Graphs Rebuttal

PAZ

5 février 2018

Packages

```
library(ggplot2)
```

Lab and other parameters

```
source("global.R")
```

Soils from Book: 06, to merge with "timeApps"

```
# Soils
soils = read.csv2("Data/MassBalance_R.csv",
                        na.strings=c('#DIV/0!', '', 'NA'), header = TRUE)
names(soils)
```

```
##  [1] "ti"                    "WeekSubWeek"
##  [3] "Event"                 "Duration.Hrs"
##  [5] "timeSinceApp"          "timeSinceApp.NoSo"
##  [7] "timeSinceApp.N"        "timeSinceApp.T"
##  [9] "timeSinceApp.S"        "diss.d13C"
## [11] "SD.d13C"               "CumOutDiss.g"
## [13] "CumOutFilt.g"          "TotSMout.g"
## [15] "TotSMout.g.SD"         "MELsm.g"
## [17] "MELsm.g.SD"            "Appl.Mass.g"
## [19] "Appl.Mass.g.OT"        "CumAppMass.g"
## [21] "CumAppMass.g.N"        "CumAppMass.g.T"
## [23] "CumAppMass.g.S"        "CumAppMass.g.OT"
## [25] "CumAppMass.g.N.OT"     "CumAppMass.g.T.OT"
## [27] "CumAppMass.g.S.OT"     "iniCo.ug.g.N"
## [29] "iniCo.ug.g.T"          "iniCo.ug.g.S"
## [31] "CumOutSmeto.g"         "CumOutMELsm.g"
## [33] "MassSoil.g.North"      "MassSoil.g.SD.North"
## [35] "Conc.mug.g.dry.soil.N" "comp.d13C.North"
## [37] "comp.d13C.SD.North"    "ID.N"
## [39] "Area.N"                "Area.T"
## [41] "Area.S"                "MassSoil.g.Talweg"
## [43] "MassSoil.g.SD.Talweg"  "Conc.mug.g.dry.soil.T"
## [45] "comp.d13C.Talweg"      "comp.d13C.SD.Talweg"
## [47] "ID.T"                  "MassSoil.g.South"
## [49] "MassSoil.g.SD.South"   "Conc.mug.g.dry.soil.S"
## [51] "comp.d13C.South"       "comp.d13C.SD.South"
## [53] "ID.S"                  "DD13C.North"
```

```
## [55] "DD13C.Talweg"          "DD13C.South"
## [57] "CatchMassSoil.g"       "CatchMassSoil.g.SD"
## [59] "BulkCatch.d13"         "BulkCatch.d13.SD"
## [61] "DD13.Bulk"             "Area.Catchment"
## [63] "BulkCatch.Conc"        "iniCo.Bulk"
```

```
colnames(soils)[colnames(soils) == "ti"] <- "Date.ti"
soils$Date.ti <- as.POSIXct(strptime(soils$Date.ti,
                                     "%Y-%m-%d %H:%M", tz="EST")) # csv typos, option 1
sum(is.na(soils$Date.ti)) == 0
```

```
## [1] TRUE
```

```
initialDelta
```

```
## [1] -32.3
```

```
# Get rid of imputed values to avoid bias
soils$DD13C.North <- (ifelse(!is.na(soils$comp.d13C.SD.North), soils$comp.d13C.North - (initialDelta),
