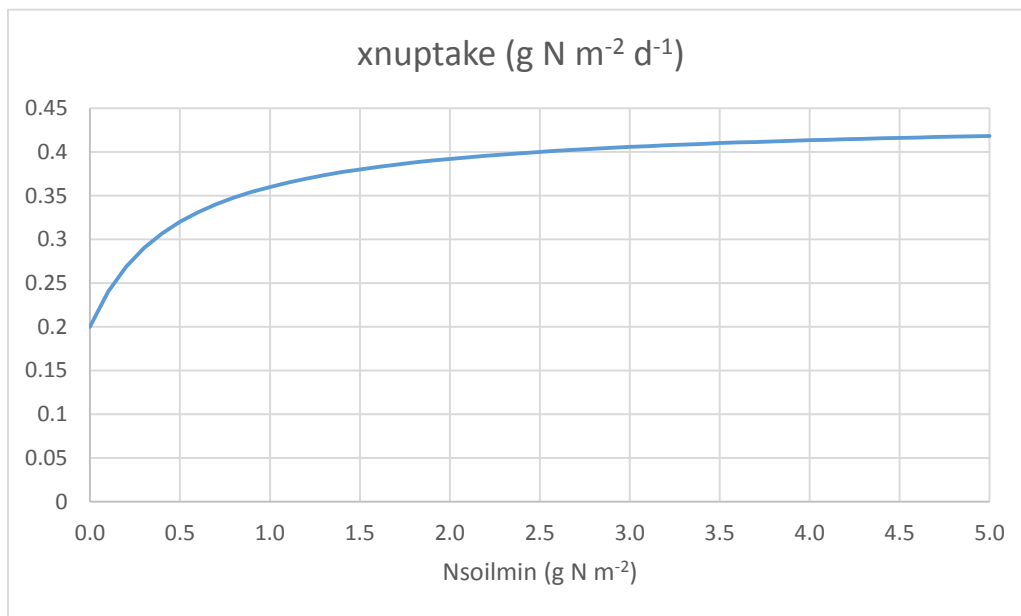


Figure 28. Actual N uptake by a plant pool ( $\text{g N m}^{-2} \text{d}^{-1}$ ). In this example,  $kminN = 0.5$ ,  $xkNlimiting = 0.8$ ,  $Nrequiremin = 0.2$ ,  $Nrequiremax = 0.5$ .

### Total plant N uptake and N allocation fractions.

These values are used in **subroutine casa\_delplant**.

$$casaf\%Nminuptake(npt) = xnuptake(npt, leaf) + xnuptake(npt, wood) + xnuptake(npt, froot)$$

$$casaf\%fracNalloc(npt, leaf) = xnuptake(npt, leaf) / casaf\%Nminuptake(npt)$$

$$casaf\%fracNalloc(npt, wood) = xnuptake(npt, wood) / casaf\%Nminuptake(npt)$$

$$casaf\%fracNalloc(npt, froot) = xnuptake(npt, froot) / casaf\%Nminuptake(npt)$$

$$casaflux\%Nupland(npt) = casaflux\%Nminuptake(npt)$$

#### END SUBROUTINE casa\_nuptake

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#### 4.4.12 Plant Net C, N, and P fluxes: (13) SUBROUTINE casa\_delplant

This subroutine calculates the change in plant C, N and P pools. The amount of N uptake by plants is computed in **subroutine casa\_nuptake**. The dC and dN values calculated here are used by **subroutine CASA-CNPcycle** to update the pools.

$$\begin{aligned} casapool\%dcplantdt(npt, nP) = & casaflux\%Cnpp(npt) * casaflux\%fracCalloc(npt, nP) \\ & - casaflux\%kplant(npt, nP) * casapool\%cplant(npt, nP) \end{aligned}$$

Calculate fraction C to labile pool **as a fraction of GPP**, not NPP.

$$\begin{aligned} casapool\%dClabiledt(npt) = & casaflux\%Cgpp(npt) * casaflux\%fracClabile(npt) \\ & - casaflux\%clabloss(npt) \end{aligned}$$

Where  $casaflux\%fracClabile(npt)$  was calculated in **subroutine casa\_xnp**, and  $casaflux\%clabloss(npt)$  was calculated in **subroutine casa\_rplant**.

#### Carbon transfers from plant to litter.

These appear to be output variables only and are not used in subsequent calculations.

$$\begin{aligned} cleaf2met(npt) &= casaflux\%fromPtoL(npt, metb, leaf) * casaflux\%kplant(npt, leaf) \\ &\quad * casapool\%cplant(npt, leaf) \\ cleaf2str(npt) &= casaflux\%fromPtoL(npt, str, leaf) * casaflux\%kplant(npt, leaf) \\ &\quad * casapool\%cplant(npt, leaf) \\ croot2met(npt) &= casaflux\%fromPtoL(npt, metb, froot) * casaflux\%kplant(npt, froot) \\ &\quad * casapool\%cplant(npt, froot) \\ croot2str(npt) &= casaflux\%fromPtoL(npt, str, froot) * casaflux\%kplant(npt, froot) \\ &\quad * casapool\%cplant(npt, froot) \\ cwood2cwd(npt) &= casaflux\%fromPtoL(npt, cwd, wood) * casaflux\%kplant(npt, wood) \\ &\quad * casapool\%cplant(npt, wood) \end{aligned}$$

#### Change in plant N pools (icycle > 1 only)

$$casapool\%dNplantdt(npt, leaf) = \begin{cases} -casaflux\%kplant(npt, leaf) * casapool\%Nplant(npt, leaf), \\ \quad \text{if } casaflux\%fracNalloc(npt, leaf) = 0.0 \\ -casaflux\%kplant(npt, leaf) * casapool\%Nplant(npt, leaf) \\ \quad * casabiome\%ftransNPtoL(iveg(npt), leaf), \\ \quad \text{otherwise} \end{cases}$$

$$casapool\%dNplantdt(npt, wood) = -casaflux\%kplant(npt, wood) * casapool\%Nplant(npt, wood) \\ * casabiome\%ftransNPtoL(iveg(npt), wood)$$

$$casapool\%dNplantdt(npt, froot) = -casaflux\%kplant(npt, froot) * casapool\%Nplant(npt, froot) \\ * casabiome\%ftransNPtoL(iveg(npt), froot)$$

Where  $casabiome\%ftransNPtoL(npt, nP)$  are biome-specific transfer rates from plant to litter

### Nitrogen transfers from plant to litter.

These appear to be output variables only and are not used in subsequent calculations.

$$nleaf2str(npt) = casaflux\%fromPtoL(npt, str, leaf) * casaflux\%kplant(npt, leaf) \\ * casapool\%cplant(npt, leaf) * ratioNCstrfix$$

$$nroot2str(npt) = casaflux\%fromPtoL(npt, str, froot) * casaflux\%kplant(npt, froot) \\ * casapool\%cplant(npt, froot) * ratioNCstrfix$$

$$nleaf2met(npt) = -casapool\%dNplantdt(npt, leaf) - nleaf2str(npt)$$

$$nroot2met(npt) = -casapool\%dNplantdt(npt, froot) - nroot2str(npt)$$

$$nwood2cwd(npt) = -casapool\%dNplantdt(npt, wood)$$

Where:

$ratioNCstrfix$  – fixed N:C ratio of structural material (1/150)

$casaflux\%kplant(npt, nP)$  – senescence rate of plant pool  $nP$  (1/day), calculated in **subroutine coeffplant**.

$casaflux\%fromPtoL(npt, nL, nP)$  – fraction of senesced plant biomass from plant pool  $nP$  transferred to litter pool  $nL$ , calculated in **subroutine casa\_coeffplant**.

Total C flux to litter is sum of all transfers of dead plant material to litter.

$$casaflux\%FluxCtolitter(npt, nL) = \sum_{nL} \sum_{nP} \left( \begin{array}{l} casaflux\%fromPtoL(npt, nL, nP) \\ *casaflux\%kplant(npt, nP) \\ *casapool\%cplant(npt, nP) \end{array} \right)$$

### N fluxes to Litter Pools (icycle > 1 only)

Total N flux to structural and metabolic litter and coarse woody debris is sum of all transfers of dead plant material to these litter pools.

### N flux to structural litter pool

$$\begin{aligned} casaflux\%FluxNtolitter(npt, str) = & casaflux\%fromPtoL(npt, str, leaf) \\ & *casaflux\%kplant(npt, leaf) \\ & *casapool\%cplant(npt, leaf) \\ & *ratioNCstrfix \\ & + casaflux\%fromPtoL(npt, str, froot) \\ & *casaflux\%kplant(npt, froot) \\ & *casapool\%cplant(npt, froot) \\ & *ratioNCstrfix \end{aligned}$$

Where:

*ratioNCstrfix* – fixed N:C ratio of structural material (1/150).

*casaflux\%kplant(npt, nP)* – senescence rate of plant pool *nP* (1/day), calculated in **subroutine coeffplant**.

*casaflux\%fromPtoL(npt, nL, nP)* – fraction of senesced plant biomass from plant pool *nP* transferred to litter pool *nL*, calculated in **subroutine casa\_coeffplant**.

### N flux to metabolic litter pool

$$\begin{aligned} casaflux\%FluxNtolitter(npt, metab) = & -casapool\%dNplantdt(npt, leaf) \\ & -casapool\%dNplantdt(npt, froot) \\ & -casaflux\%FluxNtolitter(npt, str) \end{aligned}$$

### N flux to coarse wood debris pool

$$casaflux\%FluxNtolitter(npt, cwd) = -casapool\%dNplantdt(npt, wood)$$



**N uptake by plants**

$$casapool\%dNplantdt(npt,:) = \sum_{nP} casaflux\%Nminuptake(npt) * casaflux\%fracNalloc(npt,nP)$$

where  $casaflux\%Nminuptake(npt)$  is total mineral N uptake calculated in **subroutine casa\_nuptake**, and  $casaflux\%fracNalloc(npt,nP)$  is the fraction of N allocation to each plant pool, calculated in **subroutine casa\_nuptake**.

**END SUBROUTINE casa\_delplant**

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#### 4.4.13 Update Litter and Soil Pools: (14) SUBROUTINE casa\_delsoil

This subroutine calculates changes in litter and soil pools. The dC and dN values calculated here are used by **subroutine CASA-CNPcycle** to update the pools.

**Carbon**

CO<sub>2</sub> fluxes from litter decomposition.

$$casaflux\%fluxCtoCO2(npt) = \sum_{nL} \left( casaflux\%fromLtoCO2(npt,nL) * casaflux\%klitter(npt,nL) * casapool\%clitter(npt,nL) \right)$$

C fluxes when a litter pool (nL) decomposes into an SOM pool (nS)

$$casaflux\%fluxCtoSOil(npt,nS) = \sum_{nL} \left( casaflux\%fromLtoS(npt,nS,nL) * casaflux\%klitter(npt,nL) * casapool\%clitter(npt,nL) \right)$$

CO<sub>2</sub> fluxes when one SOM pool (nSS) decomposes into another SOM pool (nS)

$$casaflux\%fluxCtoCO2(npt) += \sum_{nS} \left( casaflux\%fromStoCO2(npt,nS) * casaflux\%ksoil(npt,nS) * casapool\%csoil(npt,nS) \right)$$

C fluxes when one SOM pool (nSS) decomposes into another SOM pool (nS)

$$casaflux\%fluxCto\text{soil}(npt, nS) + = \sum_{nSS \neq nS} \left( casaflux\%fromStoS(npt, nS, nSS) * casaflux\%ksoil(npt, nSS) * casapool\%csoil(npt, nSS) \right)$$

Where the following were computed in **subroutine casa\_coefsoil**:

*casaflux%klitter(npt, nL)*: decomposition rate of litter pool *nL* (1/day)

*casaflux%ksoil(npt, nS)*: decomposition rate of soil pool *nS* (1/day)

*casaflux%fromLtoCO2(npt, nL)*: fraction of decomposed litter C pool *nL* emitted as CO<sub>2</sub>

*casaflux%fromLtoS(npt, nL, nS)*: fraction of decomposed litter pool *nL* to soil pool *nS*

*casaflux%fromStoCO2(npt, nS)*: fraction of decomposed soil C pool *nS* emitted as CO<sub>2</sub>

*casaflux%fromStoS(npt, nS, nSS)*: fraction of decomposed soil pool *nS* to another soil pool *nSS*

### Nitrogen (icycle > 1 only)

Many of these calculations are similar to those in **subroutine casa\_xkN**. However, after that function was called, *casaflux%klitter(npt, nL)* was multiplied by *xkNlimiting(npt)* (0.0 – 1.0) to reduce the litter decomposition rate if N was limiting. The value of *casaflux%ksoil(npt, nL)* was not changed.

### Mineral N fluxes

*casaflux%Nlittermin(npt)* – gross mineralization from decomposition of litter pools (positive)  
(g N m<sup>-2</sup> d<sup>-1</sup>)

*casaflux%Nsmin(npt)* – gross mineralization from decomposition of soil pools (positive) (g N m<sup>-2</sup> d<sup>-1</sup>)

*casaflux%Nsimm(npt)* – immobilization from litter and soil C flows to destination soil pools (negative)  
(g N m<sup>-2</sup> d<sup>-1</sup>)

*casaflux%Nsnet(npt)* – net mineralization (gross mineralization – immobilization), negative for net microbial uptake and positive for net release of mineral N.

### Gross mineralization from decomposition of litter

$$casaflux\%Nlittermin(npt) = \sum_{nL} casaflux\%klitter(npt, nL) * casapool\%Nlitter(npt, nL)$$

### Gross mineralization from decomposition of soil organic matter

$$casaflux\%Nsmin(npt) = \sum_{nS} casaflux\%ksoil(npt, nS) * casapool\%Nsoil(npt, nS)$$

### Immobilisation from litter to soil (from mLto nS)

$$casaf\text{lux}\% N_{\text{sim}}(npt) = \sum_{nS} \sum_{nL} \left( \begin{array}{l} -casaf\text{lux}\% \text{fromLtoS}(npt, nS, nL) \\ *casaf\text{lux}\% klitter(npt, nL) \\ *casapool\% Clitter(npt, nL) \\ *casapool\% ratioNCsoilnew(npt, nS) \end{array} \right)$$

Immobilisation from soil to soil (from nSS to nS)

$$casaf\text{lux}\% N_{\text{sim}}(npt) + = \sum_{nS} \sum_{nSS \neq nS} \left( \begin{array}{l} -casaf\text{lux}\% \text{fromStoS}(npt, nS, nSS) \\ *casaf\text{lux}\% ksoil(npt, nSS) \\ *casapool\% Csoil(npt, nSS) \\ *casapool\% ratioNCsoilnew(npt, nS) \end{array} \right)$$

Net mineralization (gross litter mineralization + gross soil mineralization – immobilization)

$$casaf\text{lux}\% N_{\text{net}}(npt) = casaf\text{lux}\% N_{\text{littermin}}(npt) + casaf\text{lux}\% N_{\text{min}}(npt) + casaf\text{lux}\% N_{\text{sim}}(npt)$$

Mineral N losses from volatilization(?) and leaching

IF(casapool%Nsoilmin(npt) > 2.0 AND casamet%tsoilavg(npt) > 273.12) THEN

$$casaf\text{lux}\% N_{\text{minloss}}(npt) = casaf\text{lux}\% fN_{\text{minloss}}(npt) * MAX(0.0, casaf\text{lux}\% N_{\text{net}}(npt))$$

$$casaf\text{lux}\% N_{\text{minleach}}(npt) = casaf\text{lux}\% fN_{\text{minleach}}(npt) * MAX(0.0, casapool\% N_{\text{soilmin}}(npt))$$

