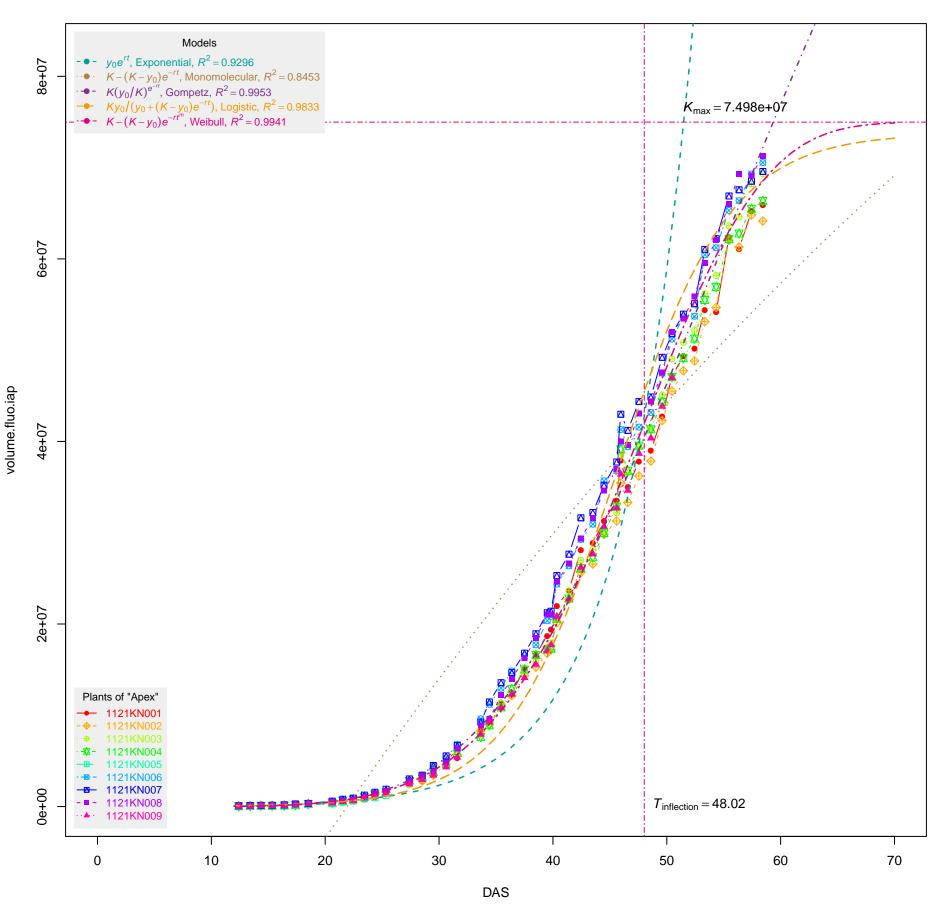
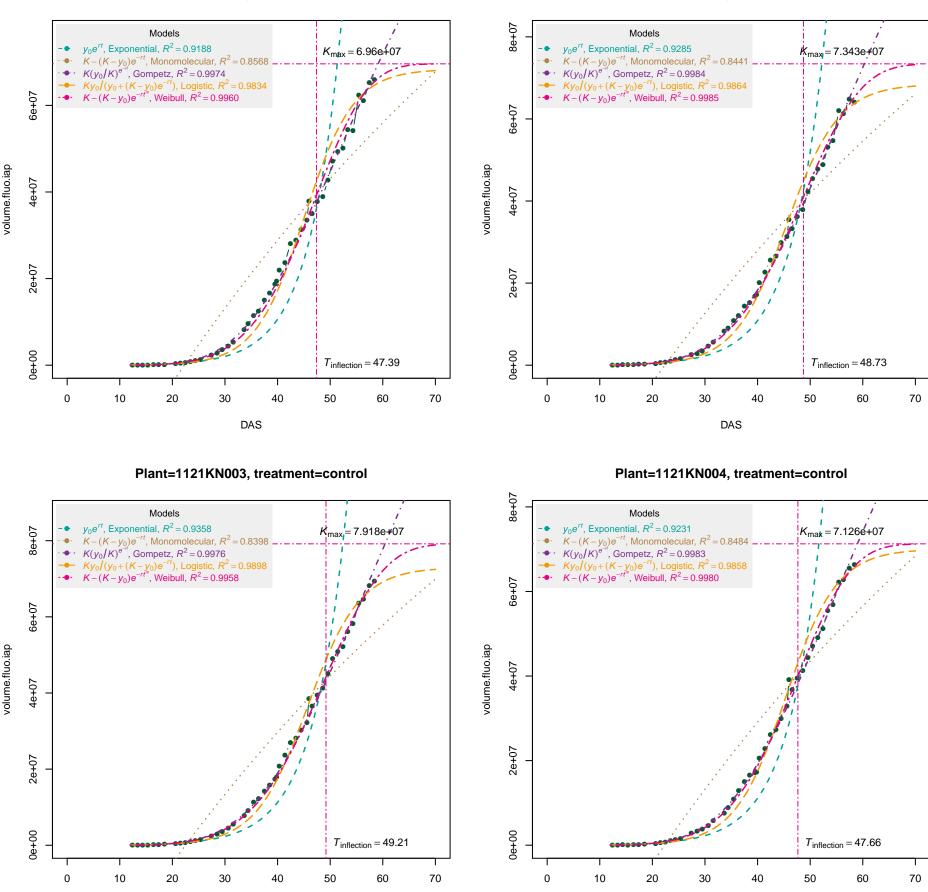
# Plant growth modeling based on trait "volume.fluo.iap"