soils$DD13C.Talweg <- (ifelse(!is.na(soils$comp.d13C.SD.Talweg), soils$comp.d13C.Talweg - (initialDelta
soils$DD13C.South <- (ifelse(!is.na(soils$comp.d13C.SD.South), soils$comp.d13C.South - (initialDelta),


dropSoil <- c("WeekSubWeek", # "Event",
              "CumOutDiss.g", "CumOutFilt.g", "CumOutAppMass.g",  "CumOutMELsm.g",
              # "CumAppMass.g",
              # "ID.N",
              "ID.T",  "Area.N", "Area.T", "Area.S",
              "comp.d13C.SE.North", "comp.d13C.SE.Talweg", "comp.d13C.SE.South",
              "ngC.SD","ngC.SE", "N_compsoil" )#, "N_ngC")
soils <- soils[ , !(names(soils) %in% dropSoil)]

soilsCheck <- soils[complete.cases(soils[ , "ID.N"]),]

names(soils)
```

```
##  [1] "Date.ti"               "Event"
##  [3] "Duration.Hrs"          "timeSinceApp"
##  [5] "timeSinceApp.NoSo"     "timeSinceApp.N"
##  [7] "timeSinceApp.T"        "timeSinceApp.S"
##  [9] "diss.d13C"             "SD.d13C"
## [11] "TotSMout.g"            "TotSMout.g.SD"
## [13] "MELsm.g"               "MELsm.g.SD"
## [15] "Appl.Mass.g"           "Appl.Mass.g.OT"
## [17] "CumAppMass.g"          "CumAppMass.g.N"
## [19] "CumAppMass.g.T"        "CumAppMass.g.S"
## [21] "CumAppMass.g.OT"       "CumAppMass.g.N.OT"
## [23] "CumAppMass.g.T.OT"     "CumAppMass.g.S.OT"
## [25] "iniCo.ug.g.N"          "iniCo.ug.g.T"
## [27] "iniCo.ug.g.S"          "CumOutSmeto.g"
## [29] "MassSoil.g.North"      "MassSoil.g.SD.North"
## [31] "Conc.mug.g.dry.soil.N" "comp.d13C.North"
## [33] "comp.d13C.SD.North"    "ID.N"
## [35] "MassSoil.g.Talweg"     "MassSoil.g.SD.Talweg"
## [37] "Conc.mug.g.dry.soil.T" "comp.d13C.Talweg"
## [39] "comp.d13C.SD.Talweg"   "MassSoil.g.South"
## [41] "MassSoil.g.SD.South"   "Conc.mug.g.dry.soil.S"
```

```
## [43] "comp.d13C.South"       "comp.d13C.SD.South"
## [45] "ID.S"                  "DD13C.North"
## [47] "DD13C.Talweg"          "DD13C.South"
## [49] "CatchMassSoil.g"       "CatchMassSoil.g.SD"
## [51] "BulkCatch.d13"         "BulkCatch.d13.SD"
## [53] "DD13.Bulk"             "Area.Catchment"
## [55] "BulkCatch.Conc"        "iniCo.Bulk"
```

```
timeApps <- soils[ , c("Date.ti", "timeSinceApp", "timeSinceApp.NoSo",
                       "timeSinceApp.N", "timeSinceApp.T" , "timeSinceApp.S",
