

# Kinetic Model Coefficient Analysis

Marc Pérez

2025-05-22

Model Agroscope

$$Y_{rel} \sim A * (1 - e^{rate * P_{CO_2} + Env})$$

Wir ersetzen nur rate mit unserer Schätzung k:

$$Y_{rel} \sim A * (1 - e^{k * P_{CO_2} + Env})$$

Sind unsere Modelparameter gute Prediktoren??

$$Y_{rel} \sim A * (1 - e^{k * PS + Env})$$

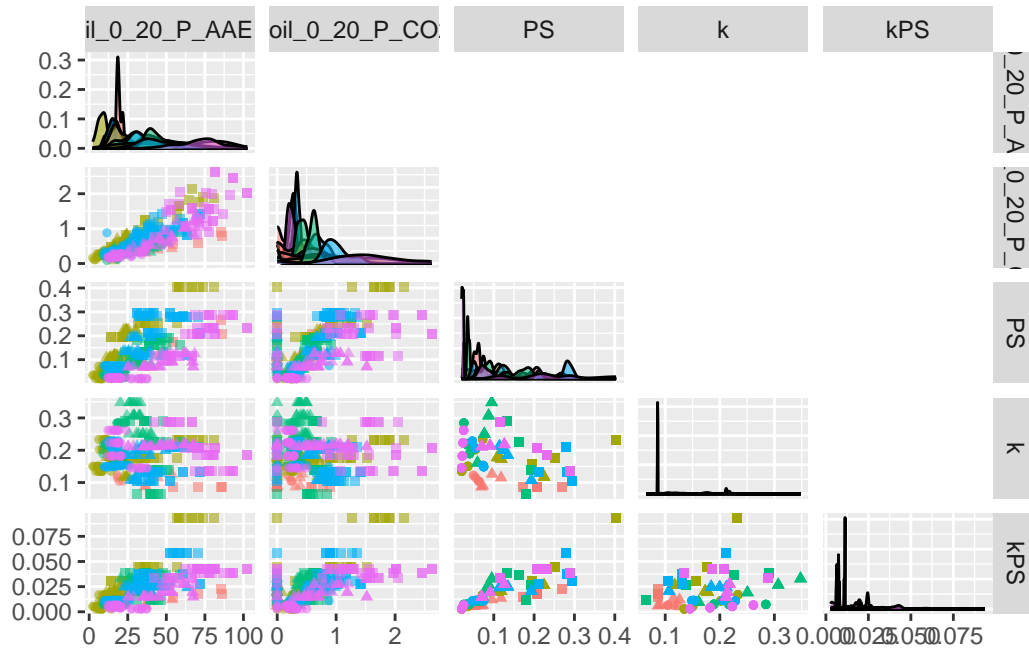
Es gibt noch die Kovariaten Niederschlag pro Jahr, Jahresdurchschnittstemperatur und Temperatur in Jugendphase

```
#|code-fold: true  
#|tidy: true
```

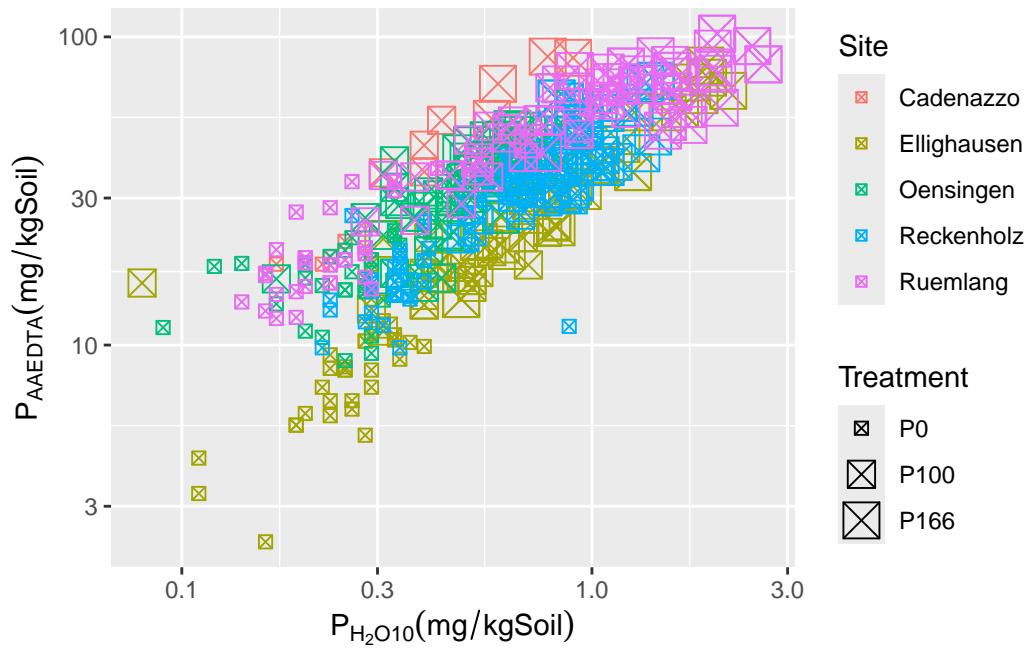
```
library(GGally)
```

```
Registered S3 method overwritten by 'GGally':  
  method from  
+ .gg      ggplot2
```