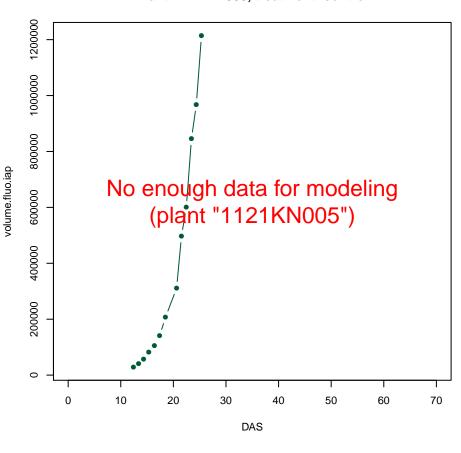
DAS

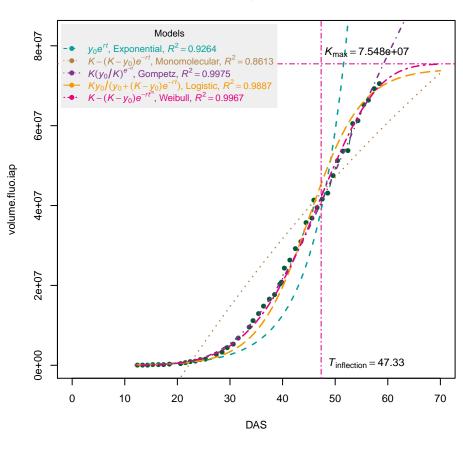
#### Plant=1121KN002, treatment=control

DAS



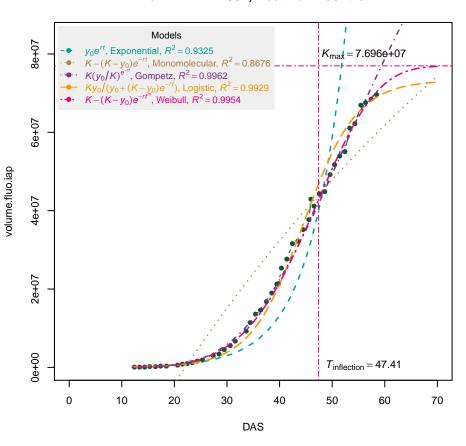
#### Plant=1121KN006, treatment=control

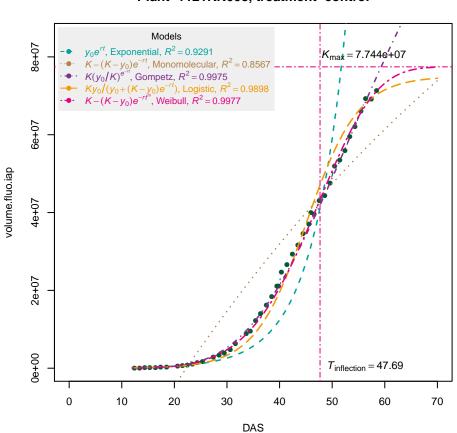




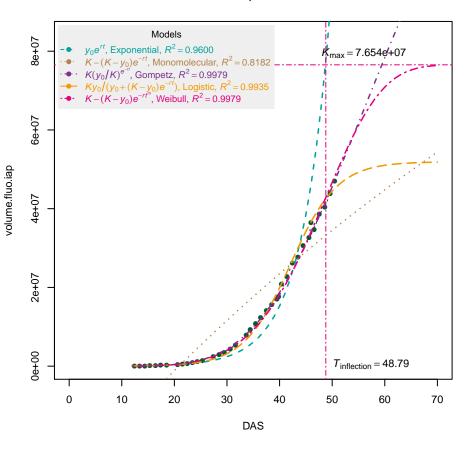
Plant=1121KN007, treatment=control

Plant=1121KN008, treatment=control

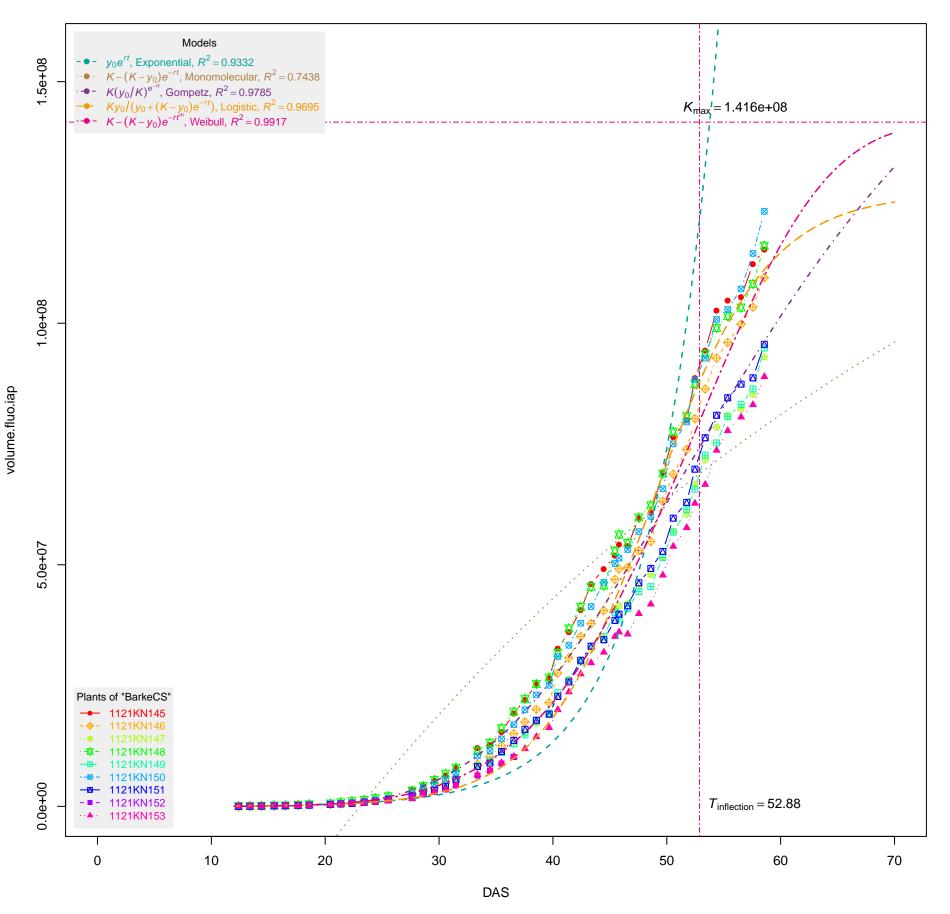




## Plant=1121KN009, treatment=control



# Genotype=BarkeCS, treatment=control



volume.fluo.iap

volume.fluo.iap

0

10

20

30

DAS

40

60

70

50

10

20

30

DAS

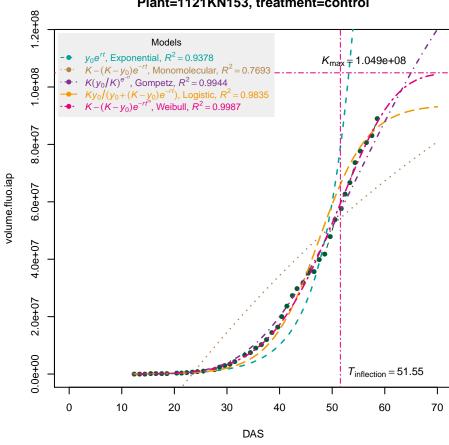
40

50

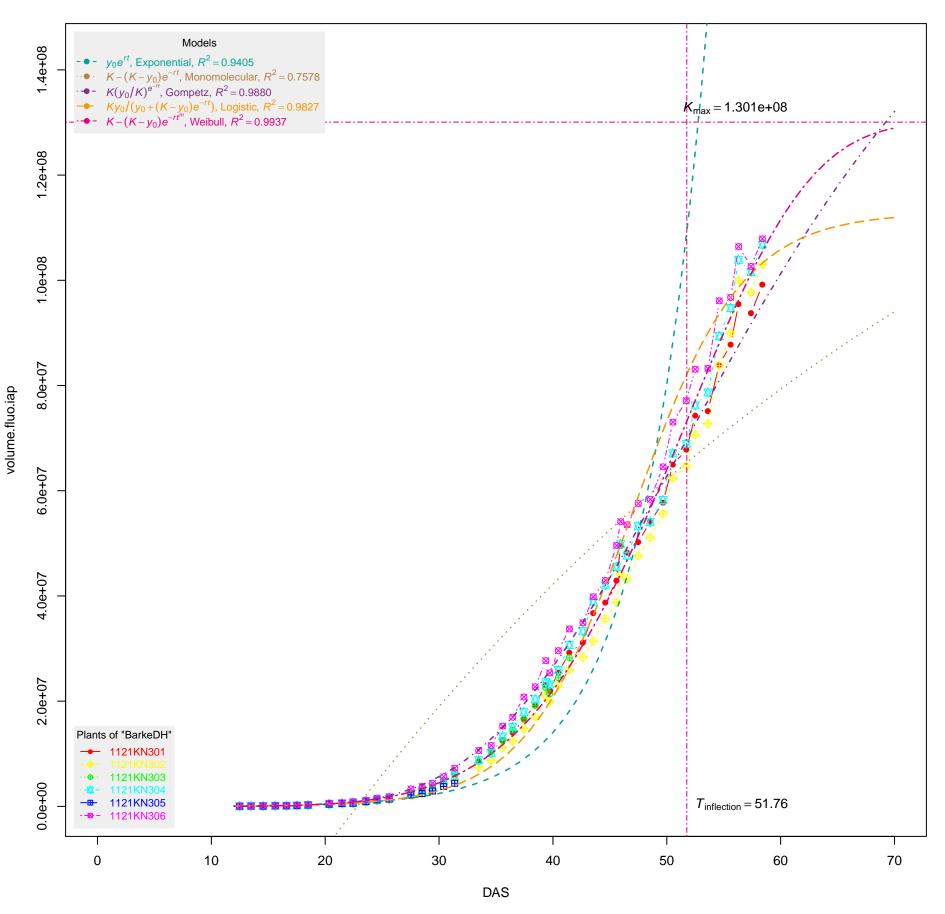
60

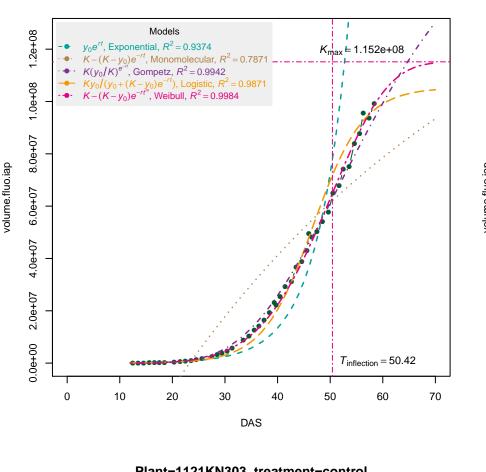
70

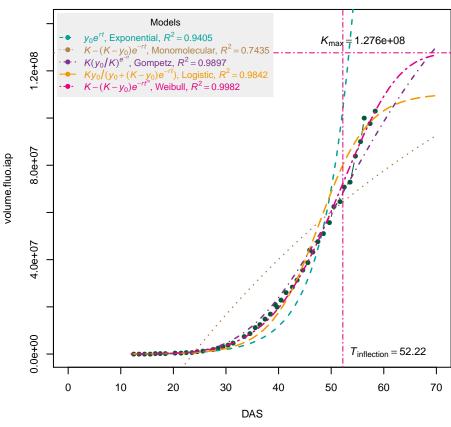
## Plant=1121KN153, treatment=control



# **Genotype=BarkeDH**, treatment=control

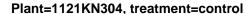


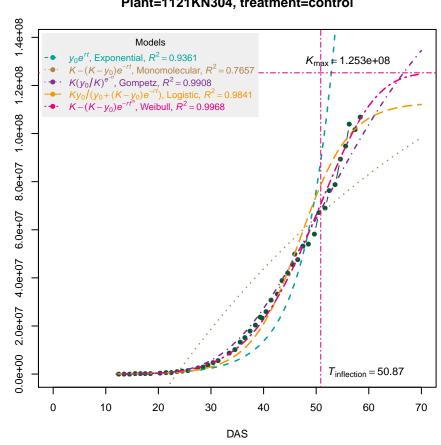




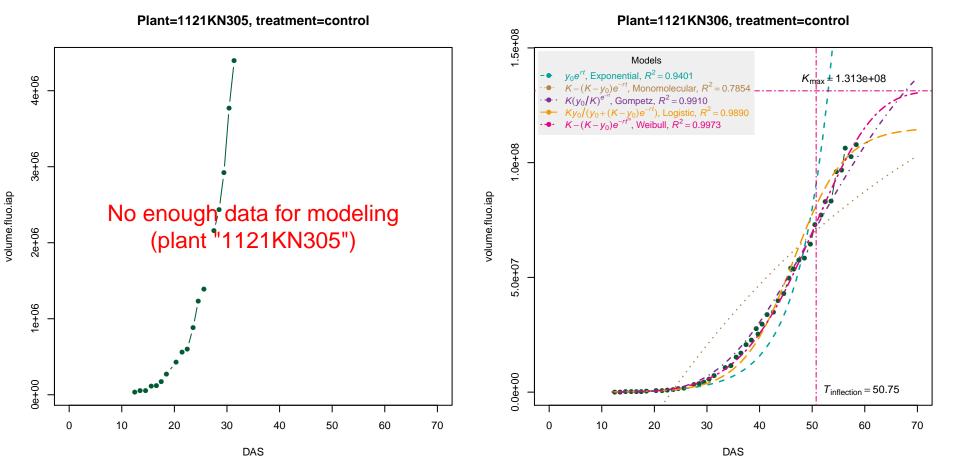
Plant=1121KN303, treatment=control

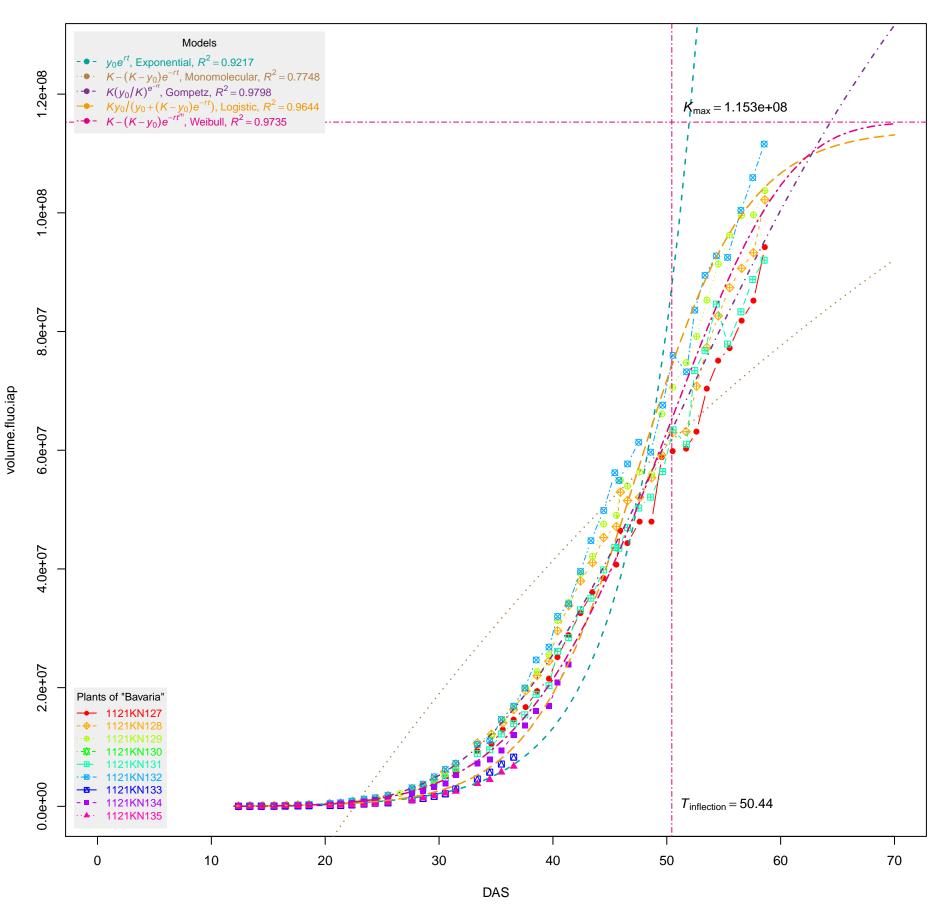
2.5e+07 2.0e+07 volume.fluo.iap No enough data for modeling (plant "1121KN303") 1.5e+07 1.0e+07 5.0e+06 0.0e+00 30 40 60 10 20 70 DAS