ELSE

$$\begin{aligned} casaf\text{lux}\% N_{\text{minloss}}(npt) &= casaf\text{lux}\% fN_{\text{minloss}}(npt) \\ &\quad * MAX(0.0, casaf\text{lux}\% N_{\text{net}}(npt)) \\ &\quad * MAX\left(0.0, \frac{casapool\% N_{\text{soilmin}}(npt)}{2.0}\right) \end{aligned}$$

$$\begin{aligned} casaf\text{lux}\% N_{\text{minleach}}(npt) &= casaf\text{lux}\% fN_{\text{minleach}}(npt) \\ &\quad * MAX(0.0, casapool\% N_{\text{soilmin}}(npt)) \\ &\quad * MAX\left(0.0, \frac{casapool\% N_{\text{soilmin}}(npt)}{2.0}\right) \end{aligned}$$

I have a question about 2 calculations above. Units are (fraction) \* (g N m<sup>-2</sup> d<sup>-1</sup>) \* (g N m<sup>-2</sup>)

Where:

*casaflex%fNminloss(npt)* – biome-specific rate of mineral N loss (fraction) (set to 0.05 for all biomes)

*casaflex%fNminleach(npt)* – biome-specific N leaching rate (1/day) (set to 0.05\*10/365 for all biomes)

### Total N fluxes to soil organic pools

$$casaflex\% FluxNto\text{soil}(npt, nS) = \sum_{nL} \sum_{nS} \left( \begin{array}{l} casaflex\% fromLtoS(npt, nS, nL) \\ *casaflex\% klitter(npt, nL) \\ *casapool\% Clitter(npt, nL) \\ *casapool\% ratioNCsoilnew(npt, nS) \end{array} \right)$$

$$casaflex\% FluxNto\text{soil}(npt, nS) += \sum_{nS} \sum_{nSS \neq nS} \left( \begin{array}{l} casaflex\% fromStoS(npt, nS, nSS) \\ *casaflex\% ksoil(npt, nSS) \\ *casapool\% Csoil(npt, nSS) \\ *casapool\% ratioNCsoilnew(npt, nS) \end{array} \right)$$

### Change in litter C pools

$$casapool\% dClitterdt(npt, nL) = casaflex\% fluxCtolitter(npt, nL) - casaflex\% klitter(npt, nL) * casapool\% clitter(npt, nL)$$

### Change in soil C pools

$$casapool\% dCsoildt(npt, nS) = casaflex\% fluxCto\text{soil}(npt, nS) - casaflex\% ksoil(npt, nS) * casapool\% csoil(npt, nS)$$

### Heterotrophic Respiration

$$casaflex\% Crsoil(npt) = casaflex\% fluxCtoCO2(npt)$$

## Nitrogen (icycle > 1 only)

### Changes to litter and soil organic matter N pools

$$\begin{aligned} \text{casapool}\%dN_{\text{litter}}dt(npt, nL) &= \text{casaflux}\%FluxN_{\text{tolitter}}(npt, nL) \\ &\quad - \text{casaflux}\%klitter(npt, nL) * \text{casapool}\%N_{\text{litter}}(npt, nL) \\ \text{casapool}\%dN_{\text{soil}}dt(npt, nS) &= \text{casaflux}\%FluxN_{\text{to soil}}(npt, nS) \\ &\quad - \text{casaflux}\%k_{\text{soil}}(npt, nS) * \text{casapool}\%N_{\text{soil}}(npt, nS) \end{aligned}$$

Where:

$\text{casaflux}\%FluxN_{\text{tolitter}}(npt)$  – Total N flux to litter, calculated in **subroutine casa\_delplant** which is called right before this subroutine ( $\text{g N m}^{-2} \text{d}^{-1}$ )

$\text{casaflux}\%FluxN_{\text{to soil}}(npt)$  – Total N flux to soil, calculated above ( $\text{g N m}^{-2} \text{d}^{-1}$ )

### Changes to mineral N pool

$$\begin{aligned} \text{casapool}\%dN_{\text{soil}}mindt(npt) &= \text{casaflux}\%Nsnet(npt) \\ &\quad + \text{casaflux}\%N_{\text{mindep}}(npt) \\ &\quad + \text{casaflux}\%N_{\text{minfix}}(npt) \\ &\quad - \text{casaflux}\%N_{\text{minloss}}(npt) \\ &\quad - \text{casaflux}\%N_{\text{minleach}}(npt) \\ &\quad - \text{casaflux}\%N_{\text{upland}}(npt) \end{aligned}$$

Where:

$\text{casaflux}\%Nsnet(npt)$  – net mineralization, calculated above ( $\text{g N m}^{-2} \text{d}^{-1}$ )

$\text{casaflux}\%N_{\text{mindep}}(npt)$  – atmospheric N deposition rate from CLM ( $\text{g N m}^{-2} \text{d}^{-1}$ )

$\text{casaflux}\%N_{\text{minfix}}(npt)$  – biome-specific N fixation rate ( $\text{g N m}^{-2} \text{d}^{-1}$ )

$\text{casaflux}\%fN_{\text{minloss}}(npt)$  – mineral N losses from volatilization, calculated above ( $\text{g N m}^{-2} \text{d}^{-1}$ ).

$\text{casaflux}\%fN_{\text{minleach}}(npt)$  – mineral N losses from leaching, calculated above ( $\text{g N m}^{-2} \text{d}^{-1}$ ).

$\text{casaflux}\%N_{\text{upland}}(npt)$  – Total mineral N uptake by plants, calculated in **subroutine casa\_nuptake** ( $\text{g N m}^{-2} \text{d}^{-1}$ ).

**END SUBROUTINE casa\_delsoil****4.4.14 Final Daily Update to all Pools: (15) SUBROUTINE casa\_cnpcycle**

This subroutine updates all pool sizes. The value of `delpool = 1` (for daily). The `dC` and `dN` values are calculated in **subroutine casa\_delplant** and **subroutine casa\_delsoil**.

**Update Plant Carbon Pools**

$$\text{casapool\%cplant}(npt, nP) = \text{casapool\%cplant}(npt, nP) + \text{casapool\%dCplantdt}(npt, nP) * \text{delpool}$$

$$\text{casapool\%clabile}(npt) = \text{casapool\%clabile}(npt) + \text{casapool\%dClabiledt}(npt) * \text{delpool}$$

$$\text{casamet\%glai}(npt) = \text{MAX}(\text{casabiome\%glaimin}(pft), \text{casabiome\%sla}(pft) * \text{casapool\%cplant}(npt, \text{leaf}))$$

$$\text{casamet\%glai}(npt) = \text{MIN}(\text{casabiome\%glaimax}(pft), \text{casamet\%glai}(npt))$$
**Update Litter and Soil Carbon Pools**

$$\text{casapool\%clitter}(npt, nL) = \text{casapool\%clitter}(npt, nL) + \text{casapool\%dClitterdt}(npt, nL) * \text{delpool}$$

$$\text{casapool\%csoil}(npt, nS) = \text{casapool\%csoil}(npt, nS) + \text{casapool\%dCsoildt}(npt, nS) * \text{delpool}$$
**Update Plant Nitrogen Pools (icycle > 1 only)**

IF(`casapool\%cplant`(`npt, leaf`) > 0.0) THEN

$$\text{casapool\%Nplant}(npt, :) = \text{casapool\%Nplant}(npt, :) + \text{casapool\%dNplantdt}(npt, :) * \text{delpool}$$
**Update Litter and Soil Nitrogen Pools (icycle > 1 only)**

$$\text{casapool\%Nlitter}(npt, nL) = \text{casapool\%Nlitter}(npt, nL) + \text{casapool\%dNlitterdt}(npt, nL) * \text{delpool}$$

$$\text{casapool\%Nsoil}(npt, nS) = \text{casapool\%Nsoil}(npt, nS) + \text{casapool\%dNsoildt}(npt, nS) * \text{delpool}$$

$$\text{casapool\%Nsoilmin}(npt) = \text{casapool\%Nsoilmin}(npt) + \text{casapool\%dNsoilmindt}(npt) * \text{delpool}$$

After the above calculations, any negative C or N pools are set to zero without adjusting the N and C balances. CASA-CNP will also produce a warning message when a negative pool is set to zero.

**END SUBROUTINE casa\_cnpcycle****5 Guidelines for adding additional SOM models to the testbed**

- Convert all code to FORTRAN 90
- If the model is a point model, then create a structure that will contain all model variables for each point. This was done for the CORPSE model to avoid modifying the original code (see type `gridcell` in `corpse_variable.f90`)
- Create model-specific versions of `casa_coeffplant`, `casa_xratesoil`, `casa_delplant`, `casa_delsoil`, `casa_cnpcycle` s needed. See “Overview of subroutine biogeochem” below.
- Create `model_inout.f90` to
  - read model-specific parameter files
  - read model restart files to initialize model variables
  - compute average annual pools and fluxes before output (once at the end-of-year)
  - output model-specific daily and annual variables to netCDF files

### 5.1 Overview of subroutine biogeochem with calls to MIMICS and CORPSE models

There are several CASA-CNP subroutines that have been modified to work with the MIMICS and CORPSE models. The numbers in front of subroutines indicate their calling position in **subroutine biogeochem** (`casa_inout.f90`) which is called once a day. The MIMICS subroutines will be found in `mimics_cycle.f90`, CORPSE subroutines are found in `corpse_cycle.f90`, and all CASA-CNP subroutines are found in `casa_cnp.f90`.

1. **phenology** – Determine current phase for each gridcell: 0=minimal LAI, 1=greenup, 2=steady LAI, 3=senescence
2. **avgsoil** – Calculate average soil moisture, average soil temperature across soil layers
3. **casa\_rplant** – Calculate maintenance respiration of woody tissue and fine roots, plant growth respiration, and nutrient unlimited NPP.
4. **casa\_allocation** – Compute fraction of new C allocated to each plant part.
5. **casa\_xrateplant** – Account for cold and drought stress on death rate of leaf: *xleafcold*, *xleafdry*
6. **if running CASA-CNP SOM model (isomModel == 1)**
  - a. **casa\_coeffplant** – Calculate plant litter fall rates (1/day) and the transfer coefficients between plant and litter pools.
  - b. **casa\_xnp** – Compute nutrient limitation on NPP.
  - c. **casa\_xratesoil** – Account for effects of temperature and water on litter and soil decomposition: *xklitter*, *xksoil*
  - d. **casa\_coeffsoil** – Calculate the litter and SOM decomposition rates (1/day), respiration rates (fraction of flow), and the transfer coefficients between litter and soil pools, and between soil pools.
  - e. **These subroutines aren’t used if icycle=1 (C only).**
    - i. **casa\_xkN** – Calls `Nrequire` to compute max and min N uptake and translocation by plant part. Computes the reduction in plant N and P uptake when N is limiting.
    - ii. **casa\_nuptake** – Calls `Nrequire` to compute max and min N uptake and translocation by plant part. (1) compute N uptake by plants; (2) allocation of uptaken N to plant pools.
    - iii. **casa\_puptake** – Calls `Prequire` to compute max and min P uptake and translocation by plant part. (1) compute P uptake by plants; (2) allocation of uptaken P to plants
  - f. **casa\_delplant** – Calculate  $\Delta C$ ,  $\Delta N$ , and  $\Delta P$  for plant parts and litter pools

- g. **casa\_delsoil** – Calculate heterotrophic respiration fluxes from litter and soil decomposition. Calculate gross and net mineralization.
- h. **casa\_cnpcycle** – Update all pool sizes. Reset negative pools to zero by calling **poolzero**.
- 7. **if running MIMICS (isomModel == 2)**
  - a. call mimics subroutines **to** update all litter, microbial, and SOM pools for the day with an hourly timestep. Calculate heterotrophic respiration also. Pertinent code was copied from **casa\_coeffplant**, **casa\_xratesoil**, **casa\_delplant**, **casa\_delsoil**, **casa\_cnpcycle**.
    - i. **call mimics\_coeffplant** – MIMICS uses some of its own parameters to partition plant litter into structural and metabolic litter. The computations for **casafux%fromPtoL(:,metb,leaf)** and **casafux%fromPtoL(:,metb,froot)** have therefore been modified.
    - ii. **call mimics\_xratesoil** – adds the **casafux%fromLtoCO2(npt,cwd)** calculation (fraction of CWD decomposition that goes to heterotrophic respiration) that is found in **casa\_coeffsoil**
    - iii. **call mimics\_delplant** – Computes C-only values. Computes MIMICS output variables for litter inputs. Computes **mimicsbiome%fmet(npt)**. Adds MIMICS **fAVAL**, **fCHEM**, and **fPHYS** calculations because **fCHEM** (and therefore **fPHYS** and **fAVAL**) depend on **themimicsbiome%fmet(npt)** calculation.
    - iv. **call mimics\_soil\_reverseMM** – the MIMICS SOC model. The hourly timestep is inside this subroutine.
    - v. **call mimics\_ccycle** – similar to **casa\_cnpcycle** but removes N,P pool updates.
    - vi. **call mimics\_caccum** – accumulate annual fluxes and convert units from **mgC/cm3** to **gC/m2**.
- 8. **if running CORPSE (isomModel == 3)**
  - a. call CORPSE subroutines **to** update all litter, microbial, and SOM pools for the day with a daily timestep.
    - i. **call casa\_coeffplant** (uses same subroutine as **CASA-CNP**)
    - ii. **call mimics\_xratesoil** (uses same subroutine as **mimics**)
    - iii. **call corpse\_delplant** – Computes C-only values. Computes **CASA-CNP** output variables for litter inputs.
    - iv. **call corpse\_soil** – the CORPSE SOC model  
**calls corpse\_caccum** – accumulate annual fluxes
    - v. **call mimics\_ccycle** (uses same subroutine as **mimics**)
- 9. IF (icycle<3) call **casa\_pdummy(casapool)** ! Update Pplant based on N:P ratio
- 10. IF (icycle<2) call **casa\_ndummy(casapool)** ! Update Nplant based on N:C ratio
- 11. **call casa\_cnppool** (*casa\_input.f90*)
- 12. **call casa\_cnpflux** (*casa\_input.f90*) – Accumulates daily **CASA-CNP** fluxes. The annual average is calculated subroutine **casa\_fluxout\***.
- 13. **call casa\_cnppool** (*casa\_input.f90*) – Accumulates daily **CASA-CNP** pool values to be averaged at the end of the year. The annual average is calculated subroutine **casa\_poolout\***.

\*MIMICS and CORPSE: **mimics\_caccum** and **corpse\_caccum** are model-specific counterparts to **casa\_cnpflux** and **casa\_cnppool**. At the end of each simulation year, **casa\_fluxout**, **casa\_poolout**, **mimics\_poolfluxout** and **corpse\_poolfluxout** are called from subroutine **CASA-CNPdriver**.

## 6 Conversions



## 6.1 g C m<sup>-2</sup> to mg C cm<sup>-3</sup>

$$\frac{\text{g C}}{\text{m}^2} * \frac{10^3 \text{ mg C}}{\text{g C}} * \frac{\text{m}^2}{10^4 \text{ cm}^2} * \frac{1}{\text{depth (cm)}} = \frac{\text{mg C}}{\text{cm}^3}$$

## 6.2 mg C cm<sup>-3</sup> to g C m<sup>-2</sup>

$$\frac{\text{mg C}}{\text{cm}^3} * \frac{10^4 \text{ cm}^2}{\text{m}^2} * \frac{\text{g C}}{10^3 \text{ mg C}} * \text{depth (cm)} = \frac{\text{g C}}{\text{m}^2}$$

# 7 Output NetCDF files

The following sections document output produced by “ncdump -h *model*\_pool\_flux.nc”, where *model* = CASA-CNP, mimics, or corpse. Some of the global attributes are specific to the run-time options selected.