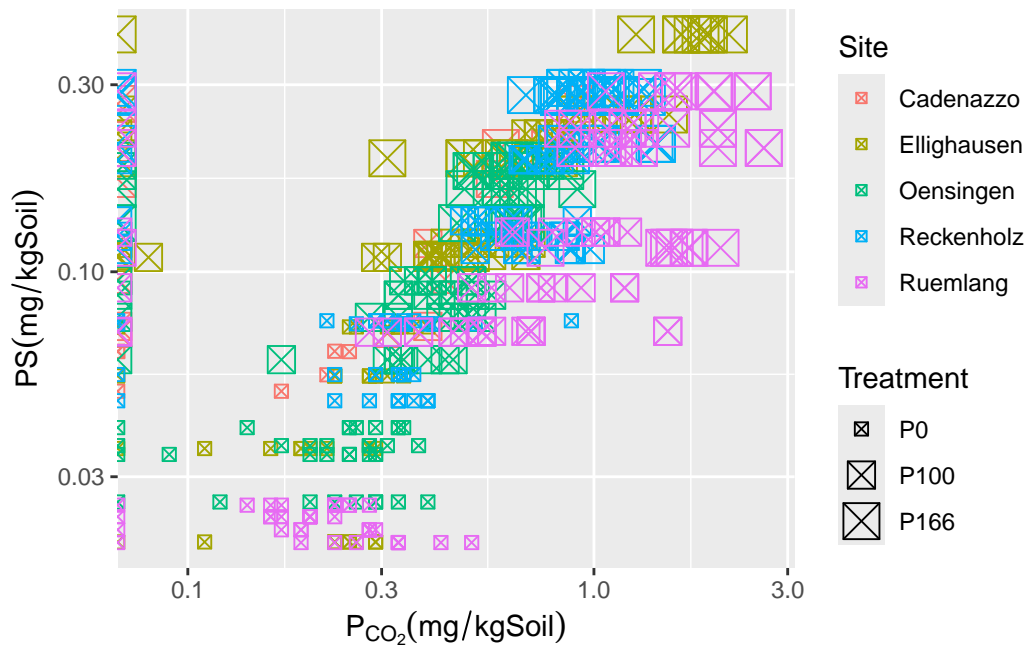
```
ggpairs(D,
  aes(col=Site, shape = Treatment,alpha = 0.6),
  columns = c("soil_0_20_P_AAE10", "soil_0_20_P_CO2", "PS", "k", "kPS"),
  lower = list(continuous = wrap("points", size = 1.3)),
  upper = list(continuous = "blank", combo = "blank", discrete = "blank")) # Adjust size here
```



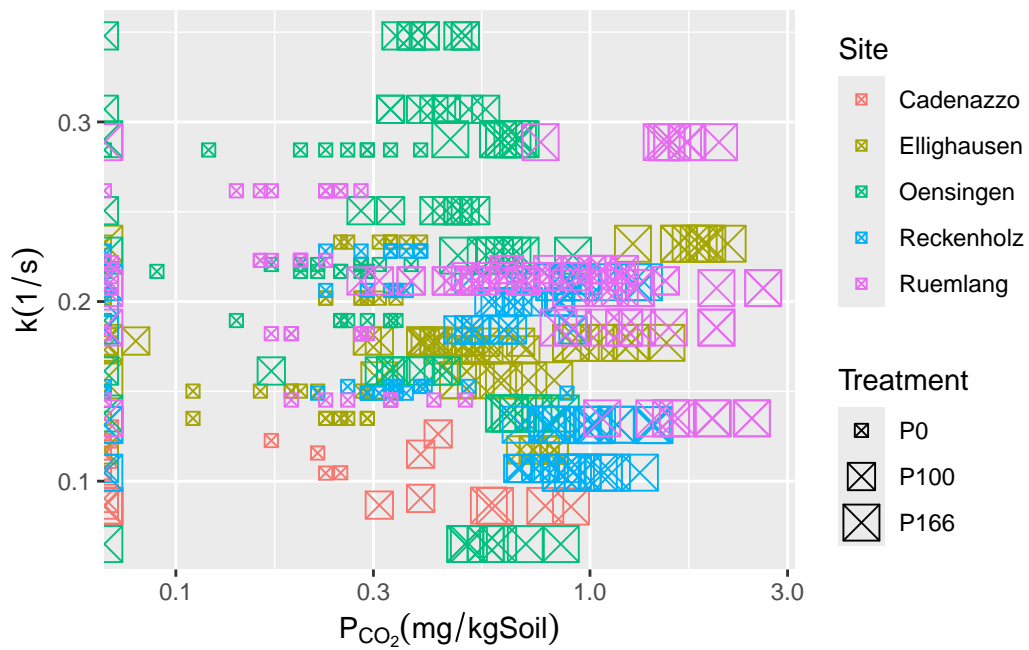
```
p6 <- ggplot(D,aes(y=soil_0_20_P_AAE10, x=soil_0_20_P_CO2, col=Site, size = Treatment)) +
  geom_point(shape = 7) +
  scale_x_log10() + scale_y_log10() +
  labs(x=TeX("$P_{H_2O10}(mg/kg Soil)$"),
       y=TeX("$P_{AAEDTA}(mg/kg Soil)$")); p6
```