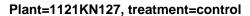




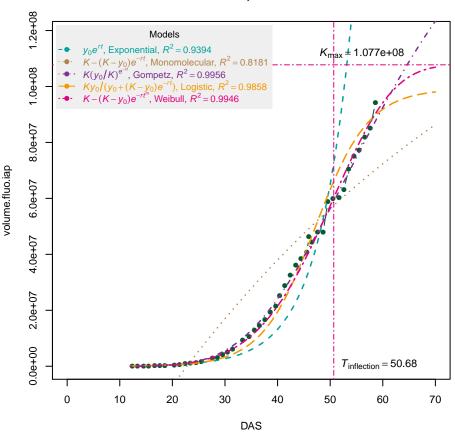
volume.fluo.iap

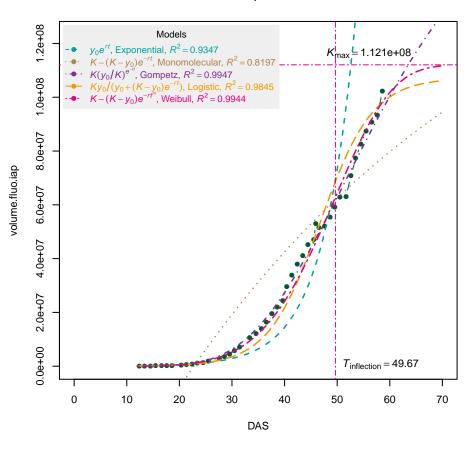






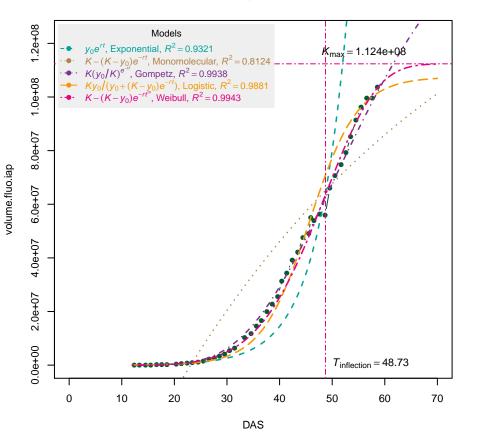
#### Plant=1121KN128, treatment=control

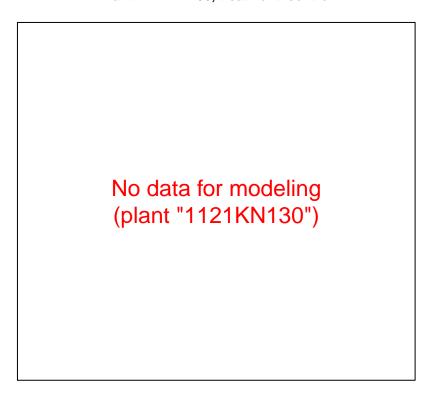


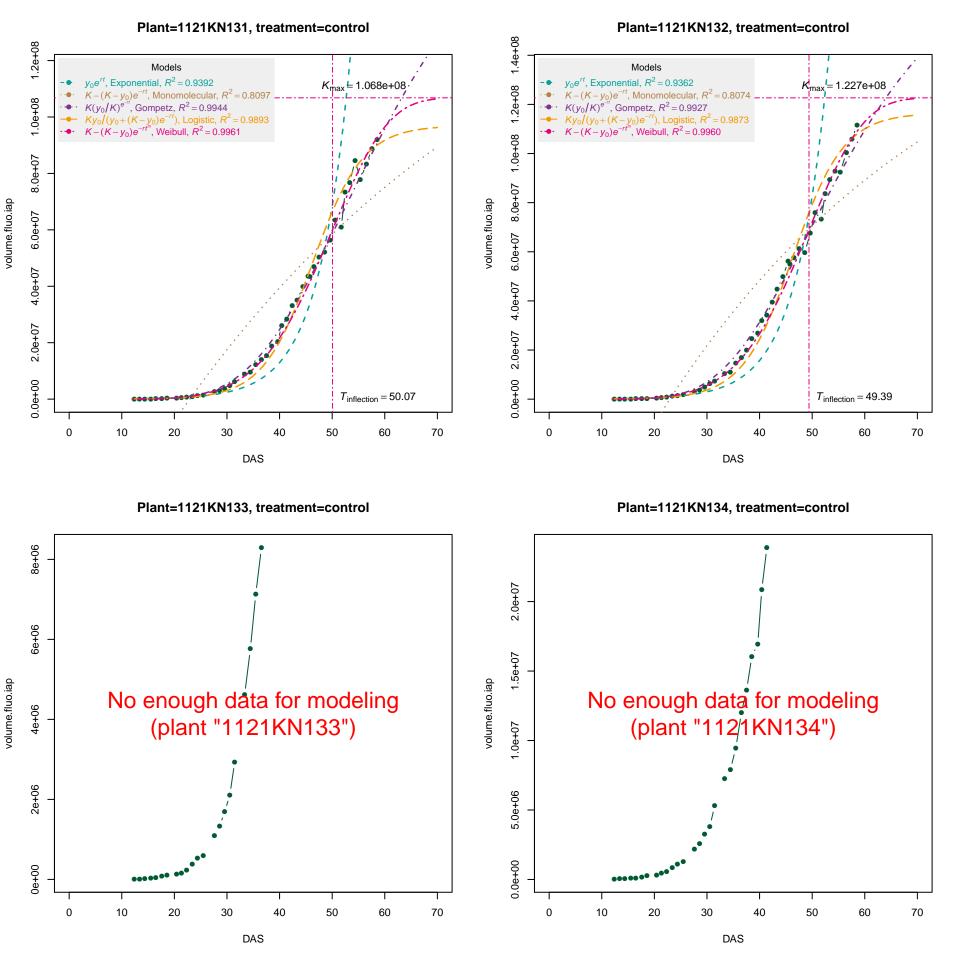


Plant=1121KN129, treatment=control

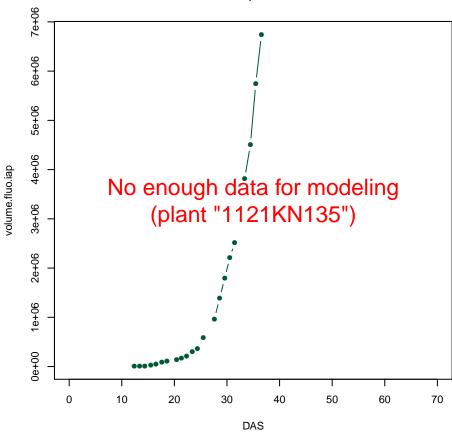
Plant=1121KN130, treatment=control



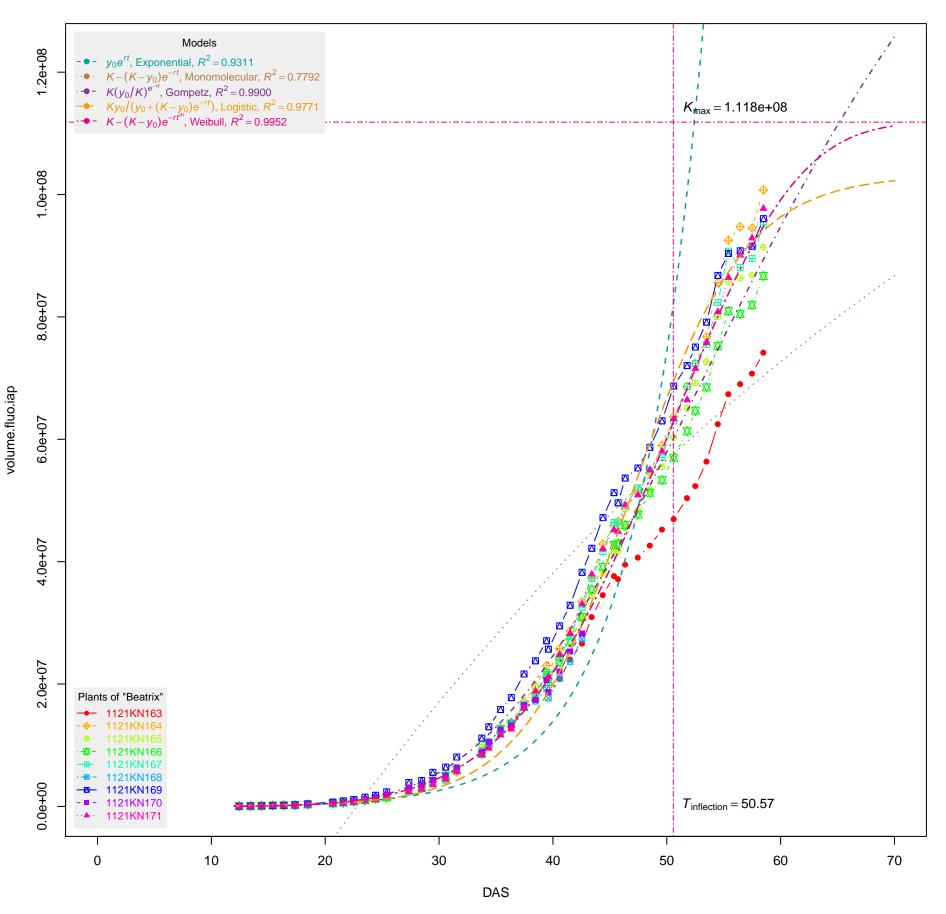




## Plant=1121KN135, treatment=control



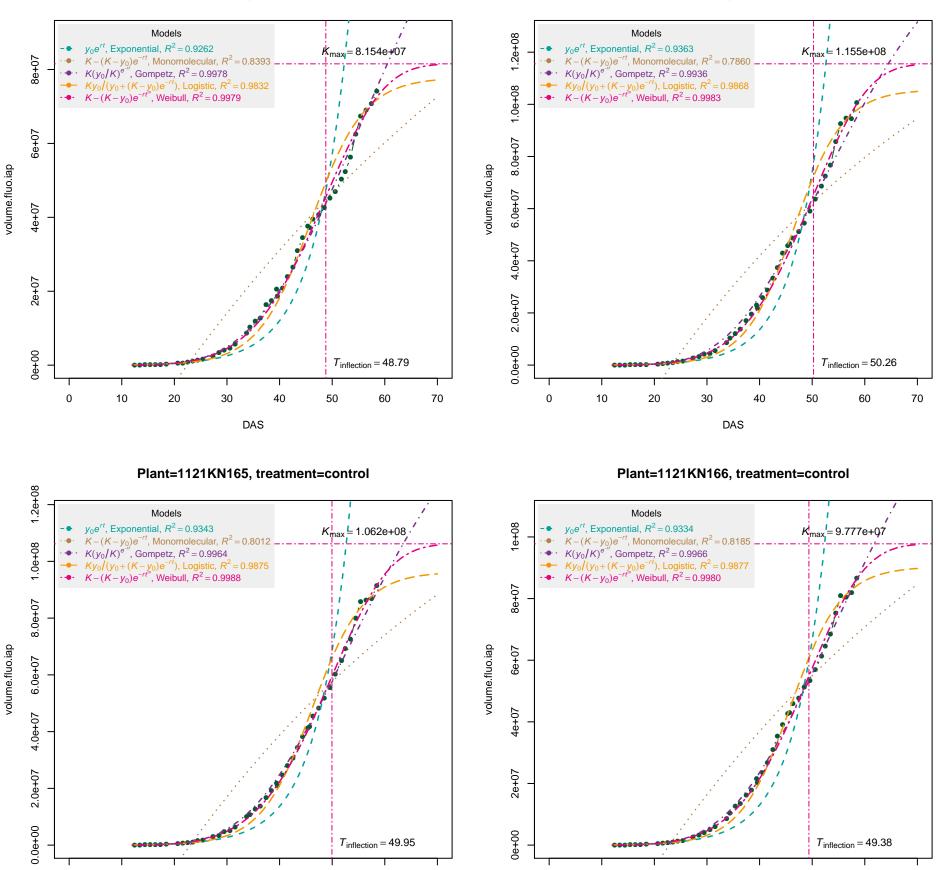
# Genotype=Beatrix, treatment=control

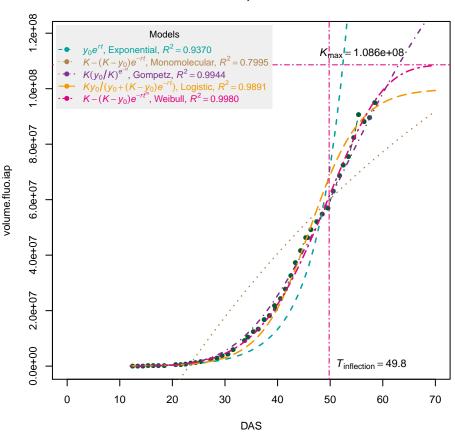


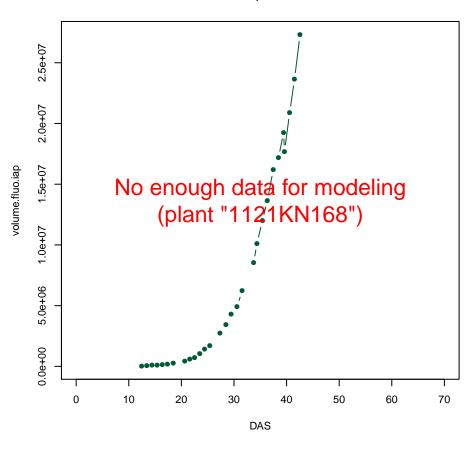
DAS

DAS

#### Plant=1121KN164, treatment=control

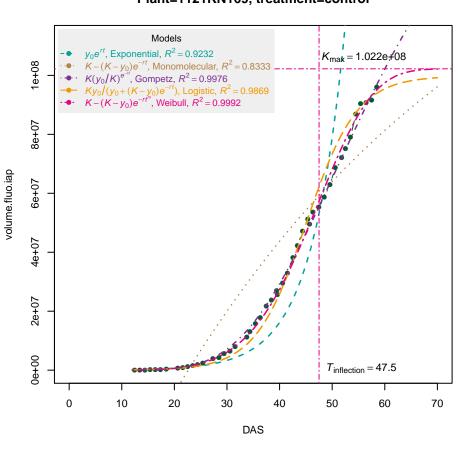