## 7.1 casaclm\_pool\_flux.nc

```
netcdf casaclm_pool_flux {
dimensions:
    lon = 144 ;
    lat = 96 ;
    time = UNLIMITED ; // (1 currently)
variables:
    float lon(lon) ;
        lon:long_name = "coordinate longitude" ;
        lon:units = "degrees_east" ;
    float lat(lat) ;
        lat:long_name = "coordinate latitude" ;
        lat:units = "degrees_north" ;
    float time(time) ;
        time:long_name = "coordinate time" ;
        time:units = "1..ntimes" ;
    int IGBP_PFT(lat, lon) ;
        IGBP_PFT:long_name = "IGBP PFT classification" ;
        IGBP_PFT:units = "1-18" ;
        IGBP_PFT:_FillValue = -9999 ;
        IGBP_PFT:missing_value = -9999 ;
    float landarea(lat, lon) ;
        landarea:long_name = "land area, icewater set to 0.0" ;
        landarea:units = "km^2" ;
        landarea:_FillValue = 1.e+36f ;
```

```

        landarea:missing_value = 1.e+36f ;
int cellMissing(lat, lon) ;
        cellMissing:long_name = "Missing Data Mask" ;
        cellMissing:units = "0=no missing data, 1=missing data" ;
int cellid(lat, lon) ;
        cellid:long_name = "Grid Cell ID" ;
        cellid:units = "1..nlat*nlon" ;
float cresp(time, lat, lon) ;
        cresp:long_name = "soil heterotrophic respiration" ;
        cresp:units = "gC m-2 year-1" ;
        cresp:_FillValue = 1.e+36f ;
        cresp:missing_value = 1.e+36f ;
float cnpp(time, lat, lon) ;
        cnpp:long_name = "net primary production" ;
        cnpp:units = "gC m-2 year-1" ;
        cnpp:_FillValue = 1.e+36f ;
        cnpp:missing_value = 1.e+36f ;
float cgpp(time, lat, lon) ;
        cgpp:long_name = "gross primary production" ;
        cgpp:units = "gC m-2 year-1" ;
        cgpp:_FillValue = 1.e+36f ;
        cgpp:missing_value = 1.e+36f ;
float cleaf(time, lat, lon) ;
        cleaf:long_name = "leaf carbon" ;
        cleaf:units = "gC m-2" ;
        cleaf:_FillValue = 1.e+36f ;
        cleaf:missing_value = 1.e+36f ;
float nleaf(time, lat, lon) ;
        nleaf:long_name = "leaf nitrogen" ;
        nleaf:units = "gN m-2" ;
        nleaf:_FillValue = 1.e+36f ;
        nleaf:missing_value = 1.e+36f ;
float cwood(time, lat, lon) ;
        cwood:long_name = "wood carbon" ;
        cwood:units = "gC m-2" ;
        cwood:_FillValue = 1.e+36f ;
        cwood:missing_value = 1.e+36f ;
float nwood(time, lat, lon) ;
        nwood:long_name = "wood nitrogen" ;
        nwood:units = "gN m-2" ;
        nwood:_FillValue = 1.e+36f ;
        nwood:missing_value = 1.e+36f ;
float cfroot(time, lat, lon) ;
        cfroot:long_name = "fine root carbon" ;
        cfroot:units = "gC m-2" ;
        cfroot:_FillValue = 1.e+36f ;
        cfroot:missing_value = 1.e+36f ;
float nfroot(time, lat, lon) ;

```

```

    nroot:long_name = "fine root nitrogen" ;
    nroot:units = "gN m-2" ;
    nroot:_FillValue = 1.e+36f ;
    nroot:missing_value = 1.e+36f ;
float clitmetb(time, lat, lon) ;
    clitmetb:long_name = "metabolic litter carbon" ;
    clitmetb:units = "gC m-2" ;
    clitmetb:_FillValue = 1.e+36f ;
    clitmetb:missing_value = 1.e+36f ;
float nlitmetb(time, lat, lon) ;
    nlitmetb:long_name = "metabolic litter nitrogen" ;
    nlitmetb:units = "gN m-2" ;
    nlitmetb:_FillValue = 1.e+36f ;
    nlitmetb:missing_value = 1.e+36f ;
float clitstr(time, lat, lon) ;
    clitstr:long_name = "structural litter carbon" ;
    clitstr:units = "gC m-2" ;
    clitstr:_FillValue = 1.e+36f ;
    clitstr:missing_value = 1.e+36f ;
float nlitstr(time, lat, lon) ;
    nlitstr:long_name = "structural litter nitrogen" ;
    nlitstr:units = "gN m-2" ;
    nlitstr:_FillValue = 1.e+36f ;
    nlitstr:missing_value = 1.e+36f ;
float clitcwd(time, lat, lon) ;
    clitcwd:long_name = "coarse woody debris carbon" ;
    clitcwd:units = "gC m-2" ;
    clitcwd:_FillValue = 1.e+36f ;
    clitcwd:missing_value = 1.e+36f ;
float nlitcwd(time, lat, lon) ;
    nlitcwd:long_name = "coarse woody debris nitrogen" ;
    nlitcwd:units = "gN m-2" ;
    nlitcwd:_FillValue = 1.e+36f ;
    nlitcwd:missing_value = 1.e+36f ;
float csoilmic(time, lat, lon) ;
    csoilmic:long_name = "microbial soil organic matter carbon" ;
    csoilmic:units = "gC m-2" ;
    csoilmic:_FillValue = 1.e+36f ;
    csoilmic:missing_value = 1.e+36f ;
float nsoilmic(time, lat, lon) ;
    nsoilmic:long_name = "microbial soil organic matter nitrogen" ;
    nsoilmic:units = "gN m-2" ;
    nsoilmic:_FillValue = 1.e+36f ;
    nsoilmic:missing_value = 1.e+36f ;
float csoilslow(time, lat, lon) ;
    csoilslow:long_name = "slow soil organic matter carbon" ;
    csoilslow:units = "gC m-2" ;
    csoilslow:_FillValue = 1.e+36f ;

```

```

        csoilslow:missing_value = 1.e+36f ;
float nsoilslow(time, lat, lon) ;
        nsoilslow:long_name = "slow soil organic matter nitrogen" ;
        nsoilslow:units = "gN m-2" ;
        nsoilslow:_FillValue = 1.e+36f ;
        nsoilslow:missing_value = 1.e+36f ;
float csoilpass(time, lat, lon) ;
        csoilpass:long_name = "passive soil organic matter carbon" ;
        csoilpass:units = "gC m-2" ;
        csoilpass:_FillValue = 1.e+36f ;
        csoilpass:missing_value = 1.e+36f ;
float nsoilpass(time, lat, lon) ;
        nsoilpass:long_name = "passive soil organic matter nitrogen" ;
        nsoilpass:units = "gN m-2" ;
        nsoilpass:_FillValue = 1.e+36f ;
        nsoilpass:missing_value = 1.e+36f ;
float tairC(time, lat, lon) ;
        tairC:long_name = "mean annual air temperature" ;
        tairC:units = "degrees C" ;
        tairC:_FillValue = 1.e+36f ;
        tairC:missing_value = 1.e+36f ;
float tsoilC(time, lat, lon) ;
        tsoilC:long_name = "mean annual soil temperature in top 50 cm" ;
        tsoilC:units = "degrees C" ;
        tsoilC:_FillValue = 1.e+36f ;
        tsoilC:missing_value = 1.e+36f ;
float litInptMet(time, lat, lon) ;
        litInptMet:long_name = "Metabolic Litter Inputs" ;
        litInptMet:units = "gC m-2 yr-1" ;
        litInptMet:_FillValue = 1.e+36f ;
        litInptMet:missing_value = 1.e+36f ;
float litInptStruc(time, lat, lon) ;
        litInptStruc:long_name = "Structural Litter Inputs" ;
        litInptStruc:units = "gC m-2 yr-1" ;
        litInptStruc:_FillValue = 1.e+36f ;
        litInptStruc:missing_value = 1.e+36f ;

// global attributes:
        :title = "CASA-CNP model output" ;
        :comment = "NOTE: None of the variables are weighted by land fraction!" ;
        :history = "created on 03/01/2017 02:36:51" ;
        :source = "CASA-CNP Model" ;
        :parameters = "./pftlookup_igbp_updated4.csv" ;
}

```

## 7.2 mimics\_pool\_flux.nc

```

netcdf mimics_pool_flux {
dimensions:
    lon = 144 ;
    lat = 96 ;
    time = UNLIMITED ; // (1 currently)
variables:
    float lon(lon) ;
        lon:long_name = "coordinate longitude" ;
        lon:units = "degrees_east" ;
    float lat(lat) ;
        lat:long_name = "coordinate latitude" ;
        lat:units = "degrees_north" ;
    float time(time) ;
        time:long_name = "coordinate time" ;
        time:units = "1..ntimes" ;
    int IGBP_PFT(lat, lon) ;
        IGBP_PFT:long_name = "IGBP PFT classification" ;
        IGBP_PFT:units = "1-18" ;
        IGBP_PFT:_FillValue = -9999 ;
        IGBP_PFT:missing_value = -9999 ;
    float landarea(lat, lon) ;
        landarea:long_name = "land area, icewater set to 0.0" ;
        landarea:units = "km^2" ;
        landarea:_FillValue = 1.e+36f ;
        landarea:missing_value = 1.e+36f ;
    int cellMissing(lat, lon) ;
        cellMissing:long_name = "Missing Data Mask" ;
        cellMissing:units = "0=no missing data, 1=missing data" ;
    int cellid(lat, lon) ;
        cellid:long_name = "Grid Cell ID" ;
        cellid:units = "1..nlat*nlon" ;
    float cLITm(time, lat, lon) ;
        cLITm:long_name = "metabolic litter carbon" ;
        cLITm:units = "gC m-2" ;
        cLITm:_FillValue = 1.e+36f ;
        cLITm:missing_value = 1.e+36f ;
    float cLITs(time, lat, lon) ;
        cLITs:long_name = "structural litter carbon" ;
        cLITs:units = "gC m-2" ;
        cLITs:_FillValue = 1.e+36f ;
        cLITs:missing_value = 1.e+36f ;
    float cMICr(time, lat, lon) ;
        cMICr:long_name = "r-selected microbial soil organic matter carbon" ;
        cMICr:units = "gC m-2" ;
        cMICr:_FillValue = 1.e+36f ;
        cMICr:missing_value = 1.e+36f ;
    float cMICK(time, lat, lon) ;
        cMICK:long_name = "k-selected microbial soil organic matter carbon" ;

```

```

        cMICK:units = "gC m-2" ;
        cMICK:_FillValue = 1.e+36f ;
        cMICK:missing_value = 1.e+36f ;
float cSOMa(time, lat, lon) ;
        cSOMa:long_name = "active soil organic matter carbon" ;
        cSOMa:units = "gC m-2" ;
        cSOMa:_FillValue = 1.e+36f ;
        cSOMa:missing_value = 1.e+36f ;
float cSOMc(time, lat, lon) ;
        cSOMc:long_name = "chemically protected soil organic matter carbon" ;
        cSOMc:units = "gC m-2" ;
        cSOMc:_FillValue = 1.e+36f ;
        cSOMc:missing_value = 1.e+36f ;
float cSOMp(time, lat, lon) ;
        cSOMp:long_name = "physically protected soil organic matter carbon" ;
        cSOMp:units = "gC m-2" ;
        cSOMp:_FillValue = 1.e+36f ;
        cSOMp:missing_value = 1.e+36f ;
float cHresp(time, lat, lon) ;
        cHresp:long_name = "soil heterotrophic respiration" ;
        cHresp:units = "gC m-2 year-1" ;
        cHresp:_FillValue = 1.e+36f ;
        cHresp:missing_value = 1.e+36f ;
float cLitInput_metbc(time, lat, lon) ;
        cLitInput_metbc:long_name = "metabolic litter inputs" ;
        cLitInput_metbc:units = "gC m-2 year-1" ;
        cLitInput_metbc:_FillValue = 1.e+36f ;
        cLitInput_metbc:missing_value = 1.e+36f ;
float cLitInput_struc(time, lat, lon) ;
        cLitInput_struc:long_name = "structural litter inputs" ;
        cLitInput_struc:units = "gC m-2 year-1" ;
        cLitInput_struc:_FillValue = 1.e+36f ;
        cLitInput_struc:missing_value = 1.e+36f ;

// global attributes:
        :title = "MIMICS model output" ;
        :comment = "NOTE: None of the variables are weighted by land fraction!" ;
        :history = "created on 03/01/2017 02:36:51" ;
        :source = "MIMICS Model" ;
        :parameters = "./pftlookup_LIDET-MIM-REV_lowerKM_v11.09.2016_e.csv" ;
}

```

### 7.3 [corpse\\_pool\\_flux.nc](#)

```

netcdf corpse_pool_flux_6300 {
dimensions:
    time = UNLIMITED ; // (1 currently)

```

```

depth = 1 ;
lat = 96 ;
lon = 144 ;
variables:
  double lon(lon) ;
    lon:long_name = "coordinate longitude" ;
    lon:units = "degrees_east" ;
  double lat(lat) ;
    lat:long_name = "coordinate latitude" ;
    lat:units = "degrees_north" ;
  double time(time) ;
    time:long_name = "simulation time in years" ;
    time:units = "1..ntimes" ;
  int IGBP_PFT(lat, lon) ;
    IGBP_PFT:units = "1-18" ;
    IGBP_PFT:_FillValue = -9999 ;
    IGBP_PFT:missing_value = -9999 ;
  double landarea(lat, lon) ;
    landarea:long_name = "land area, icewater set to 0.0" ;
    landarea:units = "km^2" ;
    landarea:_FillValue = 1.e+36 ;
    landarea:missing_value = 1.e+36 ;
  int cellMissing(lat, lon) ;
    cellMissing:long_name = "Missing Data Mask" ;
    cellMissing:units = "0=no missing data, 1=missing data" ;
  int cellid(lat, lon) ;
    cellid:long_name = "Grid Cell ID" ;
    cellid:units = "1..nlat*nlon" ;
  double SoilProtected_C1(time, lat, lon) ;
    SoilProtected_C1:long_name = "Protected soil labile C" ;
    SoilProtected_C1:units = "g C m-2" ;
    SoilProtected_C1:_FillValue = 1.e+36 ;
    SoilProtected_C1:missing_value = 1.e+36 ;
  double SoilProtected_C2(time, lat, lon) ;
    SoilProtected_C2:long_name = "Protected soil recalcitrant C" ;
    SoilProtected_C2:units = "g C m-2" ;
    SoilProtected_C2:_FillValue = 1.e+36 ;
    SoilProtected_C2:missing_value = 1.e+36 ;
  double SoilProtected_C3(time, lat, lon) ;
    SoilProtected_C3:long_name = "Protected soil dead microbe C" ;
    SoilProtected_C3:units = "g C m-2" ;
    SoilProtected_C3:_FillValue = 1.e+36 ;
    SoilProtected_C3:missing_value = 1.e+36 ;
  double Soil_C1(time, lat, lon) ;
    Soil_C1:long_name = "Unprotected soil labile C" ;
    Soil_C1:units = "g C m-2" ;
    Soil_C1:_FillValue = 1.e+36 ;
    Soil_C1:missing_value = 1.e+36 ;

