First Stage Reverse MM Kinetics

Objective

Following the discussion on https://github.com/kdorheim/MENDplus/issues/7 let's try deploying the R-MM kinetics of POM1, POM2 and MOM.

```r
# Load the required pacakges
library(magrittr)
library(MENDplus)
library(ggplot2)
library(data.table)
library(deSolve)
```

Default MEND Run   First start by setting up the default model.

```r
# Define the inital conditions the times to solve the model for.
state <- c("P" = 10, "M" = 5, "Q" = 0.1, "B" = 2, "D" = 1,
           "EP" = 1e-5, "EM" = 1e-5, 'IC' = 0, 'Tot' = 18)
times <- seq(0, 12000, by = 1)

# Solve the model and format the output
# TODO is it worth considereing wrapping this up into a function?
out <- ode(y = state, times = times, parms = default_parameters,
           func = MEND_carbon_pools, flux_function = MEND_fluxes)
results_default <- melt(as.data.table(out),  measure.vars = names(state),
                        variable.name = "C_pool", value.name = 'value')
results_default$run_name <- 'default MEND'
```

Stange 1 R-MM Run   Now we want to format the model to use R MM kinetics for decomposition of the POM1, POM2 and MOM pools.

```r
RMM_stage1_fluxes <- function(state, parms){

  # We want replace the POP and MOM break from MM to R-MM kinetics that depends on
  # concentration of the extracellular enzymes.
  functions_to_replace <-c('F3', 'F2')

  # Create a list of the carbon pool fluxes that will not change, or in otherwords
  # have the same format as the 2015 paper.
  default_fluxes <- MEND_fluxes(state, parms)
  fluxes <- default_fluxes[!names(default_fluxes) %in% functions_to_replace]

  # Format the parameters into a vector.
  p        <- parms$value
  names(p) <- parms$parameter
```

```r
  with(as.list(c(state, p)), {
    # Now cfreate the new F3 and F3 functions.
    new_fluxes <- list(
      'F3' = function(){
        # Break down of mineralized organic carbon based on R-MM kinetics.
        V.m * EM * M / (K.m + EM)
      },
      'F2' = function(){
        # POC decomposition based  R-MM kinetics.
        V.p * EP * P / (K.p + EP)
      })

    return(append(fluxes, new_fluxes))
  })


}
```

So now instead of POC decomposition $\frac{V_p*EP*P}{(K_p+P)}$ now POC break down lookts like $\frac{V_p*EP*P}{(K_p+EP)}$.