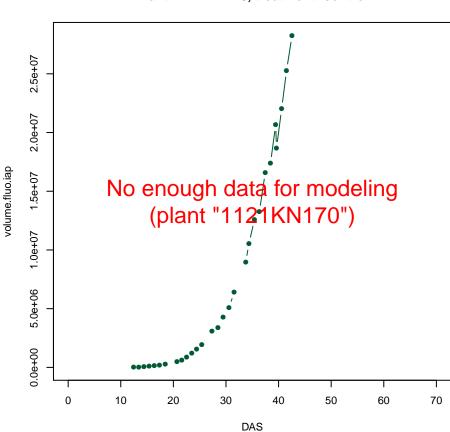




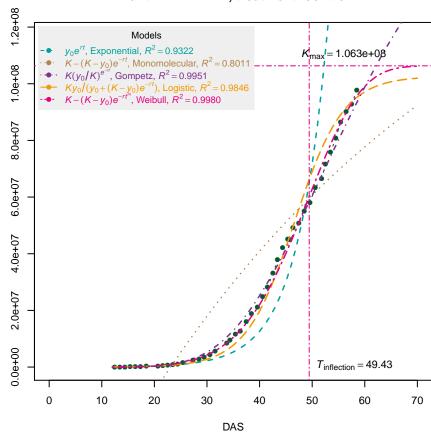
Plant=1121KN169, treatment=control

Plant=1121KN170, treatment=control



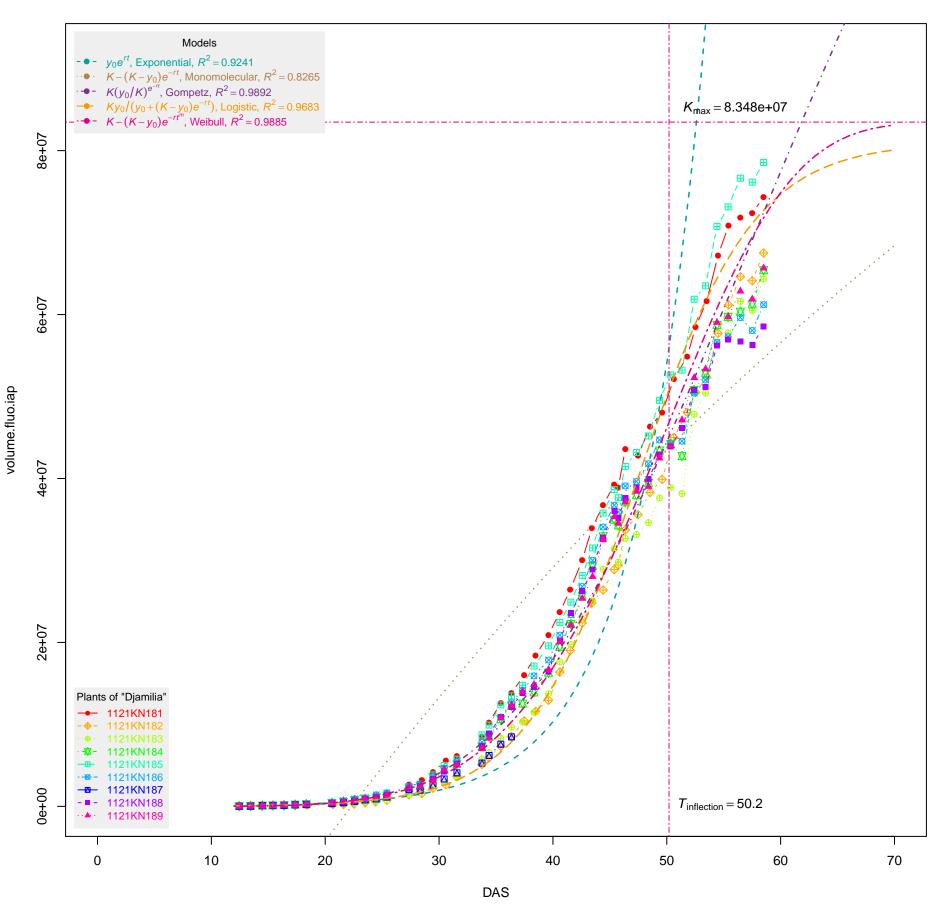


## Plant=1121KN171, treatment=control

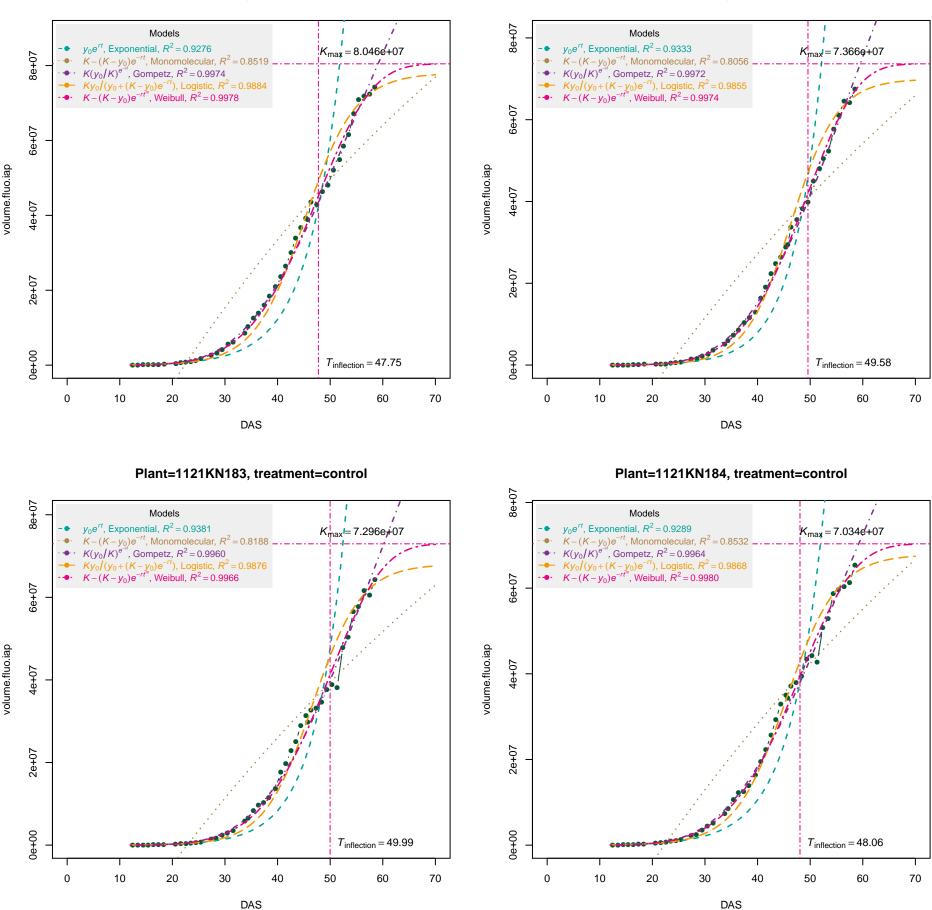


volume.fluo.iap

# **Genotype=Djamilia**, treatment=control



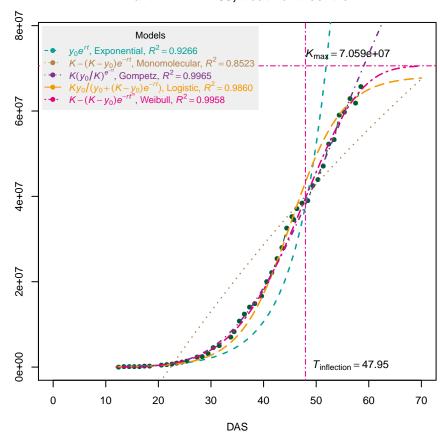
#### Plant=1121KN182, treatment=control



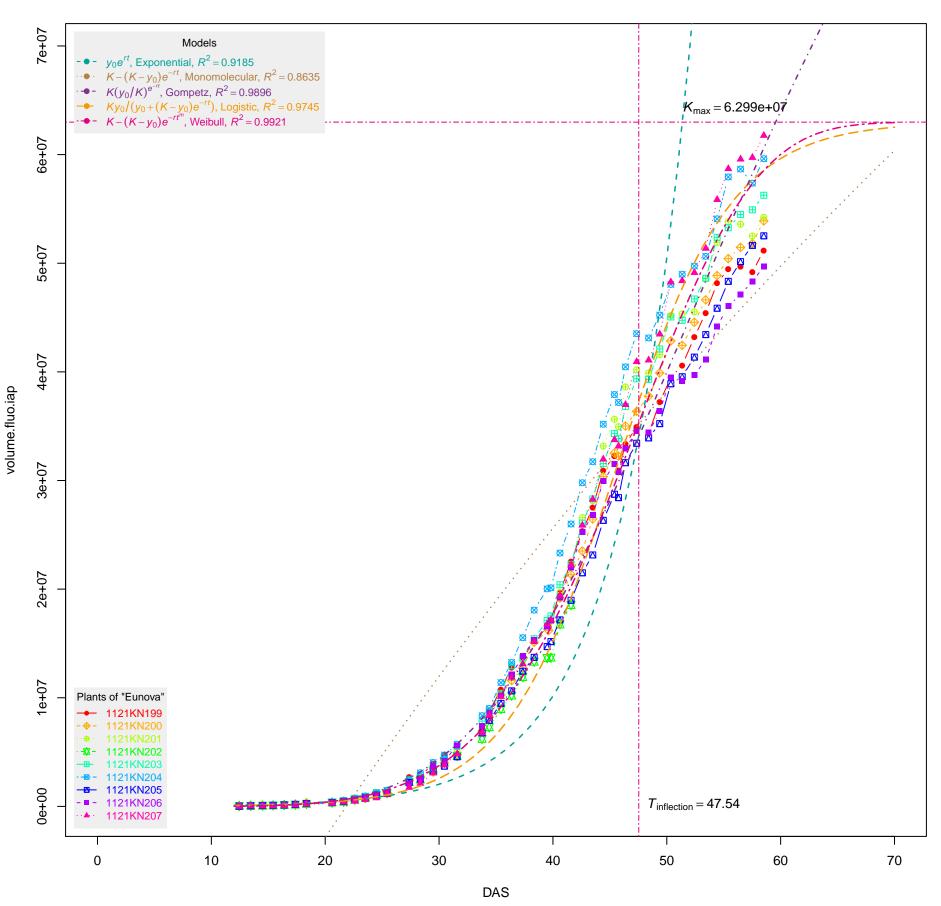
DAS

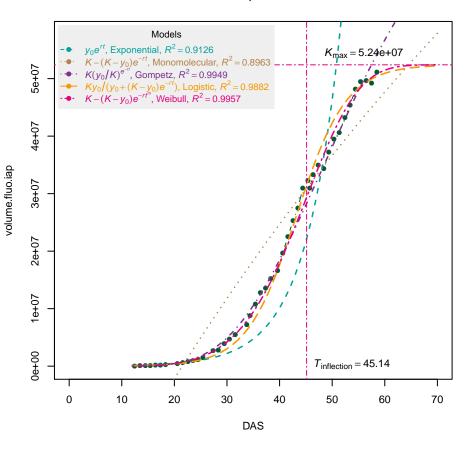
DAS

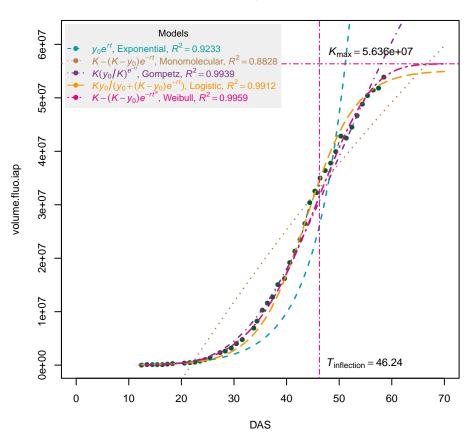
## Plant=1121KN189, treatment=control



volume.fluo.iap

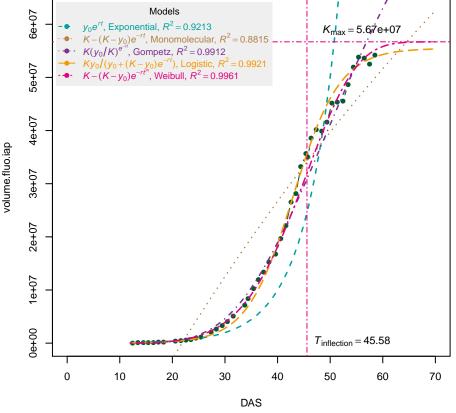


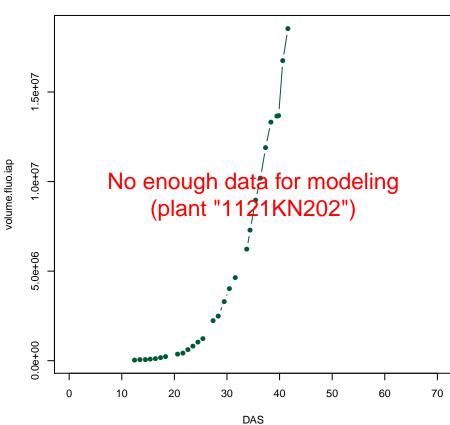


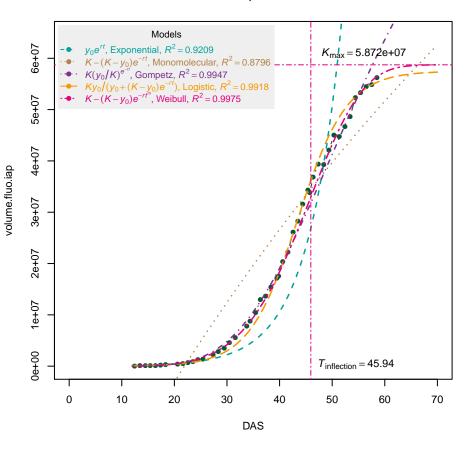