```

```

double Soil_C2(time, lat, lon) ;
    Soil_C2:long_name = "Unprotected soil recalcitrant C" ;
    Soil_C2:units = "g C m-2" ;
    Soil_C2:_FillValue = 1.e+36 ;
    Soil_C2:missing_value = 1.e+36 ;
double Soil_C3(time, lat, lon) ;
    Soil_C3:long_name = "Unprotected soil dead microbe C" ;
    Soil_C3:units = "g C m-2" ;
    Soil_C3:_FillValue = 1.e+36 ;
    Soil_C3:missing_value = 1.e+36 ;
double LitterLayer_C1(time, lat, lon) ;
    LitterLayer_C1:long_name = "Unprotected litter layer labile C" ;
    LitterLayer_C1:units = "g C m-2" ;
    LitterLayer_C1:_FillValue = 1.e+36 ;
    LitterLayer_C1:missing_value = 1.e+36 ;
double LitterLayer_C2(time, lat, lon) ;
    LitterLayer_C2:long_name = "Unprotected litter layer recalcitrant C" ;
    LitterLayer_C2:units = "g C m-2" ;
    LitterLayer_C2:_FillValue = 1.e+36 ;
    LitterLayer_C2:missing_value = 1.e+36 ;
double LitterLayer_C3(time, lat, lon) ;
    LitterLayer_C3:long_name = "Unprotected litter layer dead microbe C" ;
    LitterLayer_C3:units = "g C m-2" ;
    LitterLayer_C3:_FillValue = 1.e+36 ;
    LitterLayer_C3:missing_value = 1.e+36 ;
double Soil_LiveMicrobeC(time, lat, lon) ;
    Soil_LiveMicrobeC:long_name = "Living soil microbe C" ;
    Soil_LiveMicrobeC:units = "g C m-2" ;
    Soil_LiveMicrobeC:_FillValue = 1.e+36 ;
    Soil_LiveMicrobeC:missing_value = 1.e+36 ;
double Soil_CO2(time, lat, lon) ;
    Soil_CO2:long_name = "Mean annual soil CO2-C produced" ;
    Soil_CO2:units = "g C m-2" ;
    Soil_CO2:_FillValue = 1.e+36 ;
    Soil_CO2:missing_value = 1.e+36 ;
double LitterLayer_CO2(time, lat, lon) ;
    LitterLayer_CO2:long_name = "Mean annual litter layer CO2-C produced" ;
    LitterLayer_CO2:units = "g C m-2" ;
    LitterLayer_CO2:_FillValue = 1.e+36 ;
    LitterLayer_CO2:missing_value = 1.e+36 ;
double LitterLayer_LiveMicrobeC(time, lat, lon) ;
    LitterLayer_LiveMicrobeC:long_name = "Litter layer living microbe C" ;
    LitterLayer_LiveMicrobeC:units = "g C m-2" ;
    LitterLayer_LiveMicrobeC:_FillValue = 1.e+36 ;
    LitterLayer_LiveMicrobeC:missing_value = 1.e+36 ;
double Ts(time, lat, lon) ;
    Ts:long_name = "Soil temperature" ;
    Ts:units = "K" ;

```



```

        Ts:_FillValue = 1.e+36 ;
        Ts:missing_value = 1.e+36 ;
double Theta(time, lat, lon) ;
        Theta:long_name = "Fraction of Saturation" ;
        Theta:units = "0.0-1.0" ;
        Theta:_FillValue = 1.e+36 ;
        Theta:missing_value = 1.e+36 ;
int ncohorts(time, lat, lon) ;
        ncohorts:long_name = "Number of cohorts in layer" ;
        ncohorts:units = "1-18" ;
        ncohorts:_FillValue = -9999 ;
        ncohorts:missing_value = -9999 ;
double Soil_Depth(depth, lat, lon) ;
        Soil_Depth:long_name = "Soil depth" ;
        Soil_Depth:units = "meters" ;
        Soil_Depth:_FillValue = 1.e+36 ;
        Soil_Depth:missing_value = 1.e+36 ;

// global attributes:
        :title = "CORPSE model output" ;
        :comment = "NOTE: None of the variables are weighted by land fraction!" ;
        :history = "created on 03/14/2017 09:07:52" ;
        :source = "CORPSE Microbial Model" ;
        :parameters = "./corpse_params_new.nml" ;
}

```

## 8 Output Restart Files

The following .csv files are output every 100 simulation years and at the end of a testbed simulation. These files contain the values of the pool and can be used to initialize subsequent simulations when `initcasa > 0` in *fcasacm\_testbed.lst*. The *CASA-CNP\_pool\_end.csv* file is always generated (`isomModel=1, 2, or 3` in *fcasacm\_testbed.lst*). The *mimics\_pool\_end.csv* is generated when MIMICS is selected as the SOM model (`isomModel=2`) and *corpse\_pool\_end.csv* is generated when CORPSE is selected as the SOM model (`isomModel=3`). These are generic names for the files; the actual names of the files are specified in *fcasacm\_testbed.lst*. The files contain one line for each grid cell actually simulated. Some of the files also have a column header.

### 8.1 CASA-CNPpool\_end.csv

This file currently has no column header in first row.

Column	Variable	Description	Comments
A	ktau	Number of cycles through met.nc file	
B	n	grid cell ID	
C	veg%iveg(n)	plant functional type (PFT)	
D	soil%isoilm(n)	soil type	Not used
E	casamet%isorder(n)	soil order	Not used
F	casamet%lat(n)	latitude (decimal degrees)	
G	casamet%lon(n)	longitude (decimal degrees)	
H	casamet%areacell(n)	grid cell area (km <sup>2</sup> )	
I	casamet%glai(n)		
J	casabiome%sla(veg%iveg(n))	specific leaf area (m <sup>2</sup> /gC)	
K	casapool%clabile(n)	plant labile C (g C m <sup>-2</sup> )	
L	casapool%cplant(n:LEAF)	plant leaf C (g C m <sup>-2</sup> )	
M	casapool%cplant(n:WOOD)	plant wood C (g C m <sup>-2</sup> )	
N	casapool%cplant(n:FROOT)	plant fine root C (g C m <sup>-2</sup> )	
O	casapool%clitter(n:METB)	metabolic litter C (g C m <sup>-2</sup> )	
P	casapool%clitter(n:STR)	structural litter C (g C m <sup>-2</sup> )	
Q	casapool%clitter(n:CWD)	coarse woody debris C (g C m <sup>-2</sup> )	
R	casapool%csoil(n:MIC)	fast (microbial) soil organic C (g C m <sup>-2</sup> )	

Column	Variable	Description	Comments
S	casapool%csoil(n:SLOW)	slow soil organic C (g C m <sup>-2</sup> )	
T	casapool%csoil(n:PASS)	passive soil organic C (g C m <sup>-2</sup> )	
U	casapool%nplant(n:LEAF)	plant leaf N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
V	casapool%nplant(n:WOOD)	plant wood N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
W	casapool%nplant(n:FROOT)	plant fine root N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
X	casapool%nlitter(n:METB)	metabolic litter N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
Y	casapool%nlitter(n:STR)	structural litter N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
Z	casapool%nlitter(n:CWD)	coarse woody debris N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
AA	casapool%nsoil(n:MIC)	fast (microbial) soil organic N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
AB	casapool%nsoil(n:SLOW)	slow soil organic N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
AC	casapool%nsoil(n:PASS)	passive soil organic N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
AD	casapool%nsoilmin(n)	soil mineral N (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
AE	casapool%pplant(n:LEAF)	plant leaf P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AF	casapool%pplant(n:WOOD)	plant wood P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AG	casapool%pplant(n:FROOT)	plant fine root P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AH	casapool%plitter(n:METB)	metabolic litter P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AI	casapool%plitter(n:STR)	structural litter P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AJ	casapool%plitter(n:CWD)	coarse woody debris P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AK	casapool%psoil(n:MIC)	fast (microbial) soil organic P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AL	casapool%psoil(n:SLOW)	slow soil organic P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AM	casapool%psoil(n:PASS)	passive soil organic P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AN	casapool%psoillab(n)	soil labile mineral P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AO	casapool%psoilsorb(n)	soil sorbed mineral P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AP	casapool%psoilocc(n)	soil occluded mineral P (g P m <sup>-2</sup> )	0 unless icyle ≥ 3
AQ	casabal%sumcbal(n)	carbon balance (g C m <sup>-2</sup> )	0 unless icyle ≥ 3
AR	casabal%sumnbal(n)	nitrogen balance (g N m <sup>-2</sup> )	0 unless icyle ≥ 2
AS	casabal%sumpbal(n)	phosphorus balance (g P m <sup>-2</sup> )	0 unless icyle ≥ 3

## 8.2 mimicspool\_end.csv

Column	Variable	Description	Comments
A	iYrCnt	Number of cycles through met.nc file	
B	npt	grid cell ID	
Column	veg%iveg	plant functional type (PFT)	
D	casamet%lat	latitude (decimal degrees)	
E	casamet%lon	longitude (decimal degrees)	
F	casamet%areacell	grid cell area (km <sup>2</sup> )	
G	mimicspool%LITm	Metabolic Litter (mg C cm <sup>-3</sup> )	
H	mimicspool%LITs	Structural Litter (mg C cm <sup>-3</sup> )	
I	mimicspool%MICr	Live r-selected microbial biomass (mg C cm <sup>-3</sup> )	
J	mimicspool%MICk	Live K-selected microbial biomass (mg C cm <sup>-3</sup> )	
K	mimicspool%SOMa	Available Soil Organic Matter C (mg C cm <sup>-3</sup> )	
L	mimicspool%SOMc	Chemically Protected Soil Organic Matter C (mg C cm <sup>-3</sup> )	
M	mimicspool%SOMP	Physically Protected Soil Organic Matter C (mg C cm <sup>-3</sup> )	

### 8.3 [corpsepool\\_end.csv](#)

Column	Variable	Description	Comments
A	pt	grid cell count	
B	ijgcm	grid cell ID	
C	tcount	timestep count?	
D	time	time?	
E	lat	latitude (decimal degrees)	
F	lon	longitude (decimal degrees)	
G	veg	plant functional type (PFT)	
H	litlyr_unprotect_rhiz(LABILE)	Litter Layer Unprotected Rhizosphere Labile C (kg C m <sup>-2</sup> )	
I	litlyr_unprotect_rhiz(RECALCTRNT)	Litter Layer Unprotected Rhizosphere Recalcitrant C (kg C m <sup>-2</sup> )	

Column	Variable	Description	Comments
J	litlyr_unprotect_rhiz(DEADMICRB)	Litter Layer Unprotected Rhizosphere Dead Microbe C (kg C m <sup>-2</sup> )	
K	litlyr_unprotect_bulk(LABILE)	Litter Layer Unprotected Bulk Soil Labile C (kg C m <sup>-2</sup> )	Litter Layer has no bulk component
L	litlyr_unprotect_bulk(RECALCTRNT)	Litter Layer Unprotected Bulk Soil Recalcitrant C (kg C m <sup>-2</sup> )	Litter Layer has no bulk component
M	litlyr_unprotect_bulk(DEADMICRB)	Litter Layer Unprotected Bulk Soil Dead Microbe C (kg C m <sup>-2</sup> )	Litter Layer has no bulk component
N	litlyr_protect_rhiz(LABILE)	Litter Layer Protected Rhizosphere Labile C (kg C m <sup>-2</sup> )	Litter Layer has no protected C
O	litlyr_protect_rhiz(RECALCTRNT)	Litter Layer Protected Rhizosphere Recalcitrant C (kg C m <sup>-2</sup> )	Litter Layer has no protected C
P	litlyr_protect_rhiz(DEADMICRB)	Litter Layer Protected Rhizosphere Dead Microbe C (kg C m <sup>-2</sup> )	Litter Layer has no protected C
Q	litlyr_protect_bulk(LABILE)	Litter Layer Protected Bulk Soil Labile C (kg C m <sup>-2</sup> )	Litter Layer has no protected C
R	litlyr_protect_bulk(RECALCTRNT)	Litter Layer Protected Bulk Soil Recalcitrant C (kg C m <sup>-2</sup> )	Litter Layer has no protected C
S	litlyr_protect_bulk(DEADMICRB)	Litter Layer Protected Bulk Soil Dead Microbe C (kg C m <sup>-2</sup> )	Litter Layer has no protected C
T	litlyr_livingMicrobeC_rhiz	Litter Layer Live Microbe Rhizosphere C (kg C m <sup>-2</sup> )	
U	litlyr_livingMicrobeC_bulk	Litter Layer Live Microbe Bulk Soil C (kg C m <sup>-2</sup> )	Litter Layer has no bulk component
V	litlyr_CO2_rhiz	Cumulative Litter Layer Rhizosphere Heterotrophic Respiration (kg C m <sup>-2</sup> )	
W	litlyr_CO2_bulk	Cumulative Litter Layer Bulk Heterotrophic Respiration (kg C m <sup>-2</sup> )	Litter Layer has no bulk soil C
X	protection_rate	Rate that carbon becomes protected (yr <sup>-1</sup> or yr <sup>-1</sup> kg-microbial-biomass <sup>-1</sup> depending on microbe_driven_protection)	
Y	Qmax	Clay protection factor for litter layer	Initialized to zero
Z	litlyr_DOC(LABILE)	Litter Layer Labile DOC (kg C m <sup>-2</sup> )	Dissolved Organic C not simulated

Column	Variable	Description	Comments
AA	litlyr_DOC(RECALCTRNT)	Litter Layer Recalcitrant DOC (kg C m <sup>-2</sup> )	Dissolved Organic C not simulated
AB	litlyr_DOC(DEADMICRB)	Litter Layer Dead Microbe DOC (kg C m <sup>-2</sup> )	Dissolved Organic C not simulated
AC	soil_1_unprotect_rhiz(LABILE)	Soil Layer 1 Unprotected Rhizosphere Labile C (kg C m <sup>-2</sup> )	
AD	soil_1_unprotect_rhiz(RECALCTRNT)	Soil Layer 1 Unprotected Rhizosphere Recalcitrant C (kg C m <sup>-2</sup> )	
AE	soil_1_unprotect_rhiz(DEADMICRB)	Soil Layer 1 Unprotected Rhizosphere Dead Microbe C (kg C m <sup>-2</sup> )	
AF	soil_1_unprotect_bulk(LABILE)	Soil Layer 1 Unprotected Bulk Soil Labile C (kg C m <sup>-2</sup> )	
AG	soil_1_unprotect_bulk(RECALCTRNT)	Soil Layer 1 Unprotected Bulk Soil Recalcitrant C (kg C m <sup>-2</sup> )	
AH	soil_1_unprotect_bulk(DEADMICRB)	Soil Layer 1 Unprotected Bulk Soil Dead Microbe C (kg C m <sup>-2</sup> )	
AI	soil_1_protect_rhiz(LABILE)	Soil Layer 1 Protected Rhizosphere Labile C (kg C m <sup>-2</sup> )	
AJ	soil_1_protect_rhiz(RECALCTRNT)	Soil Layer 1 Protected Rhizosphere Recalcitrant C (kg C m <sup>-2</sup> )	
AK	soil_1_protect_rhiz(DEADMICRB)	Soil Layer 1 Protected Rhizosphere Dead Microbe C (kg C m <sup>-2</sup> )	
AL	soil_1_protect_bulk(LABILE)	Soil Layer 1 Protected Bulk Soil Labile C (kg C m <sup>-2</sup> )	
AM	soil_1_protect_bulk(RECALCTRNT)	Soil Layer 1 Protected Bulk Soil Recalcitrant C (kg C m <sup>-2</sup> )	
AN	soil_1_protect_bulk(DEADMICRB)	Soil Layer 1 Protected Bulk Soil Dead Microbe C (kg C m <sup>-2</sup> )	
AO	soil_1_livingMicrobeC_rhiz	Soil Layer 1 Live Microbe Rhizosphere C (kg C m <sup>-2</sup> )	
AP	soil_1_livingMicrobeC_bulk	Soil Layer 1 Live Microbe Bulk Soil C (kg C m <sup>-2</sup> )	
AQ	soil_1_CO2_rhiz	Cumulative Litter Layer Rhizosphere Heterotrophic Respiration (kg C m <sup>-2</sup> )	
AR	soil_1_CO2_bulk	Cumulative Litter Layer Bulk Heterotrophic Respiration (kg C m <sup>-2</sup> )	
AS	protection_rate	Rate that carbon becomes protected (yr <sup>-1</sup> or yr <sup>-1</sup> kg-microbial-biomass <sup>-1</sup> depending on microbe_driven_protection)	
AT	Qmax	Clay protection factor for soil layer 1	