                      "Event",
                      "iniCo.ug.g.N",  "iniCo.ug.g.T" , "iniCo.ug.g.S")]



# Quasi-Molten SOILS
soilGroups = read.csv2("Data/WeeklySoils_Rng.csv",
                       na.strings=c('#DIV/0!', '', 'NA'), header = TRUE)

soilGroups$Date.ti <- as.POSIXct(strptime(soilGroups$Date.ti,
                                          "%Y-%m-%d %H:%M", tz="EST")) # csv typos, option 1
sum(is.na(soilGroups$Date.ti)) == 0
```

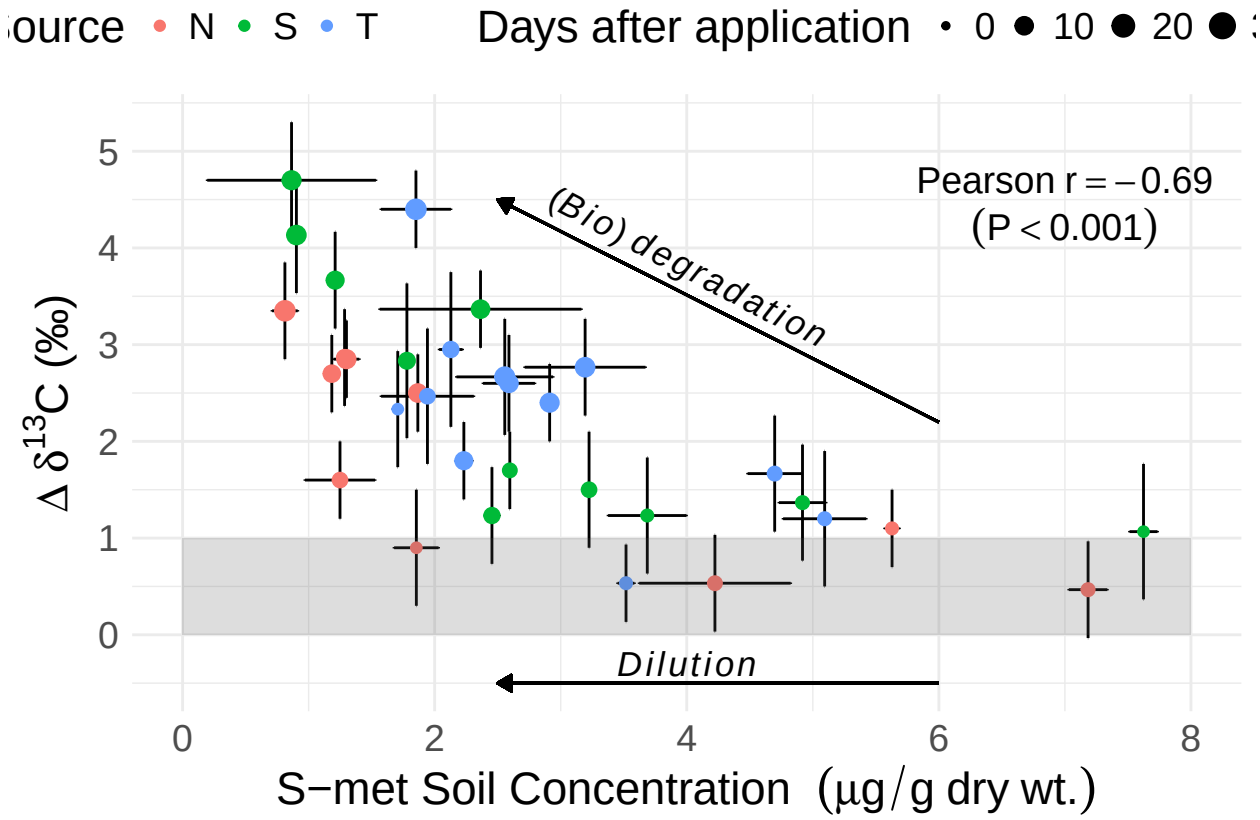
```
## [1] TRUE
```

```
soilGroups$comp.d13C <- ifelse(is.na(soilGroups$comp.d13C.SD), NA, soilGroups$comp.d13C)
# soilGroups$ngC.Label <- ifelse(soilGroups$ngC.mean < 10, "< 10 ng", "> 10 ng")

soilGroups <- subset(soilGroups, comp.d13C.SD <= 0.70)

#str(soils)

soilGrApp <- merge(soilGroups, timeApps, by = "Date.ti", all = F)
soilGrApp <- soilGrApp[complete.cases(soilGrApp[ , "timeSinceApp"]),]

soilGrApp$DD13C.comp <- ifelse(is.na(soilGrApp$comp.d13C.SD), NA, soilGrApp$DD13C.comp)
soilGrApp <- subset(soilGrApp, comp.d13C.SD <= 0.70)

# Propagated SD
soilGrApp$prop.d13C.SD = round((soilGrApp$comp.d13C.SD^2 + initialDeltaError^2)^0.5, 1)

cor.test(soilGroups$comp.d13C, soilGroups$Conc.mug.g.dry.soil)
```

```
##
##  Pearson's product-moment correlation
##
## data:  soilGroups$comp.d13C and soilGroups$Conc.mug.g.dry.soil
## t = -5.3104, df = 31, p-value = 8.817e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.8355218 -0.4545936
## sample estimates:
##       cor
## -0.6901877
```

```r
pearson_r <- cor.test(soilGroups$comp.d13C, soilGroups$Conc.mug.g.dry.soil)[4]
r_label <- sprintf("Pearson~r == %0.2f", pearson_r)
p_value <- cor.test(soilGroups$comp.d13C, soilGroups$Conc.mug.g.dry.soil)[3]

if (p_value < 0.0001){
  p_label <- "(P < 0.001)"
} else if (p_value < 0.001) {
  p_label <- "(P < 0.001)"
} else if (p_value < 0.015) {
  p_label <- ("P < 0.01")
} else {
  p_label <- "Check significance"
}

soilGrApp$Source <- ifelse(soilGrApp$Transect == "T", "Valley", "Plateau")
soilGrApp$Source <- as.factor(soilGrApp$Source)

soilGrApp.N <- subset(soilGrApp, soilGrApp$Transect == "N")
soilGrApp.T <- subset(soilGrApp, soilGrApp$Transect == "T")
soilGrApp.S <- subset(soilGrApp, soilGrApp$Transect == "S")

soilGrApp.N$timeSinceApp <- soilGrApp.N$timeSinceApp.N
soilGrApp.T$timeSinceApp <- soilGrApp.T$timeSinceApp.T