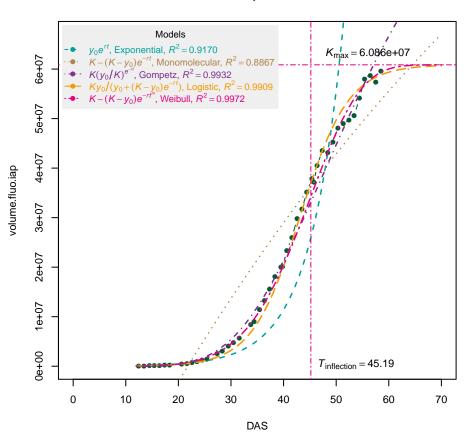
Plant=1121KN201, treatment=control

Plant=1121KN202, treatment=control



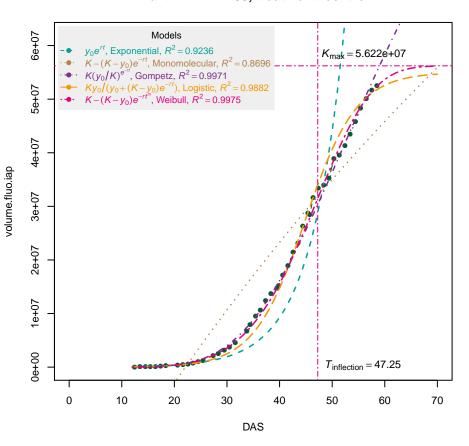


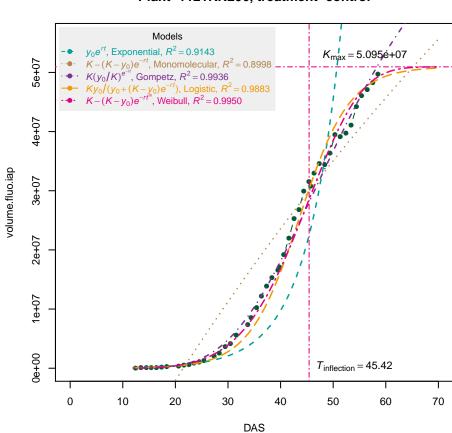




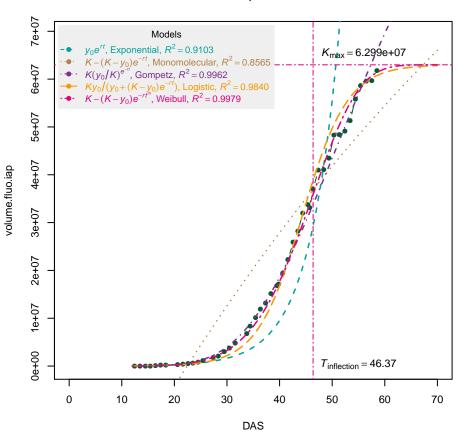
Plant=1121KN205, treatment=control

Plant=1121KN206, treatment=control

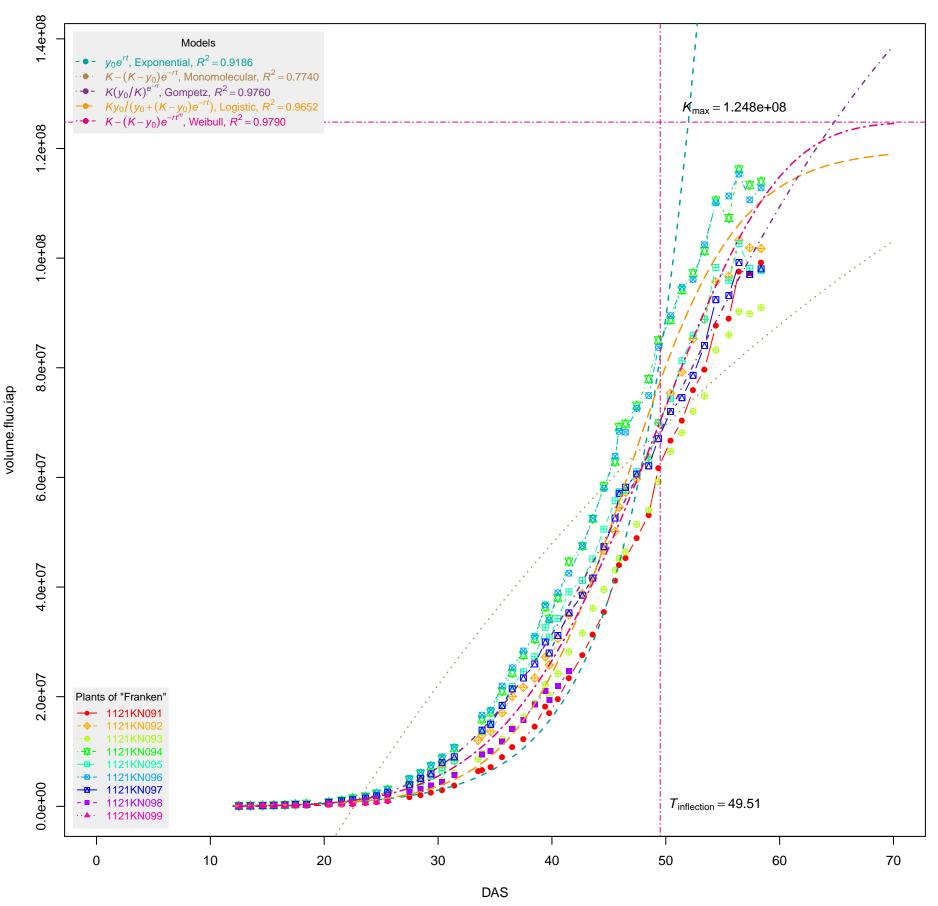


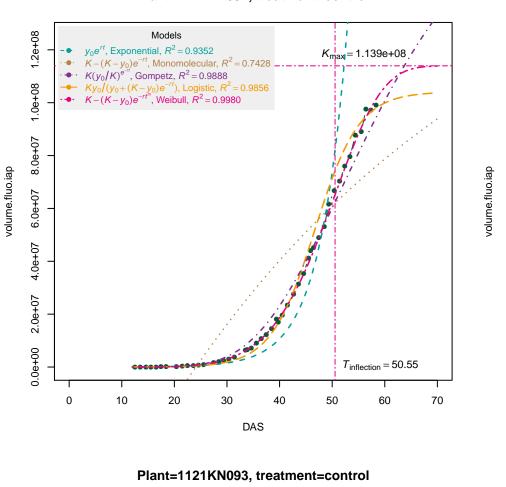


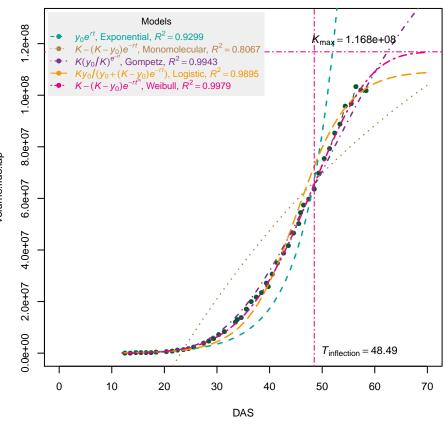
## Plant=1121KN207, treatment=control

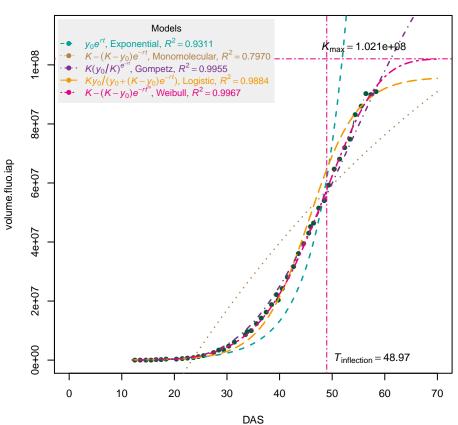


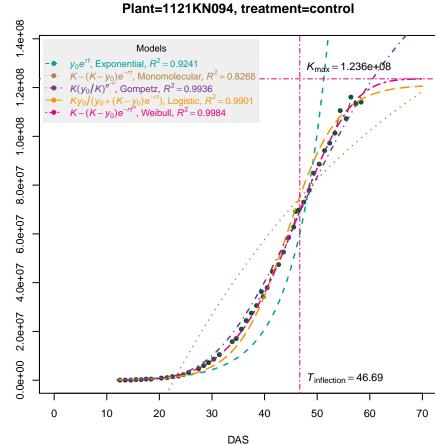
# Genotype=Franken, treatment=control



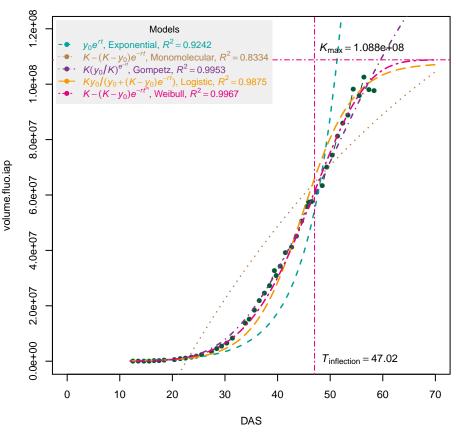


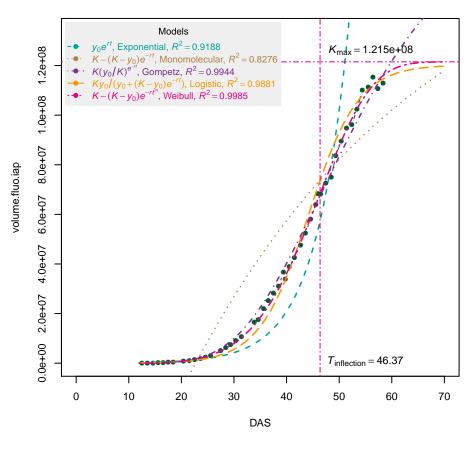


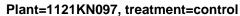


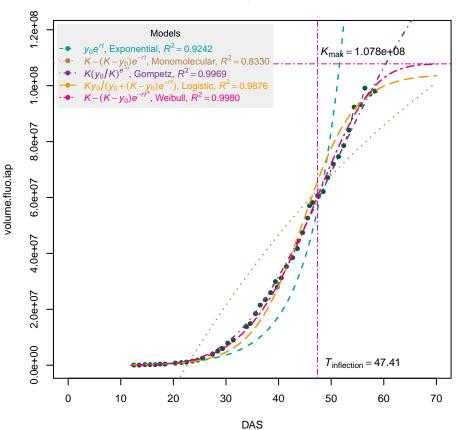