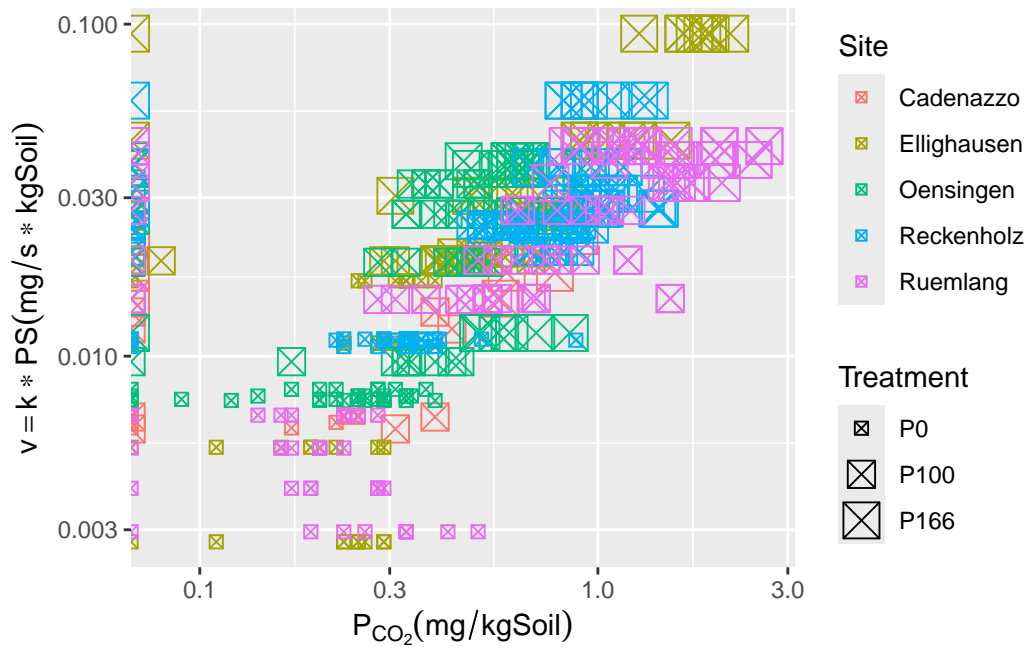
```
p7 <- ggplot(D,aes(y=PS, x=soil_0_20_P_CO2, col=Site, size = Treatment)) +
  geom_point(shape = 7) +
  scale_x_log10() + scale_y_log10() +
  labs(x=TeX("$P_{CO_2}$ (mg/kg Soil)$"),
       y=TeX("$PS$ (mg/kg Soil)$")); p7
```



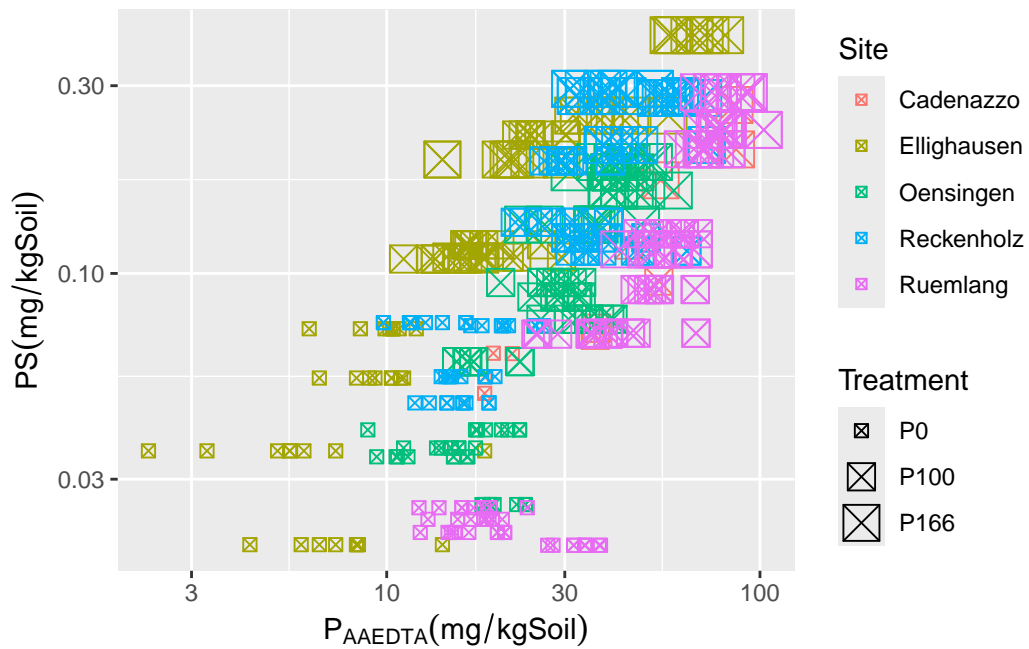
```
p8 <- ggplot(D,aes(y=k, x=soil_0_20_P_CO2, col=Site, size = Treatment)) +
  geom_point(shape = 7) +
  scale_x_log10() +
  labs(x=TeX("$P_{CO_2}$ (mg/kg Soil)$"),
       y=TeX("$k(1/s)$")); p8
```



```
p9 <- ggplot(D,aes(y=k*PS, x=soil_0_20_P_CO2, col=Site, size = Treatment)) +
  geom_point(shape = 7) +
  scale_x_log10() + scale_y_log10() +
  labs(x=TeX("$P_{CO_2}$ (mg/kg Soil)$"),
       y=TeX("$v=k*PS$ (mg/s*kg Soil)$")); p9
```