And then MOC decompostion replaced $\frac{V_m*EM*M}{K_m+M}$ with $\frac{V_m*EM*M}{K_m+EM}$.

```r
# Solve the model and format the output but use the flues that are defined with
out_RMM <- ode(y = state,
               times = times,
               parms = default_parameters,
               func = MEND_carbon_pools,
               flux_function = RMM_stage1_fluxes)
results_RMM <- melt(as.data.table(out_RMM),  measure.vars = names(state),
                    variable.name = "C_pool", value.name = 'value')
results_RMM$run_name <- 'stage 1 R-MM'
```
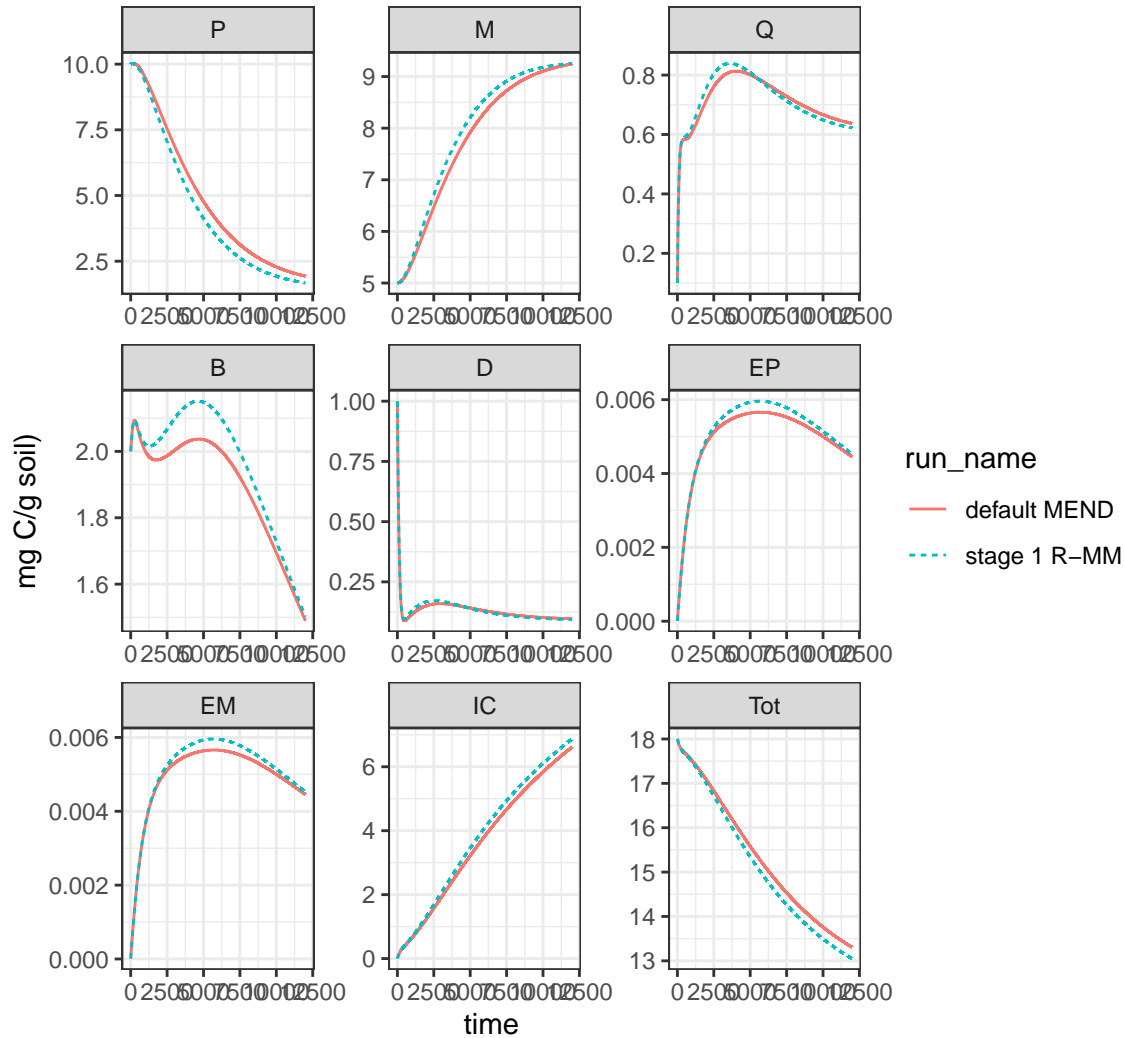
Comparison Plot

```r
ggplot(data = rbind(results_default, results_RMM)) +
  geom_line(aes(x = time, y = value, color= run_name, linetype = run_name)) +
  facet_wrap("C_pool", scales = 'free') +
  theme_bw() +
  labs(y = 'mg C/g soil)', title = 'Comparison of Default 2013 MEND with R-MM MEND',
       subtitle = 'R-MM used in MOC and POC break down')
```

Comparison of Default 2013 MEND with R–MM MEND
R–MM used in MOC and POC break down

Session Info for reproducibility

```r
sessionInfo()
```

```
## R version 3.6.3 (2020-02-29)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.6
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
```

```
## 
## other attached packages:
## [1] deSolve_1.28     data.table_1.12.8 ggplot2_3.3.2    MENDplus_0.1.0
## [5] magrittr_1.5
## 
## loaded via a namespace (and not attached):
##  [1] knitr_1.28      tidyselect_1.1.0 munsell_0.5.0    colorspace_1.4-1
##  [5] R6_2.4.1        rlang_0.4.6      dplyr_1.0.0      stringr_1.4.0
##  [9] tools_3.6.3     grid_3.6.3       gtable_0.3.0     xfun_0.14
## [13] withr_2.2.0     htmltools_0.5.0  ellipsis_0.3.1   assertthat_0.2.1
## [17] yaml_2.2.1      digest_0.6.25    tibble_3.0.1     lifecycle_0.2.0
## [21] crayon_1.3.4    farver_2.0.3     purrr_0.3.4      vctrs_0.3.1
## [25] glue_1.4.1      evaluate_0.14    rmarkdown_2.3.1  labeling_0.3
## [29] stringi_1.4.6   compiler_3.6.3   pillar_1.4.4     generics_0.0.2
## [33] scales_1.1.1    pkgconfig_2.0.3
```