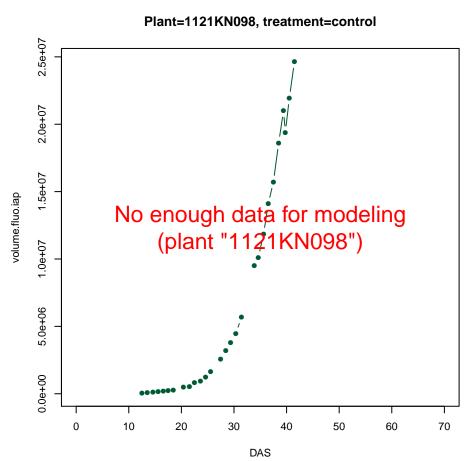
volume.fluo.iap



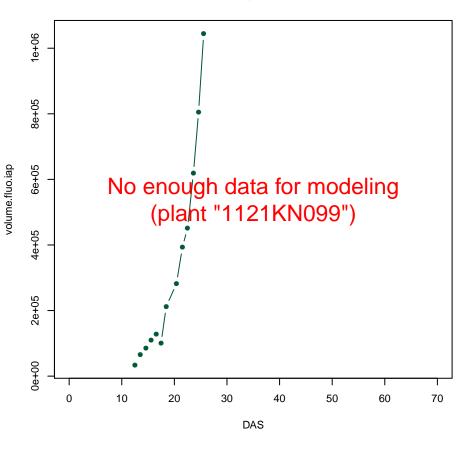




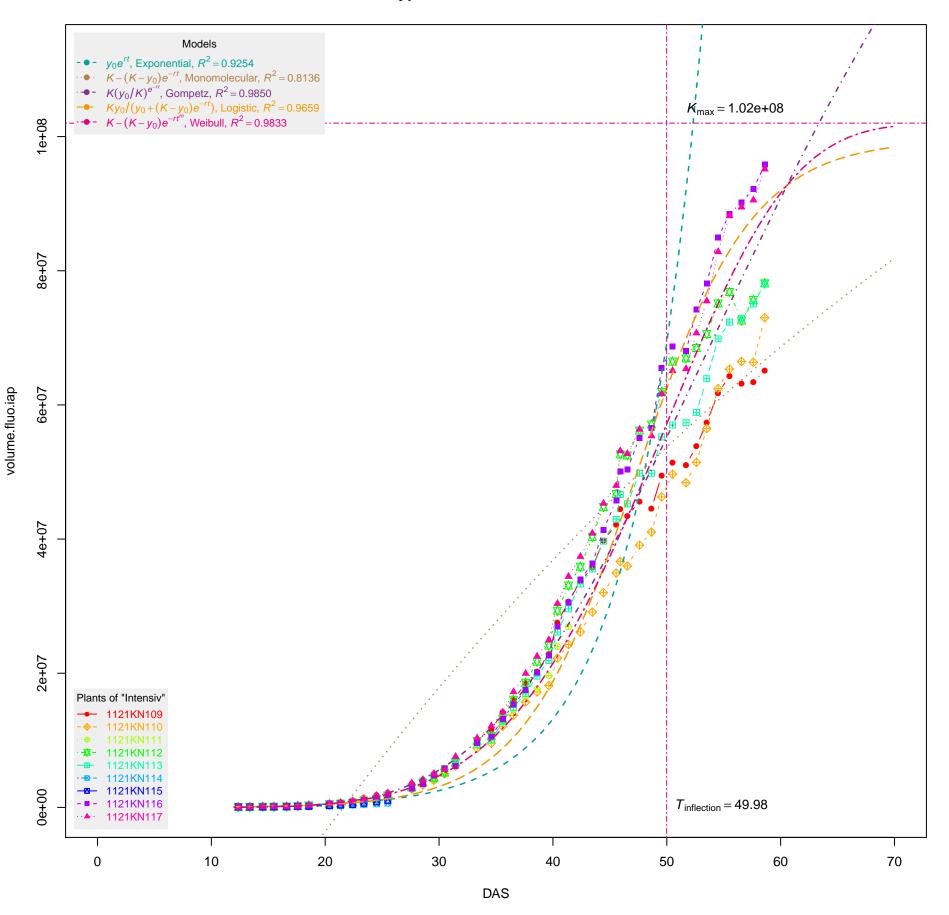




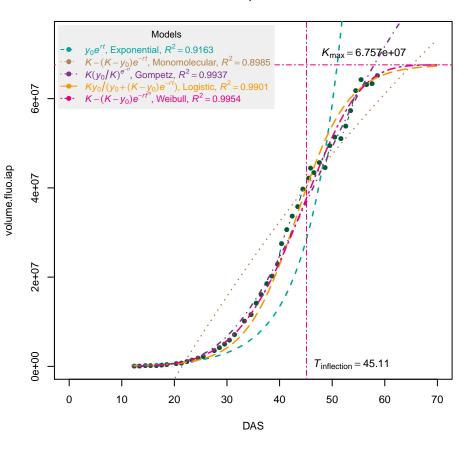
## Plant=1121KN099, treatment=control

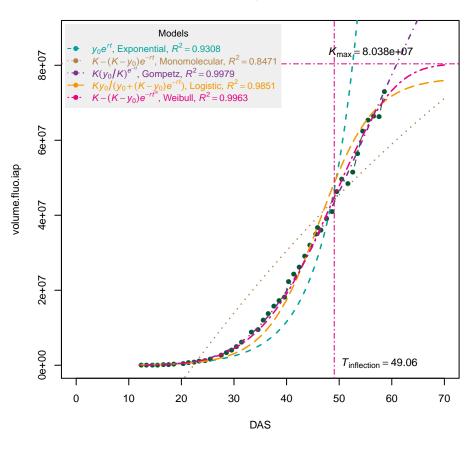


# Genotype=Intensiv, treatment=control



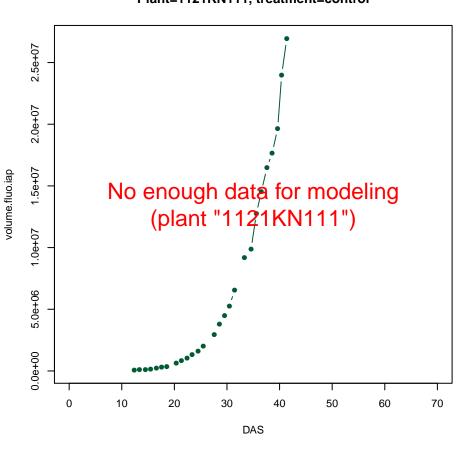
#### Plant=1121KN110, treatment=control

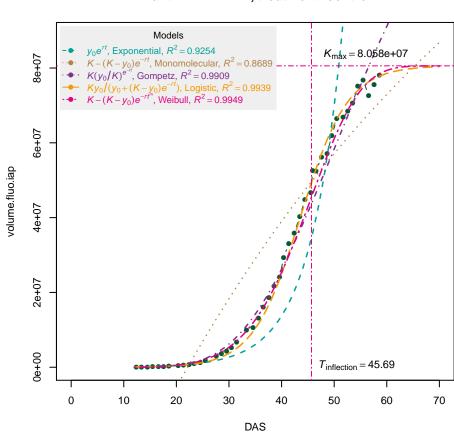


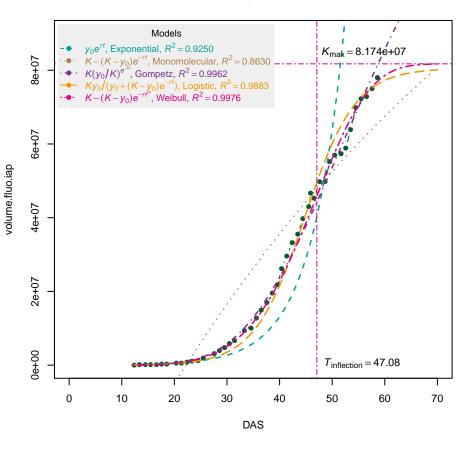


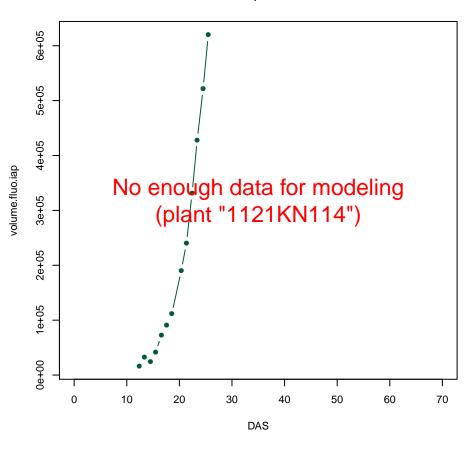
Plant=1121KN111, treatment=control

Plant=1121KN112, treatment=control







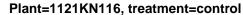


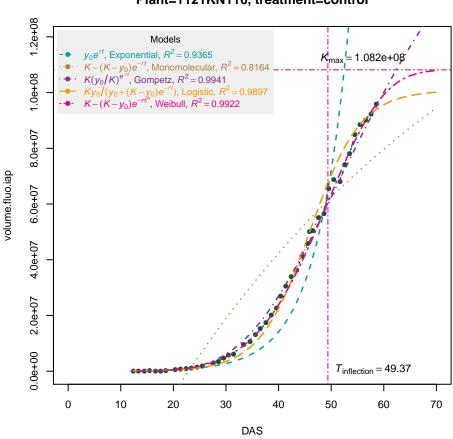
Plant=1121KN115, treatment=control

No enough data for modeling (plant "1121KN115")