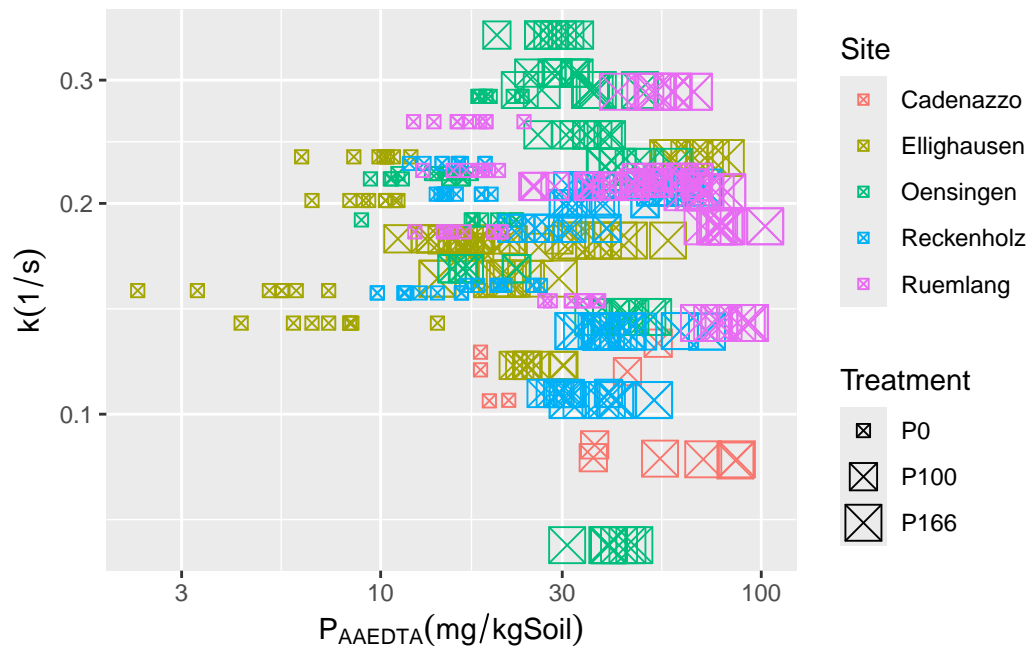


```
p11 <- ggplot(D,aes(y=PS, x=soil_0_20_P_AAE10, col=Site, size = Treatment)) +
  scale_x_log10() + scale_y_log10() +
  geom_point(shape = 7) +
  labs(x=TeX("$P_{AAEDTA}$ (mg/kg Soil)"),
       y=TeX("$PS$ (mg/kg Soil)")); p11
```



