# Model description

Equations governing the change in each carbon pool over time in the ReSOM model. All pools are in units of carbon mass per soil volume (g C m-3). Additional pool, flux, and parameter values are defined in the parameter table. For full equations, additional parameters, and model development see Tang and Riley [2015].

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| **Pool Description Differential equation** |
| *S* polymeric organic carbon (1)  *D* monomeric organic carbon (2)  *X* reserve microbial biomass (3)  *B* structural microbial biomass (4)  *E* extracellular enzymes (5)  where:  *I*S polymeric input flux (g C m-3 d-1)  *I*D monomeric input flux (g C m-3 d-1)  *F*S polymeric depolymerization flux (g C m-3 d-1)  *F*D monomeric uptake flux (g C m-3 d-1)  *Y*X yield coefficient for reserve biomass (unitless)  *f*E fraction of decayed extracellular enzymes contributing to the polymer pool (unitless)  B1 microbial mortality rate (d-1)  E enzyme turnover rate (d-1)  ** metabolic turnover rate (d-1)  *g* growth rate (d-1)  *p*E enzyme production rate (d-1) |

The ReSOM model computes depolymerization of polymers, sorption of monomers and enzymes, and uptake of monomers (i.e., microbial assimilation) using Equilibrium Chemistry Approximation (ECA) kinetics, a generalization of Michaelis-Menten (MM) kinetics [*Tang and Riley*, 2013]. ECA is more accurate than MM kinetics in approximating the law of mass action kinetics, which underlies both approaches [*Michaelis and Menten*, 1913; *Tang and Riley*, 2013; *Tang*, 2015]. ECA kinetics represents decomposition and substrate uptake as a competition between minerals and SOC for enzymes, and minerals and microbes for low molecular weight C, respectively. Two advantages of the ECA approach are the ability to (i) include distinct temperature-dependent effects on mineral sorption and microbial processes (i.e., decomposition, uptake, and maintenance) based on well-established kinetic theory and (ii) represent the multi-consumer, multi-substrate competitive environment in a computationally efficient manner. Thus, depolymerization (*F*S) and uptake (*F*C) are defined as

(8)

(9)

where *E* is the extracellular enzyme pool, *S* is the polymeric organic carbon pool, *B* is the structural microbial biomass pool, *D* is the monomeric organic carbon pool, and *M* is the mineral sorption capacity (i.e., Qmax), *V*max is the maximum rate of each process, *z* is a scaling parameter for transporter density, and *k* is the affinity parameter for decomposition (*k*ES), uptake (*k*BD), sorption to enzymes (*k*ME), and sorption to monomers (*k*MD).

Plant inputs estimated from site-level NPP are partitioned based on [*Tang and Riley*, 2015] into polymer and monomer pools, respectively, where the polymer pool represents polymeric compounds in litter (e.g., cellulose, hemicellulose, lignin) and the monomer pool represents intracellular material, easily-leached monomeric compounds in litter, and root exudates.

# General Matrix Representation (Sierra and Muller 2014, Ecological Monographs)

We converted ReSOM from the representation shown in Table 1 (i.e., a mass balance of individual fluxes) to a general matrix representation using the the form:

where dC/dt is the change in a vector of C pools, I is the input matrix, A is the matrix representing all flows of C between pools, and C are the carbon pools.

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The A matrix can be further decomposed into T and K, where T is a matrix of transfers between the pools and K is the decay rate for each pool.

# Parameter Table

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Type** | **Symbol** | **Units** | **Definition** | **Default Value** |
| **Pool** | S | g C m-3 | Polymeric organic carbon | - |
|  | D | g C m-3 | Monomeric organic C | - |
|  | Dads | g C m-3 | Adsorbed monomeric organic C | - |
|  | B | g C m-3 | Microbial structural biomass | - |
|  | X | g C m-3 | Microbial reserve biomass | - |
|  | E | g C m-3 | Extracellular enzymes | - |
|  | Eads | g C m-3 | Adsorbed extracellular enzymes | - |
|  | M | g C eqv m-3 | Mineral surfaces | - |
| **Flux** | IS | g C m-3 d-1 | Polymeric input | - |
|  | ID | g C m-3 d-1 | Monomeric input | - |
|  | FS | g C m-3 d-1 | Depolymerization | - |
|  | FD | g C m-3 d-1 | Uptake | - |
|  | FDads | g C m-3 d-1 | Monomer adsorption | - |
|  | FEads | g C m-3 d-1 | Enzyme adsorption | - |
|  | RCO2 | g C m-3 d-1 | Respiration | - |
|  | Fr | g C m-3 d-1 | C overflow | - |
| **Parameter** | B1 | d-1 | Mortality rate | - |
|  | Dads | d-1 | Turnover of adsorbed monomers | 0.006 |
|  | Eads | d-1 | Turnover of adsorbed enzymes | 0.006 |
|  | fE | - | Fraction of decayed extracellular enzyme contributing to polymer pool | 0.2 |
|  | E | d-1 | Enzyme turnover rate | 0.0061 |
|  | YX | - | Yield rate of enzyme from reserve metabolites | 0.8 |
|  | κ | d-1 | Metabolic turnover rate | 0.0537 |
|  | g | d-1 | Growth rate | - |
|  | pE | d-1 | Enzyme production rate | - |
|  | m | d-1 | Maintenance rate | - |
|  | KEQ (T) | g C | Affinity parameter at dynamic equilibrium | - |
|  | K(T0) | g C | Affinity parameter at reference temperature | - |
|  | GEQ | kJ mol-1 | Gibbs energy change at equilibrium | - |
|  |  |  | for the enzyme-mineral adsorption affinity parameter | 20 |
|  |  |  | for the monomer-mineral adsorption affinity parameter | 20 |
|  |  |  | for reserve export | 0 |
|  | VNEQ (T) | d-1 | Maximum non-equilibrium rate parameter | - |
|  |  | d-1 | for monomer adsorption | 0.01 |
|  |  | d-1 | for enzyme adsorption | 0.001 |
|  | V(T0) | d-1 | Maximum rate parameter at reference temperature | - |
|  | GNEQ | kJ mol-1 | Gibbs energy change at non-equilibrium | - |
|  | GE | kJ mol-1 | Gibbs energy change of enzyme reaction | - |
|  | R | J K-1 mol-1 | Gas constant | 8.314 |
|  | T | K | Temperature | - |
|  | T0 | K | Reference temperature | - |
|  | fact | - | Fraction enzymes active at temperature T | - |
|  | H\* | J mol-1 | Enthalpy change at T\*H | 5312.072 |
|  | S\* | J K-1 mol-1 | Entropy change at T\*S | 18.1 |
|  | T\*H | K | Convergence temperature for enthalpy | 373.6 |
|  | T\*S | K | Convergence temperature for entropy | 385.2 |
|  | CP | J mol-1 | Heat capacity change | - |
|  | n | - | Number of amino acid residues for an enzyme | 183 |
|  | NCH | - | Average number of non-polar hydrogen atoms per amino acid residue | 5.524 |
|  | VE,max | d-1 | Maximum rate of polymer degradation | 2.4133 |
|  | kES | g C | Affinity parameter for enzymatic polymer degradation | 200 |
|  | kME | g C | Affinity parameter for surface adsorption of enzymes | 50 |
|  | z | - | Scaling parameter for transporter density | 0.05 |
|  | VB,max | d-1 | Maximum rate of monomer assimilation | 10.9343 |
|  | kBD | g C | Affinity parameter for microbial monomer uptake | 1 |
|  | kMD | g C | Affinity parameter for mineral surface adsorption of monomers | 25 |