soilGrApp.S$timeSinceApp <- soilGrApp.S$timeSinceApp.S

dropAppDates <- c("timeSinceApp.NoSo", "timeSinceApp.N", "timeSinceApp.T", "timeSinceApp.S")
soilGrApp.N <- soilGrApp.N[ , !(names(soilGrApp.N) %in% dropAppDates)]
soilGrApp.T <- soilGrApp.T[ , !(names(soilGrApp.T) %in% dropAppDates)]
soilGrApp.S <- soilGrApp.S[ , !(names(soilGrApp.S) %in% dropAppDates)]

soilGrApp <- rbind(soilGrApp.N, soilGrApp.T)
soilGrApp <- rbind(soilGrApp, soilGrApp.S)

# comp.d13C.SD, replaced by: prop.d13C.SD

p <- ggplot(data = soilGrApp, aes(x=Conc.mug.g.dry.soil, y=DD13C.comp))+
  geom_errorbar(aes(ymin = DD13C.comp - prop.d13C.SD, ymax = DD13C.comp + prop.d13C.SD)) +
  geom_errorbarh(aes(xmin = Conc.mug.g.dry.soil - Conc.ComSoil.SD, xmax = Conc.mug.g.dry.soil + Conc.Co
  #stat_smooth(data = subset(soilGrApp, Conc.mug.g.dry.soil < 8),
  #            aes(x=Conc.mug.g.dry.soil, y=DD13C.comp), method = "lm", formula = y ~ poly(x, 2), se=F)
  # geom_point(aes(group = ID, size = timeSinceApp.NoSo)) + # , colour = Source)) +  # , shape = ngC.La
  geom_point(aes(group = Transect, colour = Transect, size = Wnum)) +
  # theme_bw() +
  theme_minimal() +
  theme(legend.position = "top",
        text = element_text(size=17)) +
  labs(size="   Days after application", colour="Source" ) + #, shape = "Mass Carbon") +
  ylab(expression(paste({Delta~delta}^"13","C", ' (\u2030)'))) +
  xlab(expression(paste("S-met Soil Concentration  ", {({mu}*g / g~dry~wt.)}))) +
  annotate("text", x = 7.0, y = 4.7, label = as.character(r_label), parse = T, size = 5) +
  annotate("text", x = 7.0, y = 4.2, label = p_label, parse = T, size = 5) +
  scale_size_continuous(range = c(1, 5), breaks= c(0, 10, 20, 30, 50), limits = c(0, 50)) +
  scale_y_continuous(breaks=c(0, 1, 2, 3 , 4 ,5) ) +
```

```
  # scale_size_continuous(range = c(1, 5)) +
  guides(size=guide_legend(nrow=1)) +
  annotate("text", x = 4, y = -0.3, label= "italic(Dilution)", parse=T, size = 4.5) +
  geom_segment(aes(x = 6, y = -0.5, xend = 2.5, yend = -0.5),
                   arrow = arrow(length = unit(1/2, 'picas'), type = "closed")) +
  annotate("text",
           x = 4.0, y = 3.78,
           label= "paste(\"(\", italic(Bio), \") \", italic(degradation) )", parse=T, size = 4.5, angle=
  geom_segment(aes(x = 6, y = 2.2, xend = 2.5, yend = 4.5),