Column	Variable	Description	Comments
AU	soil_1_DOC(LABILE)	Soil Layer 1 Labile DOC (kg C m <sup>-2</sup> )	Dissolved Organic C not simulated
AV	soil_1_DOC(RECALCTRNT)	Soil Layer 1 Recalcitrant DOC (kg C m <sup>-2</sup> )	Dissolved Organic C not simulated
AW	soil_1_DOC(DEADMICRB)	Soil Layer 1 Dead Microbe DOC (kg C m <sup>-2</sup> )	Dissolved Organic C not simulated

## 9 Summary of Model Parameters

### 9.1 CASA-CNP parameters in pftlookup\_igbp.csv

Table 6. IGBP plant functional types used by the CASA-CNP testbed (pftlookup\_igbp.csv).

vegtype (PFT)	(ice,water,urban:0)/ grass:1/shrub:2/woody:3	
1	3	Evergreen Needleleaf Forest
2	3	Evergreen Broadleaf Forest
3	3	Deciduous Needleleaf Forest
4	3	Deciduous Broadleaf Forest
5	3	Mixed forest
6	2	Closed shrublands
7	2	Open shrublands
8	3	woody savannas
9	3	savannas
10	1	grasslands
11	0	permanent wetlands
12	1	croplands
13	0	urban and built-up
14	1	cropland mosaic (same as 12)

vegtype (PFT)	(ice,water,urban:0)/ grass:1/shrub:2/woody:3	
15	0	permanent snow and ice
16	1	barren or sparsely vegetated
17	0	ice, water
18	1	tundra

Table 7. Rooting distribution parameters, and ?? by PFT (pftlookup\_igbp.csv).

vegtype	Kroot	rootdepth	kuptake	Krootlen	KminN (icycle ≥ 2)	Kuplabp (icycle = 3)	frac_herbivore
(PFT)	1/m	m	(not used)	m/g C	gN/m <sup>2</sup>	gP/m <sup>2</sup>	1/year
1	5.5	1.5	2	14.87805	2	0.5	0.068
2	3.9	1.5	1.9	14.38596	2	0.5	0.406
3	5.5	1.5	2	14.02597	2	0.5	0.068
4	3.9	1.5	2	18.94737	2	0.5	0.134
5	2	1.5	2	16.71642	2	0.5	0.137
6	2	0.5	1.9	0	2	0.5	0
7	2	0.5	1.8	32.30769	2	0.5	0.022
8	2	1.5	1.9	120.8	2	0.5	0.35
9	2	1.5	1.9	120.8	2	0.5	0.35
10	5.5	0.5	2	84	2	0.5	0.109
11	5.5	0.5	1.6	0	2	0.5	0
12	5.5	0.5	1.6	120.5	2	0.5	0.14
13	2	0.5	1.8	0	2	0.5	0
14	5.5	0.5	1.6	0	2	0.5	0
15	5.5	0.5	1.8	0	2	0.5	0
16	2	0.5	1.8	30.76923	2	0.5	0.01
17	5.5	1.5	1.8	0	2	0.5	0
18	5.5	0.5	2	84	2	0.5	0.109



Table 8. Mean residence times (age) for plant, litter, soil organic, and labile plant C pools, and specific leaf area (SLA) by PFT (pftlookup\_igbp.csv).

vegtype	leaf age	wood age	froot age	met age	str age	cwd age	mic age	slow age	pass age	clabile	SLA
(PFT)	year	year	year	year	year	year	year	year	year	year	m <sup>2</sup> /gC
1	2	70	18	0.04	0.23	0.824	0.137	5	222.22	0.2	0.00718
2	1.5	60	10	0.04	0.23	0.824	0.137	5	222.22	0.2	0.01532
3	0.8	80	10	0.04	0.23	0.824	0.137	5	222.22	0.2	0.0231
4	0.8	40	10	0.04	0.23	0.824	0.137	5	222.22	0.2	0.02646
5	1.2	50	10	0.04	0.23	0.824	0.137	5	222.22	0.2	0.01682
6	1	40	5	0.04	0.23	0.824	0.137	5	222.22	0.2	0.00992
7	1	40	5	0.04	0.23	0.824	0.137	5	222.22	0.2	0.00992
8	1.5	40	5	0.04	0.23	0.824	0.137	5	222.22	0.2	0.026308
9	1.5	40	3	0.04	0.23	0.824	0.137	5	222.22	0.2	0.026157
10	1	1	3	0.04	0.23	0.824	0.137	5	222.22	0.2	0.026005
11	1	1	1	0.04	0.23	0.824	0.137	5	222.22	0.2	0.02
12	1	1	0.884227	0.04	0.23	0.824	0.137	5	222.22	0.2	0.026005
13	1	1	1	0.04	0.23	0.824	0.137	5	222.22	0.2	0.02
14	1	1	1	0.04	0.23	0.824	0.137	5	222.22	0.2	0.026005
15	1	1	1	0.04	0.23	0.824	0.137	5	222.22	0.2	0.02
16	1	5	4	0.04	0.23	0.824	0.137	5	222.22	0.2	0.02447
17	1	1	1	0.04	0.23	0.824	0.137	5	222.22	0.2	0.02
18	1	1	3	0.04	0.23	0.824	0.137	5	222.22	0.2	0.026005

Table 9. Carbon allocation fractions and maintenance respiration (rm) parameters by PFT (pftlookup\_igbp.csv).

vegtype	Calloc_leaf	Calloc_wood	Calloc_froot	rmleaf	rmwood	rmfroot	rmclabile
(PFT)	fraction	fraction	fraction	1/year	1/year	1/year	1/year
1	0.42	0.33	0.25	0.1	6	6	0.5

vegtype	Calloc_leaf	Calloc_wood	Calloc_froot	rmleaf	rmwood	rmfroot	rmclabile
(PFT)	fraction	fraction	fraction	1/year	1/year	1/year	1/year
2	0.25	0.1	0.65	0.1	6	6	0.5
3	0.4	0.3	0.3	0.1	6	6	0.5
4	0.3	0.2	0.5	0.1	6	6	0.5
5	0.35	0.4	0.25	0.1	6	6	0.5
6	0.52	0.15	0.33	0.1	6	6	0.5
7	0.4	0.15	0.45	0.1	6	6	0.5
8	0.3	0.1	0.6	0.1	6	6	0.5
9	0.2	0.1	0.7	0.1	6	6	0.5
10	0.3	0	0.7	0.1	1	10	0.5
11	0.5	0	0.5	0.1	1	10	0.5
12	0.3	0	0.7	0.1	1	10	0.5
13	0.5	0	0.5	0.1	1	10	0.5
14	0.35	0	0.65	0.1	1	10	0.5
15	0.5	0	0.5	0.1	1	10	0.5
16	0.2	0.2	0.6	0.1	1	10	0.5
17	0.6	0.4	0	0.1	1	10	0.5
18	0.3	0	0.7	0.1	1	10	0.5

Table 10. Initial C:N ratios, N retranslocation parameters, and lignin content of plant parts by PFT. The C:N ratios and lignin fractions are used to compute lignin:N ratios for partitioning plant litter into structural and metabolic fraction (pftlookup\_igbp.csv).

vegtype	C:N leaf	C:N wood	C:N froot	Ntrans_leaf (icycle ≥ 2)	Ntrans_wood (icycle ≥ 2)	Ntrans_frt (icycle ≥ 2)	lignin leaf	lignin CWD	lignin froot
(PFT)	gC/gN	gC/gN	gC/gN	fraction	fraction	fraction	g lignin /gC	g lignin /gC	g lignin /gC
1	50	250	78	0.5	0.95	0.9	0.25	0.4	0.25
2	25	150	68	0.5	0.95	0.9	0.2	0.4	0.2
3	60	250	41	0.5	0.95	0.9	0.2	0.4	0.2
4	50	175	41	0.5	0.95	0.9	0.2	0.4	0.2

vegtype	C:N leaf	C:N wood	C:N froot	Ntrans_leaf (icycle ≥ 2)	Ntrans_wood (icycle ≥ 2)	Ntrans_frt (icycle ≥ 2)	lignin leaf	lignin CWD	lignin froot
(PFT)	gC/gN	gC/gN	gC/gN	fraction	fraction	fraction	g lignin /gC	g lignin /gC	g lignin /gC
5	50	175	41	0.5	0.95	0.9	0.22	0.4	0.22
6	45	150	41	0.5	0.95	0.9	0.2	0.4	0.2
7	40	150	41	0.5	0.95	0.9	0.2	0.4	0.2
8	25	150	41	0.5	0.95	0.9	0.15	0.4	0.15
9	25	150	41	0.5	0.95	0.9	0.15	0.4	0.15
10	50	150	41	0.5	0.95	0.9	0.1	0.4	0.1
11	30	150	41	0.5	0.95	0.9	0.15	0.4	0.15
12	50	125	41	0.5	0.95	0.9	0.2	0.4	0.2
13	40	150	41	0.5	0.95	0.9	0.15	0.4	0.15
14	30	125	41	0.5	0.95	0.9	0.1	0.4	0.1
15	40	150	41	0.5	0.95	0.9	0.1	0.4	0.1
16	40	150	41	0.5	0.95	0.9	0.15	0.4	0.15
17	40	135	41	0.5	0.95	0.9	0.25	0.4	0.25
18	47.6	150	41	0.5	0.95	0.9	0.166	0.4	0.166

Table 11. Initial, minimum, and maximum C:N ratios of soil organic pools (icycle ≥ 2) (pftlookup\_igbp.csv).

vegtype	C:N mic	C:N slow	C:N pass	C:Nmic_min	C:Nslow_min	C:Npass_min	C:Nmic_max	C:Nslow_max	C:Npass_max
(PFT)	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN
1	8	16.1	16.1	5.4	26.91	26.91	8	30	30
2	8	12.8	12.8	7.71	13.54	13.54	8	30	30
3	8	24.8	24.8	7.11	26.91	26.91	8	30	30
4	8	30	30	6.69	16.2	16.2	8	30	30
5	8	10.1	10.1	6.045	21.555	21.555	8	30	30
6	8	19.3	19.3	6.17	16.63	16.63	8	20	20
7	8	19.3	19.3	6.17	16.63	16.63	8	20	20

vegtype	C:N mic	C:N slow	C:N pass	C:Nmic_min	C:Nslow_min	C:Npass_min	C:Nmic_max	C:Nslow_max	C:Npass_max
(PFT)	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN	gC/gN
8	8	15	15	6.403333	14.915	14.915	8	28.33333	28.33333
9	8	15	15	6.116667	13.63	13.63	8	26.66667	26.66667
10	8	13.1	13.1	5.83	12.345	12.345	8	25	25
11	8	13.1	13.1	6.51	14.06	14.06	8	20	20
12	8	13.2	13.2	6.34	12.385	12.385	8	20	20
13	8	20	20	6.51	14.06	14.06	8	20	20
14	8	20	20	6.34	12.385	12.385	8	20	20
15	8	20	20	6.51	14.06	14.06	8	20	20
16	8	26.8	26.8	6.51	14.06	14.06	8	20	20
17	8	20	20	6.51	14.06	14.06	8	20	20
18	8	13.1	13.1	5.83	12.345	12.345	8	25	25

Table 12. Maximum and minimum LAI values by PFT (pftlookup\_igbp.csv).

vegtype	Laimax	Laimin
(PFT)	m <sup>2</sup> /m <sup>2</sup>	m <sup>2</sup> /m <sup>2</sup>
1	7	3
2	7	3
3	7	0.5
4	7	0.5
5	7	0.5
6	3	0.5
7	3	0.1
8	4	0.5
9	4	0.3
10	3	0.2
11	5	0.1

vegtype	Laimax	Laimin
(PFT)	m <sup>2</sup> /m <sup>2</sup>	m <sup>2</sup> /m <sup>2</sup>
12	6	0.5
13	6	0.5
14	6	0.5
15	0	0
16	1	0.05
17	1	0.1
18	3	0.2

Table 13. Initial Carbon values of plant, litter, and soil organic pools for spinup simulations (initcasa=0) (pftlookup\_igbp.csv).

vegtype	Leaf C	Wood C	Froot C	met C	str C	CWD C	mic C	slow C	pass C
(PFT)	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>
1	384.6037	7865.396	250	6.577021	209.1728	606.0255	528.664	13795.94	4425.396
2	273	11451	2586	44.63457	433.7626	1150.765	11.37765	311.8092	13201.81
3	96.59814	5683.402	220	7.127119	277.7733	776.7331	597.0785	16121.12	5081.802
4	150.2638	10833.74	220	10.97797	312.5492	888.5695	405.5554	11153.25	5041.192
5	166.5077	9583.492	250	14.5634	377.7089	1060.545	467.4273	11896.79	5485.779
6	0	0	0	3.229374	39.44449	111.5864	0	0	0
7	88	372	140	3.229374	39.44449	111.5864	168.0451	4465.478	1386.477
8	177.0966	1972.903	250	31.19319	206.8936	813.0919	174.5109	4782.379	2268.11
9	177.0966	1972.903	250	31.19319	206.8936	813.0919	174.5109	4782.379	2268.11
10	137.1714	0	263	28.57245	50.91091	0	425.6431	5694.437	4179.92
11	0	0	0	0	0	0	0	0	0
12	160	0	240	28.57245	50.91091	0	512.4247	6855.438	5032.137
13	0	0	0	0	0	0	0	0	0
14	0	0	0	28.57245	50.91091	0	0.041325	0.552858	0.405817

vegtype	Leaf C	Wood C	Froot C	met C	str C	CWD C	mic C	slow C	pass C
(PFT)	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>	g C/m <sup>2</sup>
15	0	0	0	0	0	0	0	0	0
16	20	17	63	1.457746	4.956338	28.44085	57.77585	1325.052	517.1719
17	0	0	0	0	0	0	0	0	0
18	137.1714	0	263	28.57245	50.91091	0	425.6431	5694.437	4179.92

Table 14. Parameters controlling plant death rates with freezing temperatures and water stress (pftlookup\_igbp.csv).

vegtype	Tkshed	xkleafcoldmax	xkleafcoldexp	xkleafdrymax	xkleafdryexp
(PFT)	K	1/year	1/year	1/year	1/year
1	268	0.2	3	0.1	3
2	260	0.1	3	0.1	3
3	263.15	0.1	3	0.1	3
4	268.15	0.6	3	1	3
5	277.15	0.4	3	0.1	3
6	268.15	0.1	3	0.1	3
7	277.15	1	3	0.1	3
8	275.15	3	3	1.5	3
9	278.15	5	3	2.5	3
10	275.15	0.2	3	0.1	3
11	277.15	0.1	3	0.1	3
12	278.15	0.3	3	0.1	3
13	277.15	0.1	3	0.1	3
14	278.15	0.3	3	0.1	3
15	283.15	0.1	3	0.1	3
16	277.15	0.1	3	0.1	3
17	277.15	0.1	3	0.1	3
18	275.15	0.2	3	0.1	3

Table 15. Phenology parameters (no longer used) (pftlookup\_igbp.csv).