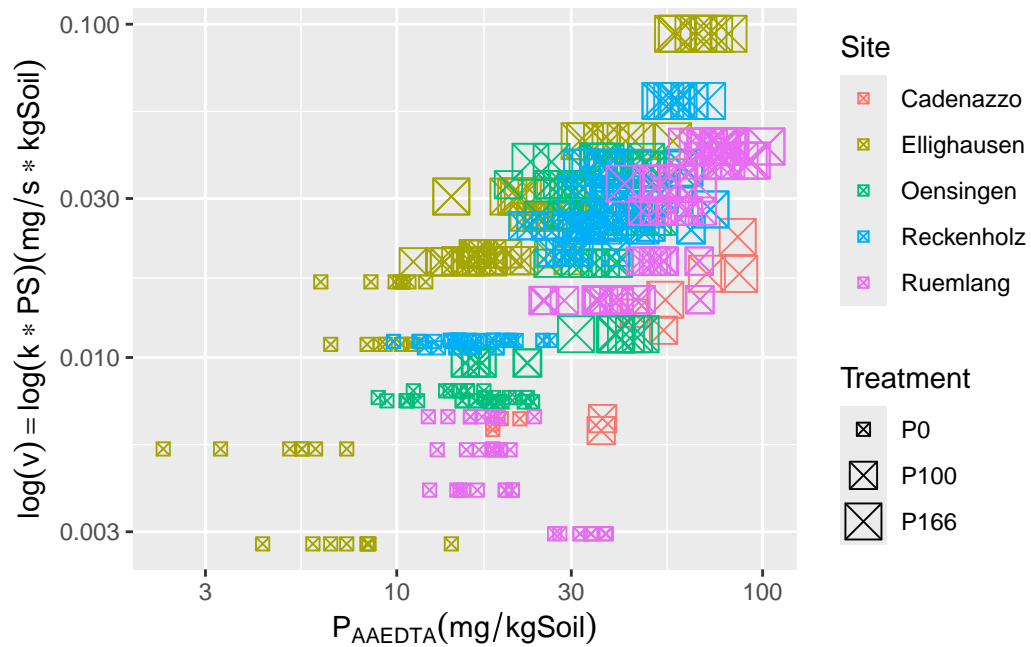
```
p12 <- ggplot(D,aes(y=k, x=soil_0_20_P_AAE10, col=Site, size = Treatment)) +
  geom_point(shape = 7) +
  scale_x_log10() + scale_y_log10() +
  labs(x=TeX("$P_{AAEDTA}(mg/kg Soil)$"),
       y=TeX("$k(1/s)$"))
```

p12



```
p13 <- ggplot(D,aes(y=k*PS, x=soil_0_20_P_AAE10, col=Site, size = Treatment)) +
  scale_x_log10() + scale_y_log10() +
  geom_point(shape = 7) +
  labs(x=TeX("$P_{AAEDTA}(mg/kg Soil)$"),
       y=TeX("$\log(v)=\log(k*PS)(mg/s*kg Soil)$"))
```

p13



Nun noch die Linearen Regressionen, die ausstehend sind:

(1|year) + (1|Site) + (1|Site:block) + (Treatment|Site)

Random intercept per year and site, block nested in site. and Treatment nested in site (could also be modelled as a random slope to allow for correlations)

```
#|code-fold: true
#|tidy: true

# Wovon hängen Modelparameter ab?

library(lmerTest)
```

Attaching package: 'lmerTest'

The following object is masked from 'package:lme4':

lmer

The following object is masked from 'package:stats':

step

```
fit.soil.PS <- lmer(log(PS) ~ soil_0_20_clay+ soil_0_20_pH_H2O + soil_0_20_Corg + soil_0_20_P_C02)
```

boundary (singular) fit: see help('isSingular')

```
fit.soil.k <- lmer(k ~ soil_0_20_clay+ soil_0_20_pH_H2O + soil_0_20_Corg + soil_0_20_P_C02)
```

boundary (singular) fit: see help('isSingular')

```
fit.soil.kPS <- lmer(I(log(k*PS))~ soil_0_20_clay+ soil_0_20_pH_H2O + soil_0_20_Corg + soil_0_20_P_C02)
```

boundary (singular) fit: see help('isSingular')

```
fit.soil.C02 <- lmer(log(soil_0_20_P_C02)~ soil_0_20_clay+ soil_0_20_pH_H2O + soil_0_20_Corg + soil_0_20_P_AAE10)
```

boundary (singular) fit: see help('isSingular')

```
fit.soil.AAE10 <- lmer(log(soil_0_20_P_AAE10)~ soil_0_20_clay+ soil_0_20_pH_H2O + soil_0_20_Corg + soil_0_20_P_C02)
```

```
fit.kin.Yrel <- lmer(Ymain_rel ~ k * log(PS) + Treatment + (1|year) + (1|Site))
```

boundary (singular) fit: see help('isSingular')

```
fit.kin.Puptake <- lmer(annual_P_uptake ~ k * log(PS) + Treatment + (1|year) + (1|Site))
```

boundary (singular) fit: see help('isSingular')

```
fit.kin.Pbalance <- lmer(annual_P_balance ~ k * log(PS) + Treatment + (1|year) + (1|Site))
```

boundary (singular) fit: see help('isSingular')

```
anova(fit.soil.PS)
```



```
Type III Analysis of Variance Table with Satterthwaite's method
```

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
soil_0_20_clay	0.0719	0.0719	1	70.835	2.3900	0.1265690
soil_0_20_pH_H2O	0.0152	0.0152	1	89.035	0.5061	0.4787086
soil_0_20_Corg	0.4704	0.4704	1	65.081	15.6423	0.0001915 ***
soil_0_20_silt	0.1061	0.1061	1	70.745	3.5286	0.0644392 .
Treatment	10.0459	5.0230	2	6.055	167.0386	5.047e-06 ***

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#summary(glht(fit.PS))
# Fazit: PS wird von treatment stark beeinflusst, k eher nicht (dafür von site)
anova(fit.soil.k)
```