                   arrow = arrow(length = unit(1/2, 'picas'), type = "closed")) +
  annotate("rect", xmin=0, xmax=8, ymin=0, ymax=propagatedError, alpha=0.2)

  # geom_rect(aes(xmin=0, xmax=8, ymin=-0.5, ymax=0.5), colour = "grey", alpha = 0.5) +
  #geom_hline(yintercept = 0.5, color = "dodgerblue4", linetype = "dotted") +
  #geom_hline(yintercept = 0, color = "dodgerblue3", linetype = "dotted") +
  #geom_hline(yintercept = -0.5, color = "dodgerblue3", linetype = "dotted")

  #scale_color_hue("Group") +
  #scale_fill_manual(
  #  "CI horizontal line", values=rep(1,4),
  #  guide=guide_legend(override.aes = list(colour=c("orange", "darkred"))),
  #  labels=c("CI of 95%", "CI of 99%")
  #)
  #geom_text_repel(data = subset(soilGrApp, (!is.na(ngC.Label) & Wnum > 10) ), aes(label=Wnum),
  #                arrow = arrow(length = unit(0.005, 'npc'), type = "closed"),
  #                force = 1,
  #                point.padding = unit(1.0, 'lines'),
  #                max.iter = 2e3,
  #                nudge_x = .2)
p
```




```
#
# ggsave(p, filename = "images/DDvsConc_soils_2.pdf", device = "pdf", dpi = 300,  scale = 2)


# Note: SD are error propagated: prop.d13C.SD
SAVE = F
PC = T
if (SAVE){
  if (PC){
    ggsave(p,
       filename = "D:/Documents/these_pablo/WriteUp/Alteck_PNAS_LaTeX/images/DDvsConc_soils.pdf",
       device = "pdf", dpi = 600,  scale = 1, # )# ,
       width = 8.7, height = 6)
  } else {
    ggsave(p,
     filename = "/Users/DayTightChunks/Documents/PhD/Writeups/PNAS/Alteck_PNAS_LaTeX/images/DDvsConc_so
      device=cairo_pdf, dpi = 600,  scale = 1, # )# ,
       width = 8.7, height = 6)
  }
}
```

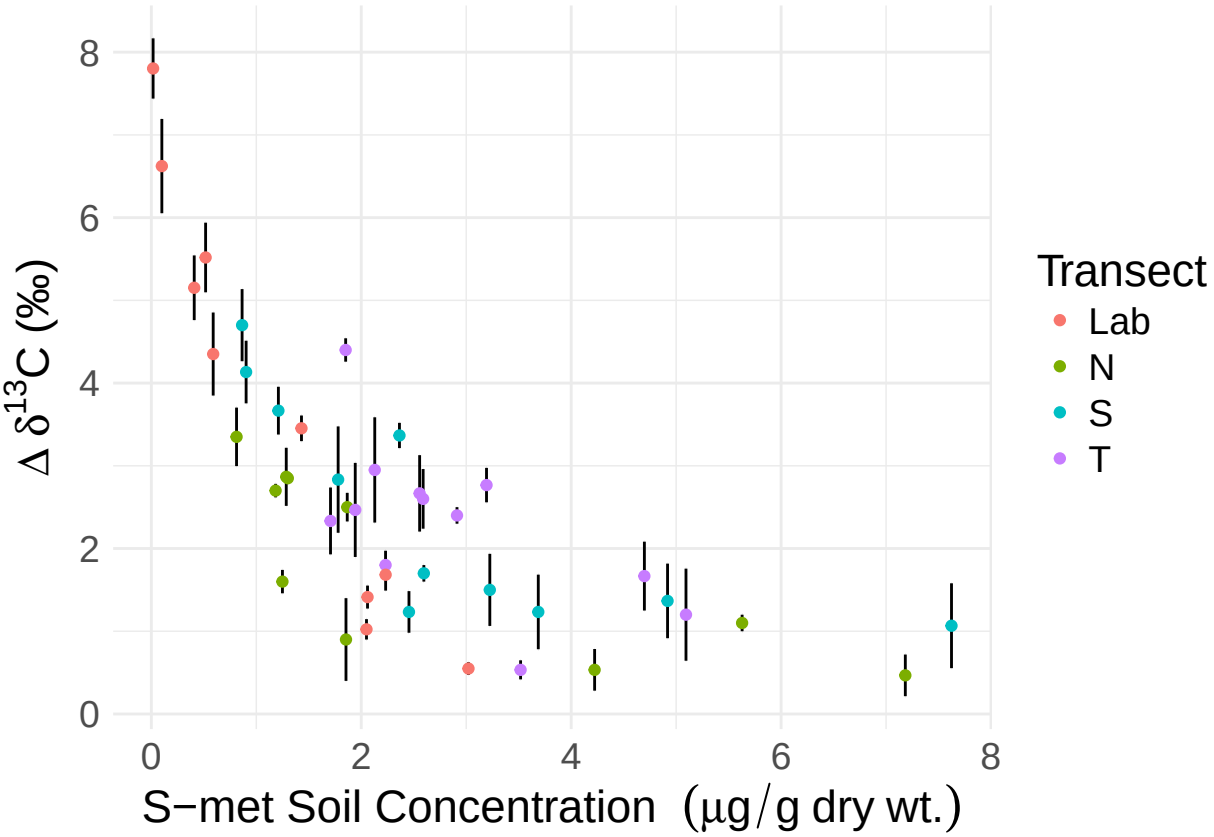
Merge with Lab experiment

```
names(soilGrApp)
```

```
##  [1] "Date.ti"             "ID"                  "Transect"
##  [4] "Wnum"                "Date.Soil"           "Conc.mug.g.dry.soil"
##  [7] "Conc.ComSoil.SD"     "Mass.Soil.g"         "theta.prct"
## [10] "N_compsoil"          "comp.d13C"           "comp.d13C.SD"
## [13] "N_isoComp"           "prctError"           "DD13C.comp"
## [16] "comp.IMP.d13C"       "MassSoil.g"          "MassSoil.g.SD"
## [19] "Area.N"              "Area.T"              "Area.S"
## [22] "timeSinceApp"        "Event"               "iniCo.ug.g.N"
## [25] "iniCo.ug.g.T"        "iniCo.ug.g.S"        "prop.d13C.SD"
## [28] "Source"
```