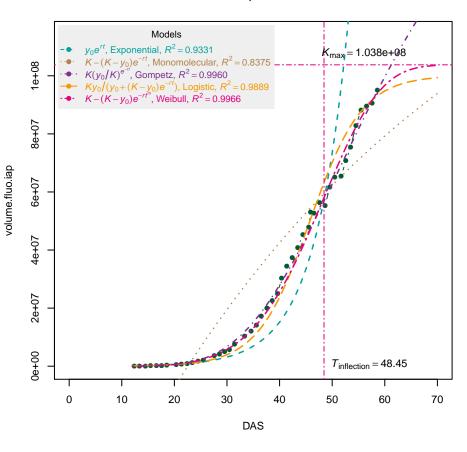
O 10 20 30 40 50 60 70

DAS

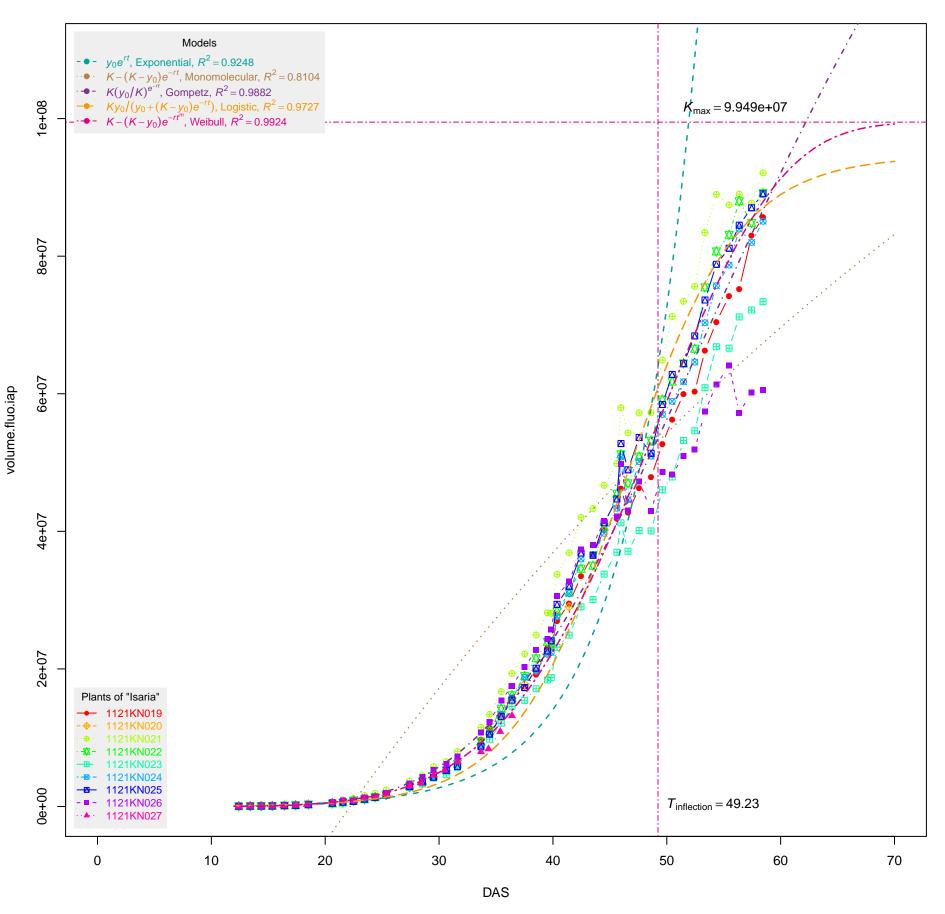


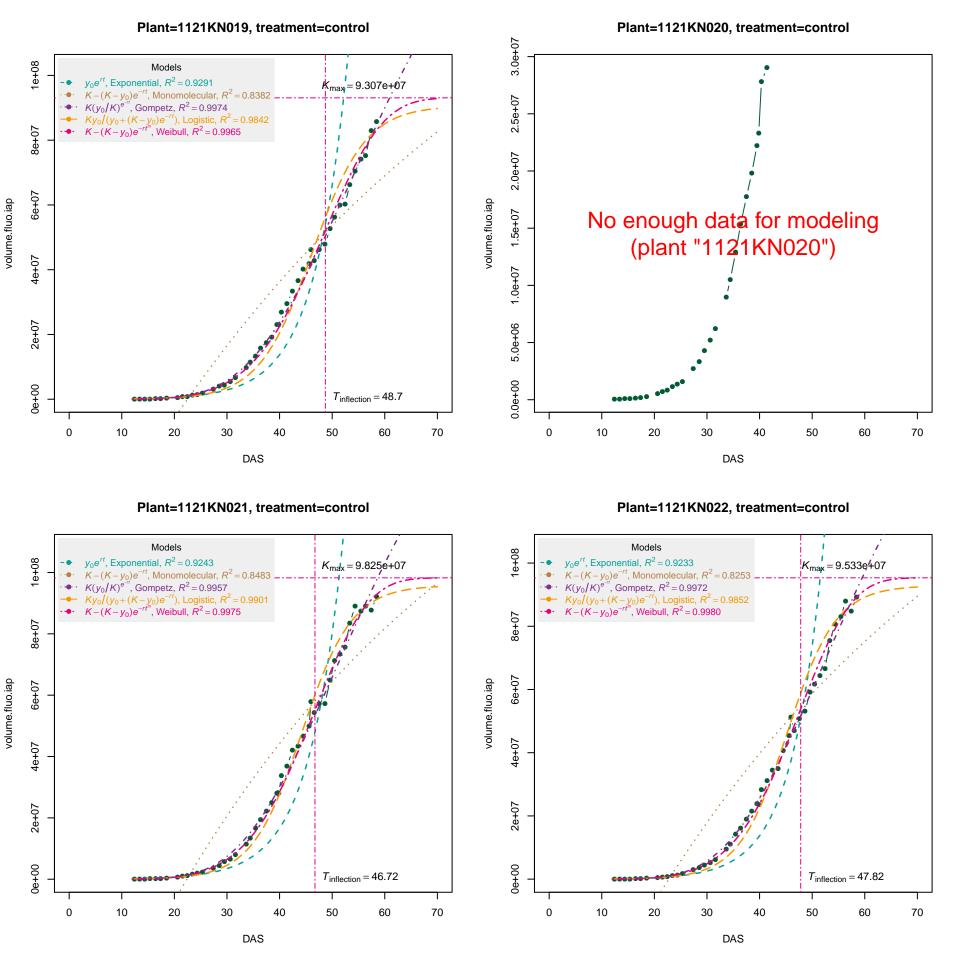


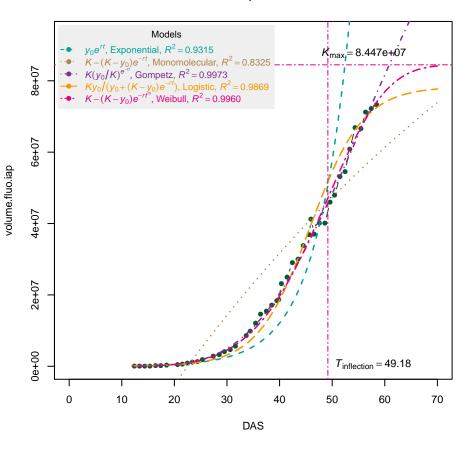
## Plant=1121KN117, treatment=control

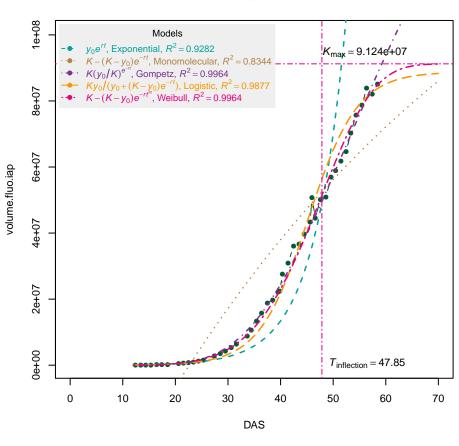


# Genotype=Isaria, treatment=control



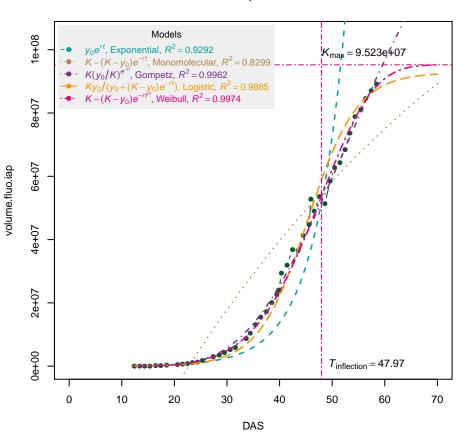


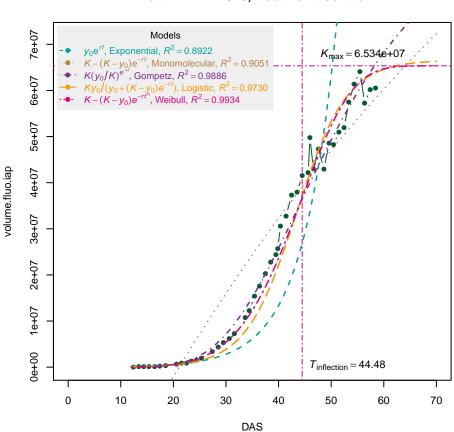




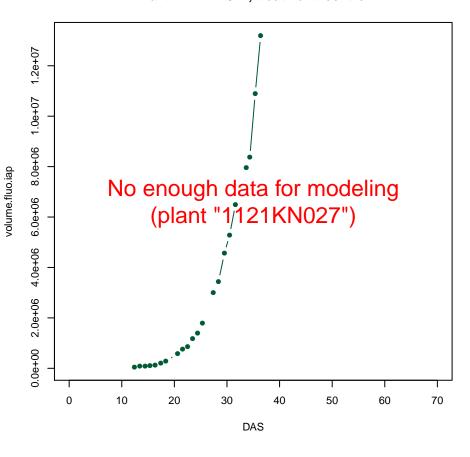
Plant=1121KN025, treatment=control

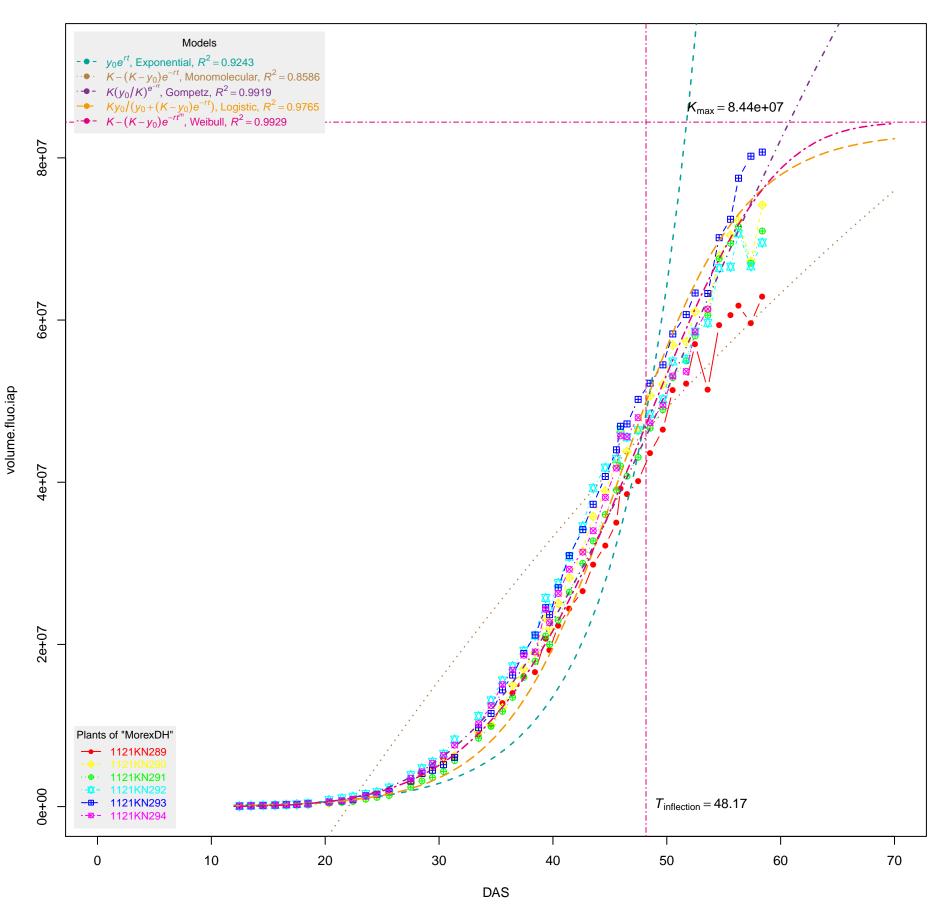
Plant=1121KN026, treatment=control

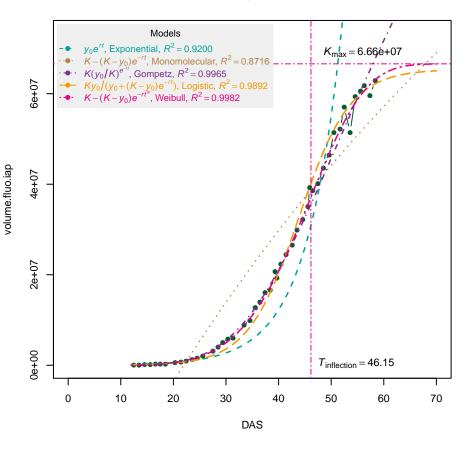


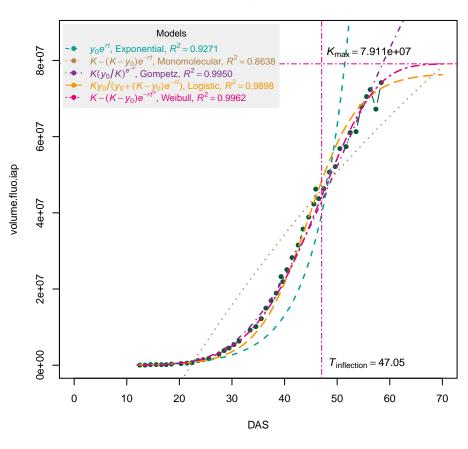


### Plant=1121KN027, treatment=control



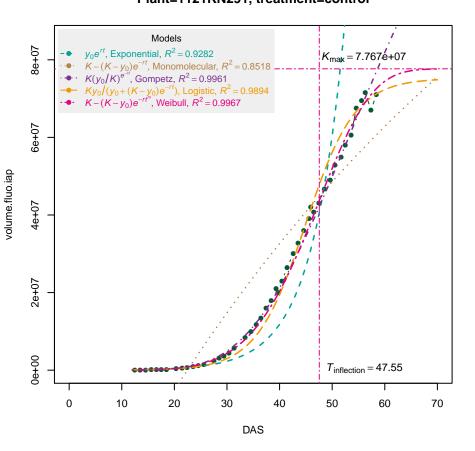


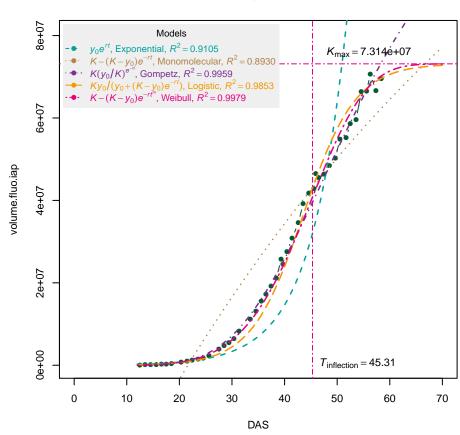


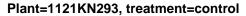


Plant=1121KN291, treatment=control