```
Type III Analysis of Variance Table with Satterthwaite's method
```

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
soil_0_20_clay	0.0098143	0.0098143	1	69.314	10.0428	0.002277 **
soil_0_20_pH_H2O	0.0091422	0.0091422	1	102.384	9.3551	0.002838 **
soil_0_20_Corg	0.0014112	0.0014112	1	98.359	1.4440	0.232372
soil_0_20_silt	0.0046704	0.0046704	1	75.910	4.7792	0.031888 *
Treatment	0.0059043	0.0029521	2	5.405	3.0209	0.131613

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(glht(fit.soil.k))
```

### Simultaneous Tests for General Linear Hypotheses

```
Fit: lmer(formula = k ~ soil_0_20_clay + soil_0_20_pH_H2O + soil_0_20_Corg +
  soil_0_20_silt + Treatment + (1 | year) + (1 | Site) + (1 |
  Site:block) + (1 | Site:Treatment), data = D)
```

#### Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept) == 0	0.074168	0.150771	0.492	0.9965
soil_0_20_clay == 0	-0.007001	0.002209	-3.169	<0.01 **
soil_0_20_pH_H2O == 0	0.033720	0.011024	3.059	0.0139 *
soil_0_20_Corg == 0	-0.034533	0.028737	-1.202	0.7769
soil_0_20_silt == 0	0.005864	0.002683	2.186	0.1662
TreatmentP100 == 0	0.003910	0.015506	0.252	0.9999

```
TreatmentP166 == 0    -0.031147    0.015685   -1.986    0.2537
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

```
anova(fit.soil.kPS)
```

```
Type III Analysis of Variance Table with Satterthwaite's method
              Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
soil_0_20_clay  0.0055 0.00551      1  77.626  0.1043 0.747639
soil_0_20_pH_H2O 0.3773 0.37731      1 101.942  7.1335 0.008807 **
soil_0_20_Corg   0.0105 0.01052      1  93.639  0.1990 0.656575
soil_0_20_silt   0.0036 0.00360      1  80.228  0.0681 0.794743
Treatment        4.0339 2.01697      2   5.847 38.1329 0.000442 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(glht(fit.soil.kPS))
```

#### Simultaneous Tests for General Linear Hypotheses

```
Fit: lmer(formula = I(log(k * PS)) ~ soil_0_20_clay + soil_0_20_pH_H2O +
      soil_0_20_Corg + soil_0_20_silt + Treatment + (1 | year) +
      (1 | Site) + (1 | Site:block) + (1 | Site:Treatment), data = D)
```

#### Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept) == 0	-6.657570	1.107392	-6.012	<0.001 ***
soil_0_20_clay == 0	-0.005316	0.016463	-0.323	0.9997
soil_0_20_pH_H2O == 0	0.216354	0.081005	2.671	0.0483 *
soil_0_20_Corg == 0	0.094691	0.212278	0.446	0.9980
soil_0_20_silt == 0	0.005221	0.020000	0.261	0.9999
TreatmentP100 == 0	1.064948	0.189188	5.629	<0.001 ***
TreatmentP166 == 0	1.634290	0.190050	8.599	<0.001 ***

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

```
anova(fit.kin.Yrel)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
k	146.11	146.11	1	151.805	0.4824	0.4884
log(PS)	44.91	44.91	1	226.958	0.1483	0.7005
Treatment	740.92	370.46	2	4.838	1.2232	0.3716
k:log(PS)	324.35	324.35	1	172.913	1.0710	0.3022

```
anova(fit.kin.Puptake)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
k	41.986	41.986	1	456.19	0.3035	0.5819
log(PS)	6.315	6.315	1	457.82	0.0457	0.8309
Treatment	129.470	64.735	2	443.37	0.4680	0.6266
k:log(PS)	39.416	39.416	1	457.86	0.2850	0.5937

```
anova(fit.soil.CO2)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
soil_0_20_clay	0.0118	0.01181	1	48.798	0.1428	0.7071250
soil_0_20_pH_H2O	0.0686	0.06858	1	65.341	0.8297	0.3657041
soil_0_20_Corg	0.2993	0.29934	1	37.017	3.6216	0.0648334 .
soil_0_20_silt	0.0665	0.06645	1	22.514	0.8040	0.3793909
Treatment	4.8977	2.44886	2	5.827	29.6281	0.0008839 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
anova(fit.soil.AAE10)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
soil_0_20_clay	0.0491	0.0491	1	58.650	1.1361	0.2908517
soil_0_20_pH_H2O	0.2473	0.2473	1	75.287	5.7214	0.0192552 *
soil_0_20_Corg	0.2830	0.2830	1	45.764	6.5490	0.0138669 *
soil_0_20_silt	0.0572	0.0572	1	87.560	1.3231	0.2531704
Treatment	7.5352	3.7676	2	4.841	87.1720	0.0001598 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
anova(fit.kin.Pbalance)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
k	20.3	20.3	1	457.51	0.0960	0.7568
log(PS)	12.9	12.9	1	455.60	0.0613	0.8046
Treatment	15488.3	7744.1	2	379.27	36.7144	2.658e-15 ***
k:log(PS)	10.1	10.1	1	455.83	0.0477	0.8272