```
soilGrApp$C.ini = ifelse(soilGrApp$Transect == "N", soilGrApp$iniCo.ug.g.N,
                         ifelse(soilGrApp$Transect == "T", soilGrApp$iniCo.ug.g.T,
                                ifelse(soilGrApp$Transect == "S", soilGrApp$iniCo.ug.g.S, NA)

))
field = soilGrApp[, c("Transect", "DD13C.comp", "comp.d13C", "comp.d13C.SD", "Conc.mug.g.dry.soil", "Co
                      )]
# Change names
names(field) <- c("Transect", "DD13", "d13", "d13.SD", "C.SM", "C.SD", "C.ini")
field$Type = "Field"

# Import raw data
enrich = read.csv2('Data/EnrichmentExp.csv', sep = ";", dec = ".", header = T)

inital = subset(enrich, Days == 1)
iniDelta = mean(inital$Delta)
enrich$DD13 <- enrich$Delta - initialDelta
enrich$DD13m <- enrich$Delta - iniDelta

biotic = subset(enrich, Type == "Biotic" & Temp == 20)
# biotic = biotic[, c("Type", "DD13m", "SD", "C.SM")] # mean initial
biotic = biotic[, c("Type", "DD13", "Delta", "SD", "C.SM")]
names(biotic) = c("Type", "DD13", "d13", "d13.SD", "C.SM")
biotic$C.ini = c_ini
biotic$C.SD = NA
biotic$Transect = NA

compare = rbind(field, biotic)
compare$Transect = as.character(compare$Transect)
compare$Transect = ifelse(is.na(compare$Transect), "Lab", compare$Transect)

mix = ggplot(data = compare, aes(x=C.SM, y=DD13))+
  geom_errorbar(aes(ymin = DD13 - d13.SD, ymax = DD13 + d13.SD)) +
  # geom_errorbarh(aes(xmin = C.SM - C.SD, xmax = C.SM + C.SD)) +
  geom_point(aes(group = Transect, colour = Transect)) +
  theme_minimal() +
  theme(legend.position = "right",
        text = element_text(size=17)) +
  guides(size=guide_legend(ncol=1)) +
```

```
  ylab(expression(paste({Delta~delta}^"13","C", ' (\u2030)'))) +
  xlab(expression(paste("S-met Soil Concentration  ", {({mu}*g / g~dry~wt.)})))

if (F) {
  mix + labs(size="   Days after application", colour="Source" ) + #, shape = "Mass Carbon") +

  annotate("text", x = 7.0, y = 4.7, label = as.character(r_label), parse = T, size = 5) +
  annotate("text", x = 7.0, y = 4.2, label = p_label, parse = T, size = 5) +
  #scale_size_continuous(range = c(1, 5), breaks= c(0, 10, 20, 30, 50), limits = c(0, 50)) +
  #scale_y_continuous(breaks=c(0, 1, 2, 3 , 4 ,5) ) +