vegtype	Tkchill	Tkwarm	GDD2stdy	nd2onset	nd2grow	nd2dorm	phena	phenb	phenc
(PFT)	K	K	DDK	day	day	day	??	??	??
1	273.15	268.15	200	30	15	10	667	-0.0304	68
2	260	260	200	30	15	10	667	-0.0304	0
3	273.15	268.15	200	30	15	10	667	-0.0304	0
4	273.15	268.15	200	30	15	10	667	-0.0304	0
5	273.15	268.15	200	30	15	10	854	-0.0172	0
6	273.15	268.15	100	30	15	10	638	-0.01	0
7	273.15	268.15	100	30	15	10	638	-0.01	68
8	273.15	268.15	100	30	15	10	638	-0.01	68
9	273.15	268.15	100	30	15	10	638	-0.01	68
10	273.15	268.15	100	30	15	10	638	-0.01	68
11	273.15	268.15	100	30	15	10	638	-0.01	68
12	273.15	268.15	100	30	15	10	638	-0.01	68
13	273.15	268.15	100	30	15	10	638	-0.01	68
14	273.15	268.15	100	30	15	10	638	-0.01	68
15	273.15	268.15	100	30	15	10	638	-0.01	68
16	273.15	268.15	100	30	15	10	638	-0.01	68
17	273.15	268.15	100	30	15	10	638	-0.01	68
18	273.15	268.15	100	30	15	10	638	-0.01	68

Table 16. Minimum and Maximum N:C ratios of plant pools, N leaching rates, and N fixation rates (icycle ≥ 2) (pftlookup\_igbp.csv).

vegtype	N/Cleafmin	N/Cleafmx	N/Cwdmin	N/Cwdmax	N/Cftrtmin	N/Cftrtmax	xNminloss	xNleach	nfixrate
(PFT)	g N/g C	g N/g C	g N/g C	g N/g C	g N/g C	g N/g C	fraction	1/year	gN/m <sup>2</sup> /yr
1	0.02	0.024	0.004	0.0048	0.012821	0.015385	0.05	0.05	0.08
2	0.025	0.048	0.006667	0.008	0.014706	0.017647	0.05	0.05	2.6
3	0.016667	0.02	0.004	0.0048	0.02439	0.029268	0.05	0.05	0.21

vegtype	N/Cleafmin	N/Cleafmx	N/Cwdmin	N/Cwdmax	N/Cfrtmin	N/Cfrtmax	xNminloss	xNleach	nfixrate
(PFT)	g N/g C	g N/g C	g N/g C	g N/g C	g N/g C	g N/g C	fraction	1/year	gN/m <sup>2</sup> /yr
4	0.02	0.024	0.005714	0.006857	0.02439	0.029268	0.05	0.05	1.64
5	0.02	0.024	0.005714	0.006857	0.02439	0.029268	0.05	0.05	1.06
6	0.02	0.026667	0.006667	0.008	0.02439	0.029268	0.05	0.05	0.37
7	0.02	0.03	0.006667	0.008	0.02439	0.029268	0.05	0.05	0.37
8	0.04	0.048	0.006667	0.008	0.02439	0.029268	0.05	0.05	4.06
9	0.04	0.048	0.006667	0.008	0.02439	0.029268	0.05	0.05	4.06
10	0.02	0.024	0.006667	0.008	0.02439	0.029268	0.05	0.05	0.95
11	0.02	0.04	0.006667	0.008	0.02439	0.029268	0.05	0.05	0
12	0.02	0.048	0.008	0.0096	0.02439	0.029268	0.05	0.05	4
13	0.02	0.03	0.006667	0.008	0.02439	0.029268	0.05	0.05	0
14	0.02	0.04	0.008	0.0096	0.02439	0.029268	0.05	0.05	4
15	0.02	0.03	0.006667	0.008	0.02439	0.029268	0.05	0.05	0
16	0.02	0.03	0.006667	0.008	0.02439	0.029268	0.05	0.05	0.35
17	0.02	0.03	0.007407	0.008889	0.02439	0.029268	0.05	0.05	0
18	0.02	0.024	0.006667	0.008	0.02439	0.029268	0.05	0.05	0.95

Table 17. Initial nitrogen pool values for spinup runs (initcasa=0, icycle ≥ 2) (pftlookup\_igbp.csv).

vegtype	N leaf	N wood	N frt	N met	N Str	N cwd	N mic	N slow	N Pass	N Nmin
(PFT)	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN /m <sup>2</sup>
1	7.541249	31.46159	6.097561	0.064481	1.394485	2.424102	52.8664	919.7293	295.0264	1000
2	9.9	102	38	0.74391	2.891751	8.524183	1.137765	20.78728	880.1209	1000
3	1.609969	22.73361	5.365854	0.059393	1.851822	3.106932	59.70785	1074.741	338.7868	1000
4	3.756594	80.24989	5.365854	0.137225	2.083661	6.581996	40.55554	743.5501	336.0795	1000
5	4.162691	47.91746	6.097561	0.182043	2.51806	5.302723	46.74273	793.1196	365.7186	1000
6	0	0	0	0.040367	0.262963	0.826566	0	0	0	1000
7	2.933333	2.755555	3.414634	0.053823	0.262963	0.826566	16.80451	297.6985	92.4318	1000
8	5.903219	14.6141	6.097561	0.519887	1.379291	6.022903	17.45109	318.8253	151.2073	1000



vegtype	N leaf	N wood	N frt	N met	N Str	N cwd	N mic	N slow	N Pass	N Nmin
(PFT)	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN/m <sup>2</sup>	gN /m <sup>2</sup>
9	5.903219	14.6141	6.097561	0.519887	1.379291	6.022903	17.45109	318.8253	151.2073	1000
10	4.572381	0	6.414634	0.476208	0.339406	0	42.56431	379.6291	278.6613	1000
11	0	0	0	0	0	0	0	0	0	1000
12	5.333333	0	5.853659	0.476208	0.339406	0	51.24247	457.0292	335.4758	1000
13	0	0	0	0	0	0	0	0	0	1000
14	0	0	0	0.476208	0.339406	0	0.004132	0.036857	0.027055	1000
15	0	0	0	0	0	0	0	0	0	1000
16	0.5	0.125926	1.536585	0.018222	0.033042	0.210673	5.777585	88.33682	34.47813	1000
17	0	0	0	0	0	0	0	0	0	1000
18	4.572381	0	6.414634	0.476208	0.339406	0	42.56431	379.6291	278.6613	1000

Table 18. N:P ratios (icycle=3) (pftlookup\_igbp.csv).

vegtype	N/Pleafmin	N/Pleafmx	N/Pwdmin	N/Pwdmax	N/Pfrtmin	N/Pfrtmax	fpptol(leaf)	fpptol(wd)	fpptol(frt)
(PFT)	gN/gP	gN/gP	gN/gP	gN/gP	gN/gP	gN/gP	fraction	fraction	fraction
1	10	10	15	15	15	15	0.5	0.95	0.9
2	20	20	15	15	15	15	0.5	0.95	0.9
3	8	8	15	15	15	15	0.5	0.95	0.9
4	10	10	15	15	15	15	0.5	0.95	0.9
5	10	10	15	15	15	15	0.5	0.95	0.9
6	8	8	15	15	15	15	0.5	0.95	0.9
7	8	8	15	15	15	15	0.5	0.95	0.9
8	20	20	15	15	15	15	0.5	0.95	0.9
9	20	20	15	15	15	15	0.5	0.95	0.9
10	15	15	15	15	15	15	0.5	0.95	0.9
11	15	15	15	15	15	15	0.5	0.95	0.9
12	10	10	15	15	15	15	0.5	0.95	0.9
13	10	10	15	15	15	15	0.5	0.95	0.9

vegtype	N/Pleafmin	N/Pleafmx	N/Pwdmin	N/Pwdmax	N/Pftrmin	N/Pftrmax	fpptol(leaf)	fpptol(wd)	fpptol(frt)
(PFT)	gN/gP	gN/gP	gN/gP	gN/gP	gN/gP	gN/gP	fraction	fraction	fraction
14	10	10	15	15	15	15	0.5	0.95	0.9
15	10	10	15	15	15	15	0.5	0.95	0.9
16	10	10	15	15	15	15	0.5	0.95	0.9
17	10	10	15	15	15	15	0.5	0.95	0.9
18	15	15	15	15	15	15	0.5	0.95	0.9

Table 19. Soil Phosphorous parameters (icycle=3). These apply to all PFTs (pftlookup\_igbp.csv).

	xkmlabp	xpsorbmax	xfpleach	N:Psoil	N:Psoil	N:Psoil	kplab	xkpsorb	kpocc
soilorder	gP/m2	gP/m2	no_dimen	mic	slow	pass	1/year	1/year	1/year
1	74.5408	439.4606	0.0005	0.00137	0.00002	0.00003	2.5	8	8
2	68.1584	937.178	0.0005	0.00137	0.00002	0.00003	2.5	8	8
3	77.952	915.3808	0.0005	0.00137	0.00001	0.00003	2.5	8	8
4	64.41918	600.8843	0.0005	0.00137	0.00001	0.00003	2.5	8	8
5	64.41918	446.9081	0.0005	0.00137	0.00002	0.00003	2.5	8	8
6	70.5856	160.5822	0.0005	0.00137	0.00002	0.00003	2.5	8	8
7	64.5888	249.5358	0.0005	0.00137	0.00002	0.00003	2.5	8	8
8	54.1692	461.3098	0.0005	0.00137	0.00002	0.00003	2.5	8	8
9	9.7704	43.63956	0.0005	0.00137	0.00003	0.00003	2.5	8	8
10	28.29	175.4926	0.0005	0.00137	0.00002	0.00003	2.5	8	8
11	63.963	227.5091	0.0005	0.00137	0.00003	0.00003	2.5	8	8
12	32.402	377.2618	0.0005	0.00137	0.00002	0.00003	2.5	8	8

Table 20. Initial Phosphorous Pool values for spinup runs by PFT (initcasa=0, icycle=3) (pftlookup\_igbp.csv).

vegtype	Pleaf	Pwood	Pfroot	Pmet	Pstr	Pcwd	Pmic	Pslow	Ppass	Plab	Psorb	Pocc
(PFT)	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2
1	0.191648	0.953979	0.076659	0.004385	0.069724	0.101004	6.872632	119.5648	38.35343	26.737	126.73	138.571

vegtype	Pleaf	Pwood	Pfroot	Pmet	Pstr	Pcwd	Pmic	Pslow	Ppass	Plab	Psorb	Pocc
(PFT)	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2	gP/m2
2	0.415	5.88	1.95	0.029756	0.144588	0.191794	0.14791	2.702347	114.4157	19.947	92.263	120.374
3	0.115988	0.64438	0.080548	0.004751	0.092591	0.129456	7.762021	139.7164	44.04228	29.107	134.639	138.22
4	0.135453	2.424778	0.141097	0.007319	0.104183	0.148095	5.27222	96.66152	43.69033	30.509	132.012	148.083
5	0.113219	2.634798	0.153318	0.009709	0.125903	0.176757	6.076555	103.1055	47.54342	25.954	143.468	138.823
6	0.022821	0	0.037083	0.002153	0.013148	0.018598	0	0	0	0	0	0
7	0.022821	0	0.037083	0.002153	0.013148	0.018598	2.184586	38.70081	12.01613	23.206	173.47	114.496
8	0.35904	0.923457	0.249333	0.020795	0.068965	0.135515	2.268642	41.44729	19.65695	23.001	125.634	129.469
9	0.35904	0.923457	0.249333	0.020795	0.068965	0.135515	2.268642	41.44729	19.65695	22.114	145.082	130.37
10	0.15125	0	0.15125	0.019048	0.01697	0	5.533361	49.35178	36.22598	25.538	186.207	145.163
11	0	0	0	0	0	0	0	0	0	0	0	0
12	0.15125	0	0.15125	0.019048	0.01697	0	6.661522	59.4138	43.61185	27.729	155.518	158.884
13	0	0	0	0	0	0	0	0	0	0	0	0
14	0.15125	0	0.15125	0.019048	0.01697	0	0.000537	0.004791	0.003517	0	0	0
15	0	0	0	0	0	0	0	0	0	0.103	1.176	0.688
16	0.007	0	0.00875	0.000972	0.001652	0	0.751086	11.48379	4.482157	21.038	255.79	108.897
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0.15125	0	0.15125	0.019048	0.01697	0	5.533361	49.35178	36.22598	25.538	186.207	145.163

Table 21. Litter and soil decomposition controls by PFT. Some parameters are only used when *icycle* ≥ 2 (*pftlookup\_igbp.csv*).

vegtype	xnpmax (icycle ≥ 2)	Q10soil	xkoplitter	xkoptsoil	prodptase (icycle=3)	cosnpup (icycle=3)	maxfineL (icycle ≥ 2)	maxcwd (icycle ≥ 2)	Nintercept (not used)	Nslope (not used)
(PFT)	unitless	unitless	unitless	unitless	year	gN/gP	gC/m <sup>2</sup>	gC/m <sup>2</sup>	μmol/m <sup>2</sup> /s	μmol/m <sup>2</sup> /s/(gN/m <sup>2</sup> )
1	1.51086	1.72	0.33	0.33	0.5	40	1524	1795	3.16	9.07
2	1.27916	1.72	0.6	0.6	0.2	25	384	613	4.19	26.19
3	1.59108	1.72	0.15	0.15	0.5	40	1527	1918	6.32	18.15
4	1.420666	1.72	0.6	0.6	0.5	40	887	1164	5.73	29.81
5	1.422382	1.72	0.4	0.495	0.5	40	1205.5	1479.5	4.445	19.44

vegtype	xnpmax (icycle ≥ 2)	Q10soil	xkoplitter	xkoptsoil	prodptase (icycle=3)	cosnpup (icycle=3)	maxfineL (icycle ≥ 2)	maxcwd (icycle ≥ 2)	Nintercept (not used)	Nslope (not used)
(PFT)	unitless	unitless	unitless	unitless	year	gN/gP	gC/m <sup>2</sup>	gC/m <sup>2</sup>	μmol/m <sup>2</sup> /s	μmol/m <sup>2</sup> /s/(gN/m <sup>2</sup> )
6	1.422382	1.72	0.4	0.5	0.5	40	157	107	14.71	23.15
7	1.358076	1.72	0.4	0.103435	0.5	40	157	107	14.71	23.15
8	1.303617	1.72	0.4	0.46494	0.5	25	689	884	5.96	28.36667
9	1.259346	1.72	0.4	0.168633	0.5	25	491	604	6.19	26.92333
10	1.456219	1.72	0.4	0.25	0.5	40	293	324	6.42	25.48
11	1.456219	1.72	0.4	1	0.5	40	100	100	14.71	23.15
12	1.210382	1.72	0.4	10	0.5	40	380	455.5	9.71	41.19
13	1.39965	1.72	0.4	0.5	0.5	40	100	100	12.80014	20.14434
14	1.210382	1.72	0.4	0.5	0.5	40	380	455.5	9.71	41.19
15	1	1.72	0.4	1	0.5	40	100	100	14.71	23.15
16	1	1.72	2	2	0.5	40	83	23	14.71	23.15
17	1	1.72	0.4	1	0.5	40	100	100	14.71	23.15
18	1.456219	1.72	0.4	0.25	0.5	40	293	324	6.42	25.48

## 9.2 MIMICS parameters

Table 22. MIMICS parameters common to all PFTs.