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
summary(fit.kin.Pbalance)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
lmerModLmerTest]

Formula: annual\_P\_balance ~ k \* log(PS) + Treatment + (1 | year) + (1 |  
Site) + (1 | Site:block) + (1 | Site:Treatment)

Data: D

REML criterion at convergence: 3854.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.8654	-0.5354	-0.0249	0.5914	3.3879

Random effects:

Groups	Name	Variance	Std.Dev.
Site:block	(Intercept)	0.00	0.000
Site:Treatment	(Intercept)	0.00	0.000
year	(Intercept)	51.80	7.197
Site	(Intercept)	21.44	4.631
Residual		210.93	14.523

Number of obs: 471, groups:

Site:block, 20; Site:Treatment, 15; year, 8; Site, 5

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	-16.980	10.354	231.810	-1.640	0.102
k	-12.679	40.918	457.507	-0.310	0.757
log(PS)	-0.916	3.701	455.596	-0.248	0.805
TreatmentP100	21.950	2.907	382.869	7.552	3.18e-13 ***

```
TreatmentP166 37.991      4.435 317.155  8.566 4.74e-16 ***
k:log(PS)      -3.788      17.345 455.832 -0.218  0.827
```

---

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Correlation of Fixed Effects:

```
          (Intr) k      lg(PS) TrP100 TrP166
k          -0.590
log(PS)      0.888 -0.713
TretmntP100 -0.542 -0.165 -0.407
TretmntP166 -0.627 -0.126 -0.481  0.868
k:log(PS)    -0.565  0.944 -0.776 -0.140 -0.126
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

```
fit.kin.Pbalance |> r.squaredGLMM()
```

```
          R2m      R2c
[1,] 0.4228263 0.5715903
```

```
fit.kin.Puptake |> r.squaredGLMM()
```

```
          R2m      R2c
[1,] 0.01723874 0.6121275
```

```
fit.kin.Yrel |> r.squaredGLMM()
```

```
          R2m      R2c
[1,] 0.03304352 0.8042098
```

```
# Verhalten der Modelparameter und Ertragsdaten auf P-CO2 und P-AAE10
```

Since we now model two measurement methods, we do not expect correlations by Site/year/etc

```
#|code-fold: true
#|tidy: true
# fit.PS      <- lm(PS ~ soil_0_20_P_CO2 + soil_0_20_P_AAE10, D)
fit.grud.PS   <- lm(log(PS) ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10), D)
```

```

fit.grud.k      <- lm(k ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10), D)
fit.grud.kPS    <- lm(I(log(k*PS)) ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10), D)

fit.grud.Yrel   <- lmer(Ymain_rel ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10) + 1)

# this is hopeless, since cannot log becaus of 0's
fit.grud.Puptake <- lmer(annual_P_uptake ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10), D)

```

boundary (singular) fit: see help('isSingular')

```

fit.grud.Pbalance <- lmer(annual_P_balance ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10), D)

```

boundary (singular) fit: see help('isSingular')

```

#summary(glht(fit.PS))
# Fazit: PS wird von treatment stark beeinflusst, k eher nicht (dafür von site)
summary(glht(fit.grud.PS))

```

#### Simultaneous Tests for General Linear Hypotheses

```

Fit: lm(formula = log(PS) ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10),
data = D)

```

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept) == 0	-1.59063	0.23863	-6.666	<1e-04 ***
log(soil_0_20_P_CO2) == 0	1.02613	0.06084	16.866	<1e-04 ***
log(soil_0_20_P_AAE10) == 0	-0.02995	0.06127	-0.489	0.793

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Adjusted p values reported -- single-step method)

```

summary(glht(fit.grud.k))

```

#### Simultaneous Tests for General Linear Hypotheses

```

Fit: lm(formula = k ~ log(soil_0_20_P_CO2) + log(soil_0_20_P_AAE10),
data = D)

```

```
data = D)
```

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept) == 0	0.103889	0.028977	3.585	< 0.001 ***
log(soil_0_20_P_C02) == 0	-0.026427	0.007388	-3.577	< 0.001 ***
log(soil_0_20_P_AAE10) == 0	0.021027	0.007440	2.826	0.00847 **

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

```
summary(glht(fit.grud.kPS))
```

#### Simultaneous Tests for General Linear Hypotheses

```
Fit: lm(formula = I(log(k * PS)) ~ log(soil_0_20_P_C02) + log(soil_0_20_P_AAE10),  
data = D)
```

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept) == 0	-3.63331	0.24159	-15.039	<0.001 ***
log(soil_0_20_P_C02) == 0	0.90485	0.06160	14.690	<0.001 ***
log(soil_0_20_P_AAE10) == 0	0.04814	0.06203	0.776	0.587

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

```
summary(fit.grud.Yrel)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
lmerModLmerTest]

Formula:

```
Ymain_rel ~ log(soil_0_20_P_C02) + log(soil_0_20_P_AAE10) + Treatment +  
(1 | year) + (1 | Site) + (1 | Site:block) + (1 | Site:Treatment)
```