  # scale_size_continuous(range = c(1, 5)) +

  annotate("text", x = 4, y = -0.3, label= "italic(Dilution)", parse=T, size = 4.5) +
  geom_segment(aes(x = 6, y = -0.5, xend = 2.5, yend = -0.5),
                   arrow = arrow(length = unit(1/2, 'picas'), type = "closed")) +
  annotate("text",
           x = 4.0, y = 3.78,
           label= "paste(\"(\", italic(Bio), \") \", italic(degradation) )", parse=T, size = 4.5, angle=
  geom_segment(aes(x = 6, y = 2.2, xend = 2.5, yend = 4.5),
                   arrow = arrow(length = unit(1/2, 'picas'), type = "closed")) +
  annotate("rect", xmin=0, xmax=8, ymin=0, ymax=propagatedError, alpha=0.2)
}

mix
```



```
# ggsave(mix, filename = "D:/Documents/these_pablo/WriteUp/Images/DDvsConc_soils.png" , width = 8.7, he
```

Rayleigh

```
# compare$yRaleigh <- log((1000+initialDelta+compare$DD13)/(1000+initialDelta)) # Elsner 2005
compare$yRaleigh = 1000*log( (10^-3*compare$d13+1) / (10^-3*initialDelta+1)) # Van Breukelen, 2007
compare$xRaleigh <- log(compare$C.SM/compare$C.ini)

compare.lm <-lm(yRaleigh~xRaleigh, data= subset(compare, Type == "Biotic"))
cofsoil <- as.numeric(coef(compare.lm)[2])

summary(compare.lm)
```

```
##
## Call:
## lm(formula = yRaleigh ~ xRaleigh, data = subset(compare, Type ==
##     "Biotic"))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.16976 -0.88704  0.00485  0.74926  1.54389
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.7194     0.4370   3.935  0.00433 **
## xRaleigh     -1.4763     0.2048  -7.208 9.17e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.009 on 8 degrees of freedom
## Multiple R-squared:  0.8666, Adjusted R-squared:  0.8499
## F-statistic: 51.96 on 1 and 8 DF,  p-value: 9.17e-05
```

```
rexp = ggplot(data = subset(compare,  !is.na(yRaleigh) ), aes(x=xRaleigh, y=yRaleigh, group = Type, col
  geom_point() +
  theme_minimal() +
  stat_smooth(method = "lm", formula = y ~ x, se=F) +
  theme(legend.position = "right",
        text = element_text(size=17)) +
  guides(size=guide_legend(ncol=1)) +
  ylab(expression(paste(ln~(R["C"["t"]]/R["C"["0"]])))) +
  xlab(expression(paste(ln~("C"["t"]/"C"["0"]))))

ggsave(rexp, filename = "D:/Documents/these_pablo/WriteUp/Images/Rayleigh.png" , width = 8.7, height = 
```

Color pallette

```
library(scales)
## Color palette
```

```
show_col(hue_pal()(12))
```