<b>Vmax(T)– temperature sensitive maximum reaction velocities (mg C (mg MIC)<sup>-1</sup> h<sup>-1</sup>)</b>			
$Vmax_{[rk]}(T) = \exp(Vslope_{[rk]} \cdot T_{soil} + Vint_{[rk]}) \cdot av_{[rk]} \cdot Vmod_{[rk]}$			
0.063	Vslope(r1)	Vmax regression slope (ln(mg Cs (mg MIC) <sup>-1</sup> h <sup>-1</sup> ) C <sup>-1</sup> )	LITm to MICr
0.063	Vslope(r2)	Vmax regression slope (ln(mg Cs (mg MIC) <sup>-1</sup> h <sup>-1</sup> ) C <sup>-1</sup> )	LITs to MICr
0.063	Vslope(r3)	Vmax regression slope (ln(mg Cs (mg MIC) <sup>-1</sup> h <sup>-1</sup> ) C <sup>-1</sup> )	SOMa to MICr
0.063	Vslope(k1)	Vmax regression slope (ln(mg Cs (mg MIC) <sup>-1</sup> h <sup>-1</sup> ) C <sup>-1</sup> )	LITm to MICK
0.063	Vslope(k2)	Vmax regression slope (ln(mg Cs (mg MIC) <sup>-1</sup> h <sup>-1</sup> ) C <sup>-1</sup> )	LITs to MICK
0.063	Vslope(k3)	Vmax regression slope (ln(mg Cs (mg MIC) <sup>-1</sup> h <sup>-1</sup> ) C <sup>-1</sup> )	SOMa to MICK

5.47	Vint(r1)	Vmax regression intercept ( $\ln(\text{mg Cs (mg MIC)}^{-1} \text{ h}^{-1})$ )	LITm to MICr
5.47	Vint(r2)	Vmax regression intercept ( $\ln(\text{mg Cs (mg MIC)}^{-1} \text{ h}^{-1})$ )	LITs to MICr
5.47	Vint(r3)	Vmax regression intercept ( $\ln(\text{mg Cs (mg MIC)}^{-1} \text{ h}^{-1})$ )	SOMa to MICr
5.47	Vint(k1)	Vmax regression intercept ( $\ln(\text{mg Cs (mg MIC)}^{-1} \text{ h}^{-1})$ )	LITm to MICK
5.47	Vint(k2)	Vmax regression intercept ( $\ln(\text{mg Cs (mg MIC)}^{-1} \text{ h}^{-1})$ )	LITs to MICK
5.47	Vint(k3)	Vmax regression intercept ( $\ln(\text{mg Cs (mg MIC)}^{-1} \text{ h}^{-1})$ )	SOMa to MICK
1.25E-08	av(r1)	Vmax tuning coefficient	LITm to MICr
1.25E-08	av(r2)	Vmax tuning coefficient	LITs to MICr
1.25E-08	av(r3)	Vmax tuning coefficient	SOMa to MICr
1.25E-08	av(k1)	Vmax tuning coefficient	LITm to MICK
1.25E-08	av(k2)	Vmax tuning coefficient	LITs to MICK
1.25E-08	av(k3)	Vmax tuning coefficient	SOMa to MICK
<b>Km(T) – Temperature sensitive reverse Michaelis-Menton half-saturation coefficient</b>			
$Km_{[rk]}(T) = \exp(Kslope_{[rk]} * T_{soil} + Kint_{[rk]}) * ak_{[rk]} / Kmod_{[rk]}$			
$Km_{[r3]}(T) = \exp(Kslope_{[r3]} * T_{soil} + Kint_{[r3]}) * ak_{[r3]} / (Kmod_{[r3]} * Pscalar)$			
$Km_{[k3]}(T) = \exp(Kslope_{[k3]} * T_{soil} + Kint_{[k3]}) * ak_{[k3]} / (Kmod_{[k3]} * Pscalar)$			
0.02	Kslope(r1)	Km regression slope (reverse MM)	LITm to MICr
0.02	Kslope(r2)	Km regression slope (reverse MM)	LITs to MICr
0.02	Kslope(r3)	Km regression slope (reverse MM)	SOMa to MICr
0.02	Kslope(k1)	Km regression slope (reverse MM)	LITm to MICK
0.02	Kslope(k2)	Km regression slope (reverse MM)	LITs to MICK
0.02	Kslope(k3)	Km regression slope (reverse MM)	SOMa to MICK
3.19	Kint(r1)	Km regression intercept	LITm to MICr
3.19	Kint(r2)	Km regression intercept	LITs to MICr
3.19	Kint(r3)	Km regression intercept	SOMa to MICr
3.19	Kint(k1)	Km regression intercept	LITm to MICK
3.19	Kint(k2)	Km regression intercept	LITs to MICK
3.19	Kint(k3)	Km regression intercept	SOMa to MICK

0.015625	ak(r1)	Km tuning coefficient	LITm to MICr
0.015625	ak(r2)	Km tuning coefficient	LITs to MICr
0.015625	ak(r3)	Km tuning coefficient	SOMa to MICr
0.015625	ak(k1)	Km tuning coefficient	LITm to MICK
0.015625	ak(k2)	Km tuning coefficient	LITs to MICK
0.015625	ak(k3)	Km tuning coefficient	SOMa to MICK
<b>Vmax modifier (see Vmax(T) calculation above)</b>			
10	Vmod(r1)	modifies Vmax[r1]	LITm to MICr
2	Vmod(r2)	modifies Vmax[r2]	LITs to MICr
10	Vmod(r3)	modifies Vmax[r3]	SOMa to MICr
3	Vmod(k1)	modifies Vmax[k1]	LITm to MICK
3	Vmod(k2)	modifies Vmax[k2]	LITs to MICK
2	Vmod(k3)	modifies Vmax[k3]	SOMa to MICK
<b>Km modifier (see Km(T) calculation above)</b>			
8	Kmod(r1)	modifies Km[r1]	LITm to MICr
2	Kmod(r2)	modifies Km[r2]	LITs to MICr
4	Kmod(r3)	modifies Km[r3]	SOMa to MICr
2	Kmod(k1)	modifies Km[k1]	LITm to MICK
4	Kmod(k2)	modifies Km[k2]	LITs to MICK
6	Kmod(k3)	modifies Km[k3]	SOMa to MICK
<b>Oxidation of SOMc</b>			
$OXIDAT = \left( \frac{MICr \cdot Vmax[r2] \cdot SOMc}{KO[1] \cdot Km[r2] + MICr} \right) + \left( \frac{MICK \cdot Vmax[k2] \cdot SOMc}{KO[2] \cdot Km[k2] + MICK} \right)$			
6	KO(1)	modifies Km[r2] for oxidation of SOMc	
6	KO(2)	modifies Km[k2] for oxidation of SOMc	
<b>Microbial Growth Efficiency</b>			
0.5	MGE(1)	microbial growth efficiency for C fluxes from LITm or SOMa into MICr (mg mg <sup>-1</sup> )	
0.25	MGE(2)	microbial growth efficiency for C fluxes from LITs into MICr (mg mg <sup>-1</sup> )	
0.7	MGE(3)	microbial growth efficiency for C fluxes from LITm or SOMa into MICK (mg mg <sup>-1</sup> )	

0.35	MGE(4)	microbial growth efficiency for C fluxes from LITs into MICk (mg mg <sup>-1</sup> )
<b>Microbial turnover of r-selected and K-selected (tauR and tauK)</b>		
0.00052	tau_r(1)	tauR(npt) = tau_r(1) * exp(tau_r(2) * fmet(npt)) * tauMod(npt)
0.3	tau_r(2)	tauR(npt) = tau_r(1) * exp(tau_r(2) * fmet(npt)) * tauMod(npt)
0.00024	tau_k(1)	tauK(npt) = tau_k(1) * exp(tau_k(2) * fmet(npt)) * tauMod(npt)
0.1	tau_k(2)	tauK(npt) = tau_k(1) * exp(tau_k(2) * fmet(npt)) * tauMod(npt)
100	tauModDenom	tauMod(npt) = SQRT(NPP <sub>AN</sub> (npt)/tauModDenom)
0.6	tauMod_MIN	tauMod(npt) = MAX(tauMod_MIN, tauMod(npt))
1.3	tauMod_MAX	tauMod(npt) = MIN(tauMod_MAX, tauMod(npt))
<b>Fraction of physically protected carbon (fPHYS)</b>		
<i>fPHYSr</i> – fraction of $\tau_r$ partitioned into <i>SOMp</i> (0.0 – 1.0)		
<i>fPHYSk</i> – fraction of $\tau_k$ partitioned into <i>SOMp</i> (0.0 – 1.0)		
0.15	fPHYS_r(1)	fPHYSr(npt,1) = fPHYS_r(1) * exp(fPHYS_r(2) * clay(npt))
1.3	fPHYS_r(2)	fPHYSr(npt,1) = fPHYS_r(1) * exp(fPHYS_r(2) * clay(npt))
0.1	fPHYS_K(1)	fPHYSk(npt,2) = fPHYS_K(1) * exp(fPHYS_K(2) * clay(npt))
0.8	fPHYS_K(2)	fPHYSk(npt,2) = fPHYS_K(1) * exp(fPHYS_K(2) * clay(npt))
<i>fCHEMr</i> – fraction of $\tau_r$ partitioned into <i>SOMc</i> (0.0 – 1.0)		
<i>fCHEMk</i> – fraction of $\tau_k$ partitioned into <i>SOMc</i> (0.0 – 1.0)		
0.1	fCHEM_r(1)	fCHEMr(npt) = fCHEM_r(1) * exp(fCHEM_r(2) * fmet(npt)) * fCHEM_r(3)
-3	fCHEM_r(2)	fCHEMr(npt) = fCHEM_r(1) * exp(fCHEM_r(2) * fmet(npt)) * fCHEM_r(3)
3	fCHEM_r(3)	fCHEMr(npt) = fCHEM_r(1) * exp(fCHEM_r(2) * fmet(npt)) * fCHEM_r(3)
0.3	fCHEM_K(1)	fCHEMk(npt) = fCHEM_K(1) * exp(fCHEM_K(2) * fmet(npt)) * fCHEM_K(3)
-3	fCHEM_K(2)	fCHEMk(npt) = fCHEM_K(1) * exp(fCHEM_K(2) * fmet(npt)) * fCHEM_K(3)
3	fCHEM_K(3)	fCHEMk(npt) = fCHEM_K(1) * exp(fCHEM_K(2) * fmet(npt)) * fCHEM_K(3)
<b>Desorption of physically protected SOM to available SOM (hr<sup>-1</sup>)</b>		
$DE_{sorb} = SOMp \cdot 1.5 \times 10^{-5} \cdot \exp(-1.5 \cdot f_{clay})$		
1.00E-05	fSOM_p(1)	desorb(npt) = fSOM_p(1) * exp(fSOM_p(2) * clay(npt))
-3.5	fSOM_p(2)	desorb(npt) = fSOM_p(1) * exp(fSOM_p(2) * clay(npt))
<b>Physical protection modifier on consumption of SOMa (Pscalar)</b>		

See $K_{m_{r3}}(T)$ and $K_{m_{k3}}(T)$ calculations above.		
3	phys_scalar(1)	$P_{\text{scalar}} = \text{phys\_scalar}(1) * \exp(\text{phys\_scalar}(2) * \text{SQRT}(\text{clay}(\text{npt})))$
-2	phys_scalar(2)	$P_{\text{scalar}} = \text{phys\_scalar}(1) * \exp(\text{phys\_scalar}(2) * \text{SQRT}(\text{clay}(\text{npt})))$
<b>Direct litter transfer to SOMp and SOMc</b>		
0.05	FI(metb)	fraction of metabolic litter inputs transferred to SOMp, the remaining goes to the metabolic litter pool.
0.05	FI(struc)	fraction of structural litter inputs transferred to SOMc, the remaining goes to the structural litter pool.
<b>fmet = fraction of plant residue transferred to metabolic litter (0.0 – 1.0) (structural litter fraction = 1 – fmet)</b>		
0.75	fmet_p(1)	$\text{fmet}(\text{npt}) = \text{fmet\_p}(1) * (\text{fmet\_p}(2) - \text{fmet\_p}(3) * \text{ligninNratioAvg}(\text{npt}))$
0.85	fmet_p(2)	$\text{fmet}(\text{npt}) = \text{fmet\_p}(1) * (\text{fmet\_p}(2) - \text{fmet\_p}(3) * \text{ligninNratioAvg}(\text{npt}))$
0.013	fmet_p(3)	$\text{fmet}(\text{npt}) = \text{fmet\_p}(1) * (\text{fmet\_p}(2) - \text{fmet\_p}(3) * \text{ligninNratioAvg}(\text{npt}))$

Table 23. MIMICS PFT-specific soil depths.

vegtype (PFT)	SOM depth (cm)
1	100
2	100
3	100
4	100
5	100
6	100
7	100
8	100
9	100
10	100
11	100
12	100
13	100
14	100



15	100
16	100
17	100
18	100

### 9.3 CORPSE parameters from corpse\_params\_new.nml

Table 24. CORPSE model parameters common to all PFTs (CORPSE has no PFT-specific parameters).

soil_carbon_nml	Description
Vmaxref = 4500e0, 25e0, 600e0	Vmax at reference temperature ( $\text{yr}^{-1}$ ) for labile, recalcitrant, and dead microbe pools
Ea = 37e3, 54e3, 50e3	Activation energy (kJ/mol) for labile, recalcitrant, and dead microbe pools
kC = 0.01, 0.01, 0.01	Michaelis-Menton C parameter (dimensionless microbe fraction of total C) for labile, recalcitrant, and dead microbe pools
minMicrobeC = 1e-3	Minimum microbial biomass (fraction of total C)
Tmic = 0.25	Microbial turnover rate ( $\text{yr}^{-1}$ )
eup = 0.6, 0.05, 0.6	Microbial uptake efficiency (dimensionless fraction) for labile, recalcitrant, and dead microbe pools
protection_rate = 1.5	Rate that carbon becomes protected ( $\text{yr}^{-1}$ or $\text{yr}^{-1} \text{ kg-microbial-biomass}^{-1}$ depending on microbe_driven_protection)
microbe_driven_protection = .FALSE.	Whether to use microbial biomass in protection rate
protection_species = 1.0, 0.001, 1.0	Relative protection rate of each carbon species (between 0 and 1) for labile, recalcitrant, and dead microbe pools
tProtected = 45.0	Turnover time for protected carbon transition back to unprotected pool (years)
protected_carbon_decomp_factor = 0.0	vmaxref for protected carbon is multiplied by this (0.0 if protected C is inaccessible to microbial decomposition)
soilMaxCohorts = 2	Maximum number of cohorts in each soil carbon pool
gas_diffusion_exp = 2.5	Exponent for gas diffusion power law dependence on theta (Meslin, Adler et al. 2010)
et = 0.6	Fraction of microbial turnover not converted to $\text{CO}_2$
leaching_solubility = 0.0	Rate carbon dissolves in soil water at saturated moisture ( $\text{yr}^{-1}$ )
DOC_deposition_rate = 1.0e10	Rate carbon is deposited from DOC ( $\text{yr}^{-1}$ ) -- currently set very high so there is no persistent DOC

<b>soil_carbon_nml</b>	<b>Description</b>
flavor_relative_solubility = 1.0, 0.1, 1.0	Relative solubility of for labile, recalcitrant, and dead microbe pools (0.0 – 1.0)
protected_relative_solubility = 0.0	Relative solubility of protected carbon (0.0 – 1.0)
litterDensity = 22.0	C density of litter layer (kg/m <sup>3</sup> ) (22.0 roughly from Gaudinsky et al. 2000)
<b>CORPSE_casa_nml</b>	
initial_C = 0.0, 2.0, 0.0	Initial C values for labile, recalcitrant, and dead microbe pools (initcasa=0 only) (kg C /m <sup>2</sup> )
exudate_npp_frac = 0.02, 0.0, 0.0	Fraction of annual NPP going to root exudation for labile, recalcitrant, and dead microbe pools
rhizosphere_frac = 0.3	Fraction of soil pool located in the rhizosphere (0.0 – 1.0)

## 10 References

National Center for Atmospheric Research Staff (Eds). Last modified 10 Feb 2017. "The Climate Data Guide: CERES: IGBP Land Classification." Retrieved from <https://climatedataguide.ucar.edu/climate-data/ceres-igbp-land-classification>.