Data: D

REML criterion at convergence: 1726.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

-2.98805 -0.62531 -0.03449 0.57660 3.15994

Random effects:

Groups	Name	Variance	Std.Dev.
Site:block	(Intercept)	1.815	1.347
Site:Treatment	(Intercept)	26.585	5.156
year	(Intercept)	175.180	13.236
Site	(Intercept)	22.431	4.736
Residual		194.780	13.956

Number of obs: 212, groups:

Site:block, 16; Site:Treatment, 12; year, 5; Site, 4

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	70.659	16.451	69.722	4.295	5.54e-05 ***
log(soil_0_20_P_CO2)	1.155	3.967	152.164	0.291	0.7713
log(soil_0_20_P_AAE10)	8.099	4.176	78.407	1.939	0.0561 .
TreatmentP100	4.062	5.052	9.299	0.804	0.4414
TreatmentP166	1.599	6.208	18.950	0.258	0.7996

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	l(_0_20_P_C	l(_0_20_P_A	TrP100
l(_0_20_P_C	0.722			
l(_0_20_P_A	-0.867	-0.602		
TretmntP100	0.019	-0.179	-0.278	
TretmntP166	0.013	-0.329	-0.307	0.663

```
summary(fit.grud.Puptake)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]

Formula: annual\_P\_uptake ~ log(soil\_0\_20\_P\_CO2) + log(soil\_0\_20\_P\_AAE10) + Treatment + (1 | year) + (1 | Site) + (1 | Site:block) + (1 | Site:Treatment)

Data: D

REML criterion at convergence: 3112.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----



-2.5656 -0.4852 0.0615 0.5877 4.0429

Random effects:

Groups	Name	Variance	Std.Dev.
Site:block	(Intercept)	0.000	0.000
Site:Treatment	(Intercept)	0.000	0.000
year	(Intercept)	144.870	12.036
Site	(Intercept)	8.992	2.999
Residual		107.132	10.350

Number of obs: 412, groups:

Site:block, 20; Site:Treatment, 15; year, 7; Site, 5

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	14.2487	8.9343	57.6545	1.595	0.116
log(soil_0_20_P_C02)	2.0836	1.9505	283.2590	1.068	0.286
log(soil_0_20_P_AAE10)	0.8228	2.0797	128.3639	0.396	0.693
TreatmentP100	1.5242	1.8127	372.9659	0.841	0.401
TreatmentP166	1.1812	2.5495	364.9432	0.463	0.643

Correlation of Fixed Effects:

```
(Intr) 1(_0_20_P_C 1(_0_20_P_A TrP100
1(_0_20_P_C 0.679
1(_0_20_P_A -0.808 -0.613
TretmntP100 0.109 -0.267 -0.374
TretmntP166 0.071 -0.408 -0.357 0.797
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

```
summary(fit.grud.Pbalance)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
lmerModLmerTest]

Formula: annual\_P\_balance ~ log(soil\_0\_20\_P\_C02) + log(soil\_0\_20\_P\_AAE10) +  
Treatment + (1 | year) + (1 | Site) + (1 | Site:block) +  
(1 | Site:Treatment)

Data: D

REML criterion at convergence: 3269.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

-4.3875 -0.5837 -0.1052 0.6817 2.9298

Random effects:

Groups	Name	Variance	Std.Dev.
Site:block	(Intercept)	0.00	0.000
Site:Treatment	(Intercept)	0.00	0.000
year	(Intercept)	61.91	7.868
Site	(Intercept)	10.76	3.280
Residual		160.52	12.670

Number of obs: 412, groups:

Site:block, 20; Site:Treatment, 15; year, 7; Site, 5

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	-16.640	9.699	84.718	-1.716	0.0899 .
log(soil_0_20_P_CO2)	-5.004	2.365	257.039	-2.116	0.0353 *
log(soil_0_20_P_AAE10)	-1.120	2.504	104.202	-0.447	0.6556
TreatmentP100	22.377	2.210	361.468	10.127	<2e-16 ***
TreatmentP166	38.888	3.105	349.644	12.523	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

```
(Intr) l(_0_20_P_C l(_0_20_P_A TrP100
l(_0_20_P_C 0.751
l(_0_20_P_A -0.895 -0.609
TretmntP100 0.114 -0.273 -0.369
TretmntP166 0.072 -0.414 -0.354 0.796
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

```
fit.grud.Pbalance |> r.squaredGLMM()
```

```
          R2m          R2c
[1,] 0.4145326 0.5969757
```

```
fit.grud.Puptake |> r.squaredGLMM()
```

```
          R2m          R2c
[1,] 0.02058153 0.5979709
```

```
fit.grud.Yrel |> r.squaredGLMM()
```

```
           R2m      R2c  
[1,] 0.09773311 0.5823498
```

```
save.image(file = "~/Documents/Master Thesis/Master-Thesis-P-kinetics/data/results_coefficien
```