Koven, C. D., et al. (2013). "The effect of vertically-resolved soil biogeochemistry and alternate soil C and N models on C dynamics of CLM4." *Biogeosciences* **10**: 7109-7131.

Loveland, T. R., et al. (2000). "Development of a global land cover characteristics database and IGBP DISCover from 1 km AVHRR data." *International Journal of Remote Sensing* **21**(6-7): 1303-1330.

Researchers from the U.S. Geological Survey, University of Nebraska-Lincoln and the European Commission's Joint Research Centre, Ispra, Italy produced a 1 km resolution global land cover characteristics database for use in a wide range of continental- to global-scale environmental studies. This database provides a unique view of the broad patterns of the biogeographical and ecoclimatic diversity of the global land surface, and presents a detailed interpretation of the extent of human development. The project was carried out as an International Geosphere-Biosphere Programme, Data and Information Systems (IGBP-DIS) initiative. The IGBP DISCover global land cover product is an integral component of the global land cover database. DISCover includes 17 general land cover classes defined to meet the needs of IGBP core science projects. A formal accuracy assessment of the DISCover data layer will be completed in 1998.

The 1 km global land cover database was developed through a continent-by-continent unsupervised classification of 1 km monthly Advanced Very High Resolution Radiometer (AVHRR) Normalized Difference Vegetation Index (NDVI) composites covering 1992-1993. Extensive post-classification stratification was necessary to resolve spectral/temporal confusion between disparate land cover types. The complete global database consists of 961 seasonal land cover regions that capture patterns of land cover, seasonality and relative primary productivity. The seasonal land cover regions were aggregated to produce seven separate land cover data sets used for global environmental modelling and assessment. The data sets include IGBP DISCover, U.S. Geological Survey Anderson System, Simple Biosphere Model, Simple Biosphere Model 2, Biosphere Atmosphere Transfer Scheme, Olson Ecosystems and Running Global Remote Sensing Land Cover. The database also includes all digital sources that were used in the classification. The complete database can be sourced from the website: <http://edcwww.cr.usgs.gov/landdaac/glcc/glcc.html>.

Meslin, P. Y., et al. (2010). "Diffusive transport of gases in wet porous media. Application to radon." *Soil Science Society Of America Journal* **74**: 1871-1885.

Oleson, K., et al. (2013). Technical description of version 4.5 of the Community Land Model (CLM). NCAR Technical Note NCAR/TN-503+STR: 420.

Oleson, K. W., et al. (2013). Technical description of version 4.5 of the Community Land Model (CLM), NCAR/TN-503+STR NCAR Technical Note. Boulder, CO, National Center for Atmospheric Research: 420.

Potter, C. S., et al. (1993). "Terrestrial Ecosystem Production - a Process Model-Based on Global Satellite and Surface Data." Global Biogeochemical Cycles **7**(4): 811-841.

This paper presents a modeling approach aimed at seasonal resolution of global climatic and edaphic controls on patterns of terrestrial ecosystem production and soil microbial respiration. We use satellite imagery (Advanced Very High Resolution Radiometer and International Satellite Cloud Climatology Project solar radiation), along with historical climate (monthly temperature and precipitation) and soil attributes (texture, C and N contents) from global (1-degrees) data sets as model inputs. The Carnegie-Ames-Stanford approach (CASA) Biosphere model runs on a monthly time interval to simulate seasonal patterns in net plant carbon fixation, biomass and nutrient allocation, litterfall, soil nitrogen mineralization, and microbial CO<sub>2</sub> production. The model estimate of global terrestrial net primary production is 48 Pg C yr<sup>-1</sup> with a maximum light use efficiency of 0.39 g C MJ<sup>-1</sup> PAR. Over 70% of terrestrial net production takes place between 30-degrees-N and 30-degrees-S latitude. Steady state pools of standing litter represent global storage of around 174 Pg C (94 and 80 Pg C in nonwoody and woody pools, respectively), whereas the pool of soil C in the top 0.3 m that is turning over on decadal time scales comprises 300 Pg C. Seasonal variations in atmospheric CO<sub>2</sub> concentrations from three stations in the Geophysical Monitoring for Climate Change Flask Sampling Network correlate significantly with estimated net ecosystem production values averaged over 50-degrees-80-degrees-N, 10-degrees-30-degrees-N, and 0-degrees-10-degrees-N.

Randerson, J. T., et al. (1997). "The contribution of terrestrial sources and sinks to trends in the seasonal cycle of atmospheric carbon dioxide." Global Biogeochemical Cycles **11**(4): 535-560.

We characterized decadal changes in the amplitude and shape of the seasonal cycle of atmospheric CO<sub>2</sub> with three kinds of analysis. First, we calculated the trends in the seasonal cycle of measured atmospheric CO<sub>2</sub> at observation stations in the National Oceanic and Atmospheric Administration Climate Monitoring and Diagnostic Laboratory network. Second, we assessed the impact of terrestrial ecosystems in various localities on the mean seasonal cycle of CO<sub>2</sub> at observation stations using the Carnegie-Ames-Stanford Approach terrestrial biosphere model and the Goddard Institute for Space Studies (GISS) atmospheric tracer transport model. Third, we used the GISS tracer model to quantify the contribution of terrestrial sources and sinks to trends in the seasonal cycle of atmospheric CO<sub>2</sub> for the period 1961–1990, specifically examining the effects of biomass burning, emissions from fossil fuel combustion, and regional increases in net primary production (NPP). Our analysis supports results from previous studies that indicate a significant positive increase in the amplitude of the seasonal cycle of CO<sub>2</sub> at Arctic and subarctic observation stations. For stations north of 55°N the amplitude increased at a mean rate of 0.66% yr<sup>-1</sup> from 1981 to 1995. From the analysis of ecosystem impacts on the mean seasonal cycle we find that tundra, boreal forest, and other northern ecosystems are responsible for most of the seasonal variation in CO<sub>2</sub> at stations north of 55°N. The effects of tropical biomass burning on trends in the seasonal cycle are minimal at these stations, probably because of strong vertical convection in equatorial regions. From 1981 to 1990, fossil fuel emissions contributed a trend of 0.20% yr<sup>-1</sup> to the seasonal cycle amplitude at Mauna Loa and less than 0.10% yr<sup>-1</sup> at stations north of 55°N. To match the observed amplitude increases at Arctic and subarctic stations with NPP increases, we find that north of 30°N a 1.7 Pg C yr<sup>-1</sup> terrestrial sink would be required. In contrast, over regions south of 30°N, even large NPP

increases and accompanying terrestrial sinks would be insufficient to account for the increase in high-latitude amplitudes.

Randerson, J. T., et al. (1996). "Substrate limitations for heterotrophs: Implications for models that estimate the seasonal cycle of atmospheric CO<sub>2</sub>." Global Biogeochemical Cycles **10**(4): 585-602.

We examine the sensitivity of the seasonal cycle of heterotrophic respiration to model estimates of litterfall seasonality, herbivory, plant allocation, tissue chemistry, and land use. As a part of this analysis, we compare heterotrophic respiration models based solely on temperature and soil moisture controls (zero-order models) with models that depend on available substrate as well (first-order models). As indicators of regional and global CO<sub>2</sub> exchange, we use maps of monthly global net ecosystem production, growing season net flux (GSNF), and simulated atmospheric CO<sub>2</sub> concentrations from an atmospheric tracer transport model. In one first-order model, CASA, variations on the representation of the seasonal flow of organic matter from plants to heterotrophs can increase global GSNF as much as 60% (5.7 Pg C yr<sup>-1</sup>) above estimates obtained from a zero-order model. Under a new first-order scheme that includes separate seasonal dynamics for leaf litterfall, fine root mortality, coarse woody debris, and herbivory, we observe an increase in GSNF of 8% (0.7 Pg C yr<sup>-1</sup>) over that predicted by the zero-order model. The increase in seasonality of CO<sub>2</sub> exchange in first-order models reflects the dynamics of labile litter fractions; specifically, the rapid decomposition of a pulse of labile leaf and fine root litter that enters the heterotrophic community primarily from the middle to the end of the growing season shifts respiration outside the growing season. From the perspective of a first-order model, we then explore the consequences of land use change and winter temperature anomalies on the amplitude of the seasonal cycle of atmospheric CO<sub>2</sub>. Agricultural practices that accelerate decomposition may drive a long-term increase in the amplitude, independent of human impacts on plant production. Consideration of first-order litter decomposition dynamics may also help explain year-to-year variation in the amplitude.

Sitch, S., et al. (2003). "Evaluation of ecosystem dynamics, plant geography and terrestrial carbon cycling in the LPJ dynamic global vegetation model." Global Change Biology **9**(2): 161-185.

The Lund–Potsdam–Jena Dynamic Global Vegetation Model (LPJ) combines process-based, large-scale representations of terrestrial vegetation dynamics and land-atmosphere carbon and water exchanges in a modular framework. Features include feedback through canopy conductance between photosynthesis and transpiration and interactive coupling between these ‘fast’ processes and other ecosystem processes including resource competition, tissue turnover, population dynamics, soil organic matter and litter dynamics and fire disturbance. Ten plants functional types (PFTs) are differentiated by physiological, morphological, phenological, bioclimatic and fire-response attributes. Resource competition and differential responses to fire between PFTs influence their relative fractional cover from year to year. Photosynthesis, evapotranspiration and soil water dynamics are modelled on a daily time step, while vegetation structure and PFT population densities are updated annually. Simulations have been made over the industrial period both for specific sites where field measurements were available for model evaluation, and globally on a 0.5° × 0.5° grid. Modelled vegetation patterns are consistent with observations, including remotely sensed vegetation structure and phenology. Seasonal cycles of net ecosystem exchange and soil moisture compare well with local measurements. Global carbon exchange fields used as input to an atmospheric tracer transport model (TM2) provided

a good fit to observed seasonal cycles of CO<sub>2</sub> concentration at all latitudes. Simulated inter-annual variability of the global terrestrial carbon balance is in phase with and comparable in amplitude to observed variability in the growth rate of atmospheric CO<sub>2</sub>. Global terrestrial carbon and water cycle parameters (pool sizes and fluxes) lie within their accepted ranges. The model is being used to study past, present and future terrestrial ecosystem dynamics, biochemical and biophysical interactions between ecosystems and the atmosphere, and as a component of coupled Earth system models.

Sulman, B. N., et al. (2014). "Microbe-driven turnover offsets mineral-mediated storage of soil carbon under elevated CO<sub>2</sub>." Nature Climate Change **4**(12): 1099-1102.

Wang, Y. P., et al. (2010). "A global model of carbon, nitrogen and phosphorus cycles for the terrestrial biosphere." Biogeosciences **7**(7): 2261-2282.

Carbon storage by many terrestrial ecosystems can be limited by nutrients, predominantly nitrogen (N) and phosphorus (P), in addition to other environmental constraints, water, light and temperature. However the spatial distribution and the extent of both N and P limitation at the global scale have not been quantified. Here we have developed a global model of carbon (C), nitrogen (N) and phosphorus (P) cycles for the terrestrial biosphere. Model estimates of steady state C and N pool sizes and major fluxes between plant, litter and soil pools, under present climate conditions, agree well with various independent estimates. The total amount of C in the terrestrial biosphere is 2767 Gt C, and the C fractions in plant, litter and soil organic matter are 19%, 4% and 77%. The total amount of N is 135 Gt N, with about 94% stored in the soil, 5% in the plant live biomass, and 1% in litter. We found that the estimates of total soil P and its partitioning into different pools in soil are quite sensitive to biochemical P mineralization. The total amount of P (plant biomass, litter and soil) excluding occluded P in soil is 17 Gt P in the terrestrial biosphere, 33% of which is stored in the soil organic matter if biochemical P mineralization is modelled, or 31 Gt P with 67% in soil organic matter otherwise. This model was used to derive the global distribution and uncertainty of N or P limitation on the productivity of terrestrial ecosystems at steady state under present conditions. Our model estimates that the net primary productivity of most tropical evergreen broadleaf forests and tropical savannahs is reduced by about 20% on average by P limitation, and most of the remaining biomes are N limited; N limitation is strongest in high latitude deciduous needle leaf forests, and reduces its net primary productivity by up to 40% under present conditions.

Wieder, W. R., et al. (2014). "Integrating microbial physiology and physio-chemical principles in soils with the MIMICS model." Biogeosciences **11**: 3899–3917.

Wieder, W. R., et al. (2015). "Representing life in the Earth system with soil microbial functional traits in the MIMICS model." Geoscientific Model Development **8**(6): 1789-1808.

Projecting biogeochemical responses to global environmental change requires multi-scaled perspectives that consider organismal diversity, ecosystem processes, and global fluxes. However, microbes, the drivers of soil organic matter decomposition and stabilization, remain notably absent from models used to project carbon (C) cycle-climate feedbacks. We used a microbial trait-based soil C model with two physiologically distinct microbial communities, and

evaluate how this model represents soil C storage and response to perturbations. Drawing from the application of functional traits used to model other ecosystems, we incorporate copiotrophic and oligotrophic microbial functional groups in the Microbial-Mineral Carbon Stabilization (MIMICS) model; these functional groups are akin to 'gleaner' vs. 'opportunistic' plankton in the ocean, or r- vs. K-strategists in plant and animal communities. Here we compare MIMICS to a conventional soil C model, DAYCENT (the daily time-step version of the CENTURY model), in cross-site comparisons of nitrogen (N) enrichment effects on soil C dynamics. MIMICS more accurately simulates C responses to N enrichment; moreover, it raises important hypotheses involving the roles of substrate availability, community-level enzyme induction, and microbial physiological responses in explaining various soil biogeochemical responses to N enrichment. In global-scale analyses, we show that MIMICS projects much slower rates of soil C accumulation than a conventional soil biogeochemistry in response to increasing C inputs with elevated carbon dioxide (CO<sub>2</sub>) - a finding that would reduce the size of the land C sink estimated by the Earth system. Our findings illustrate that tradeoffs between theory and utility can be overcome to develop soil biogeochemistry models that evaluate and advance our theoretical understanding of microbial dynamics and soil biogeochemical responses to environmental change.

Zhang, X., et al. (2006). "Global vegetation phenology from Moderate Resolution Imaging Spectroradiometer (MODIS): Evaluation of global patterns and comparison with in situ measurements." Journal of Geophysical Research: Biogeosciences **111**(G4): n/a-n/a.

In the last two decades the availability of global remote sensing data sets has provided a new means of studying global patterns and dynamics in vegetation. The vast majority of previous work in this domain has used data from the Advanced Very High Resolution Radiometer, which until recently was the primary source of global land remote sensing data. In recent years, however, a number of new remote sensing data sources have become available that have significantly improved the capability of remote sensing to monitor global ecosystem dynamics. In this paper, we describe recent results using data from NASA's Moderate Resolution Imaging Spectroradiometer to study global vegetation phenology. Using a novel new method based on fitting piecewise logistic models to time series data from MODIS, key transition dates in the annual cycle(s) of vegetation growth can be estimated in an ecologically realistic fashion. Using this method we have produced global maps of seven phenological metrics at 1-km spatial resolution for all ecosystems exhibiting identifiable annual phenologies. These metrics include the date of year for (1) the onset of greenness increase (greenup), (2) the onset of greenness maximum (maturity), (3) the onset of greenness decrease (senescence), and (4) the onset of greenness minimum (dormancy). The three remaining metrics are the growing season minimum, maximum, and summation of the enhanced vegetation index derived from MODIS. Comparison of vegetation phenology retrieved from MODIS with in situ measurements shows that these metrics provide realistic estimates of the four transition dates identified above. More generally, the spatial distribution of phenological metrics estimated from MODIS data is qualitatively realistic, and exhibits strong correspondence with temperature patterns in mid- and high-latitude climates, with rainfall seasonality in seasonally dry climates, and with cropping patterns in agricultural areas.