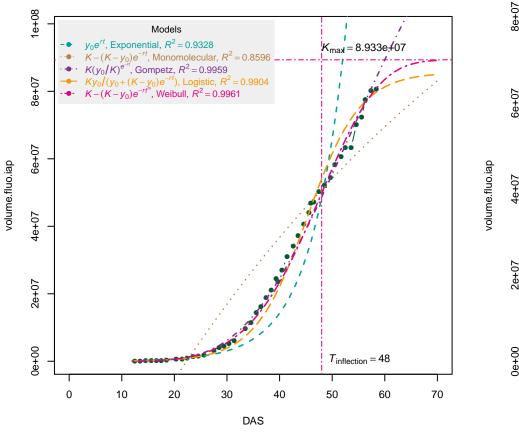
Plant=1121KN292, treatment=control

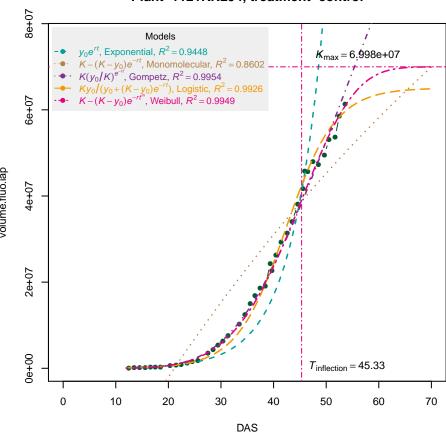


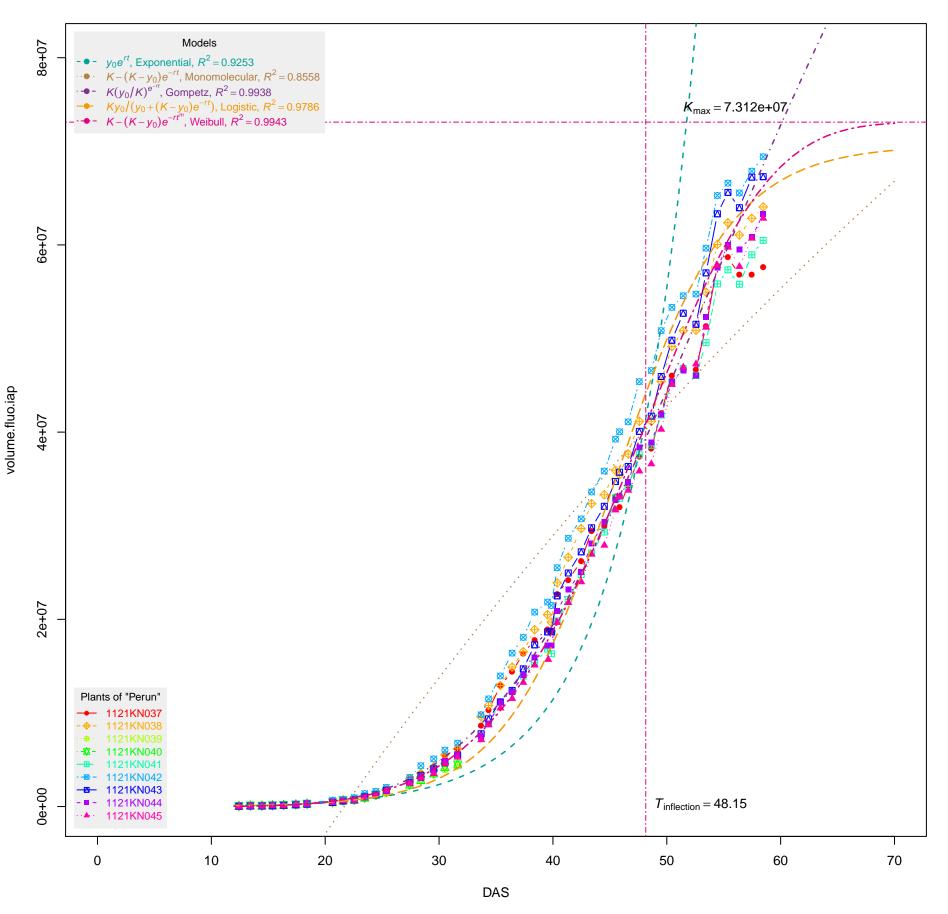




#### Plant=1121KN294, treatment=control







0e+00

10

30

DAS

40

50

60

70

volume.fluo.iap

volume.fluo.iap

30

DAS

10

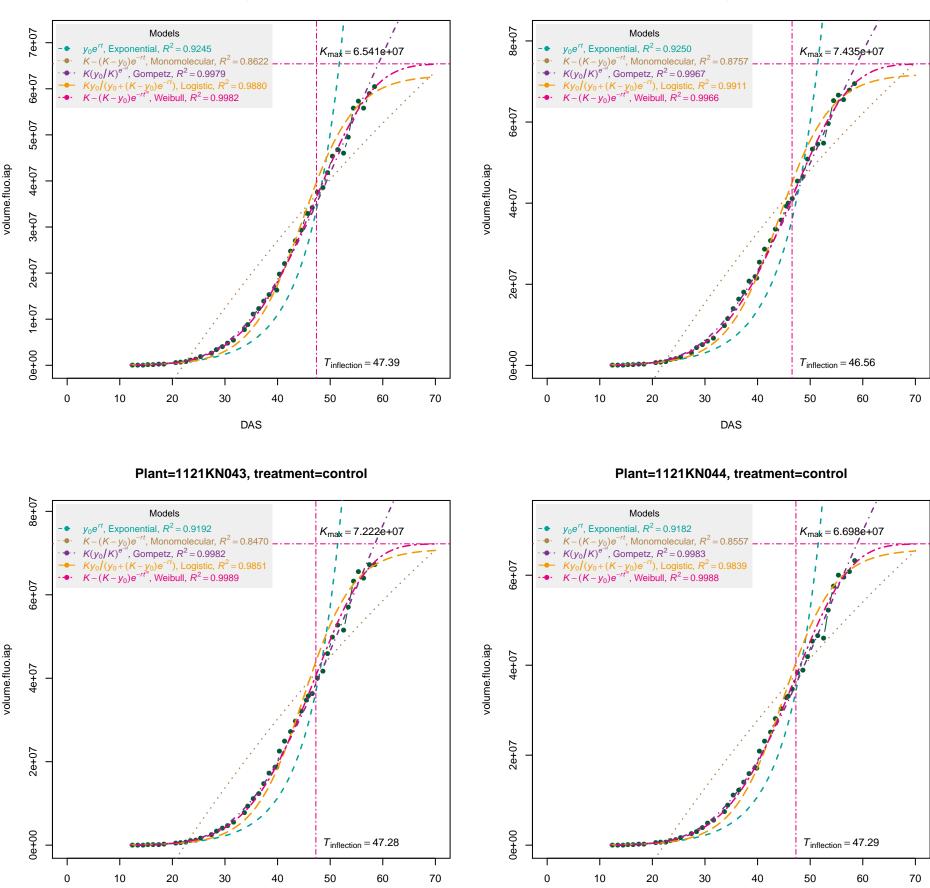
20

40

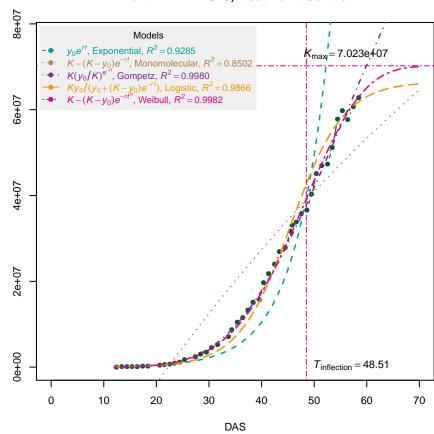
60

DAS

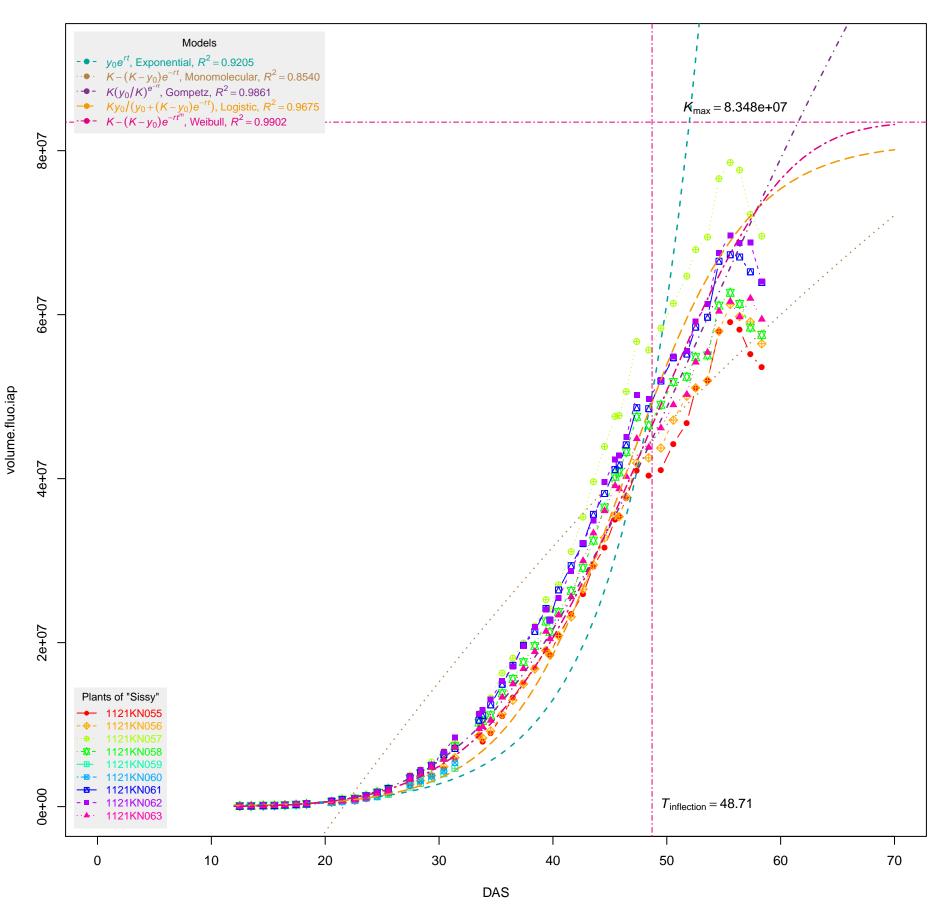
DAS

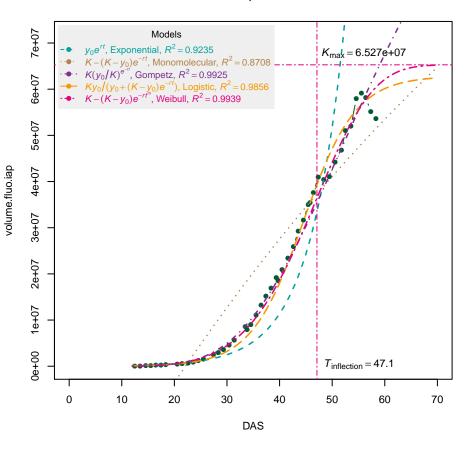


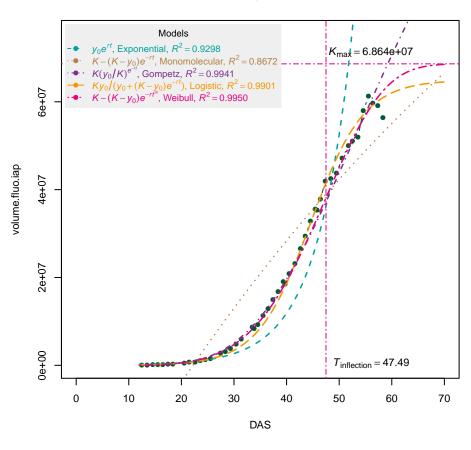
### Plant=1121KN045, treatment=control



volume.fluo.iap

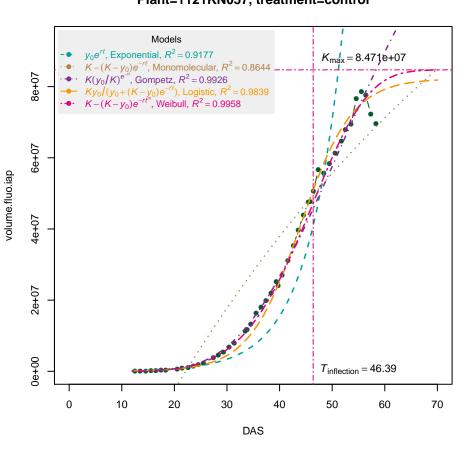


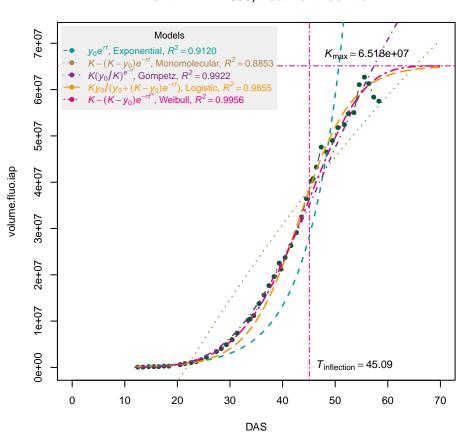




Plant=1121KN057, treatment=control

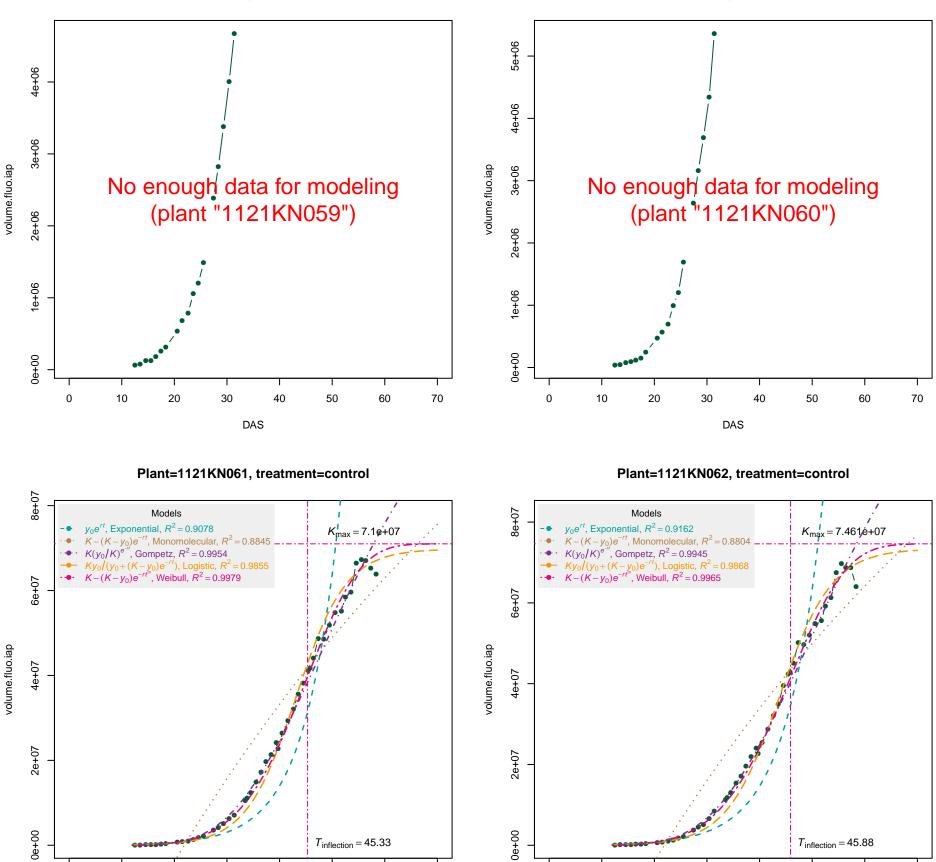
Plant=1121KN058, treatment=control



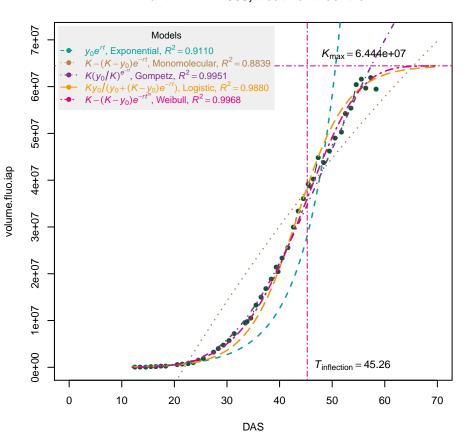


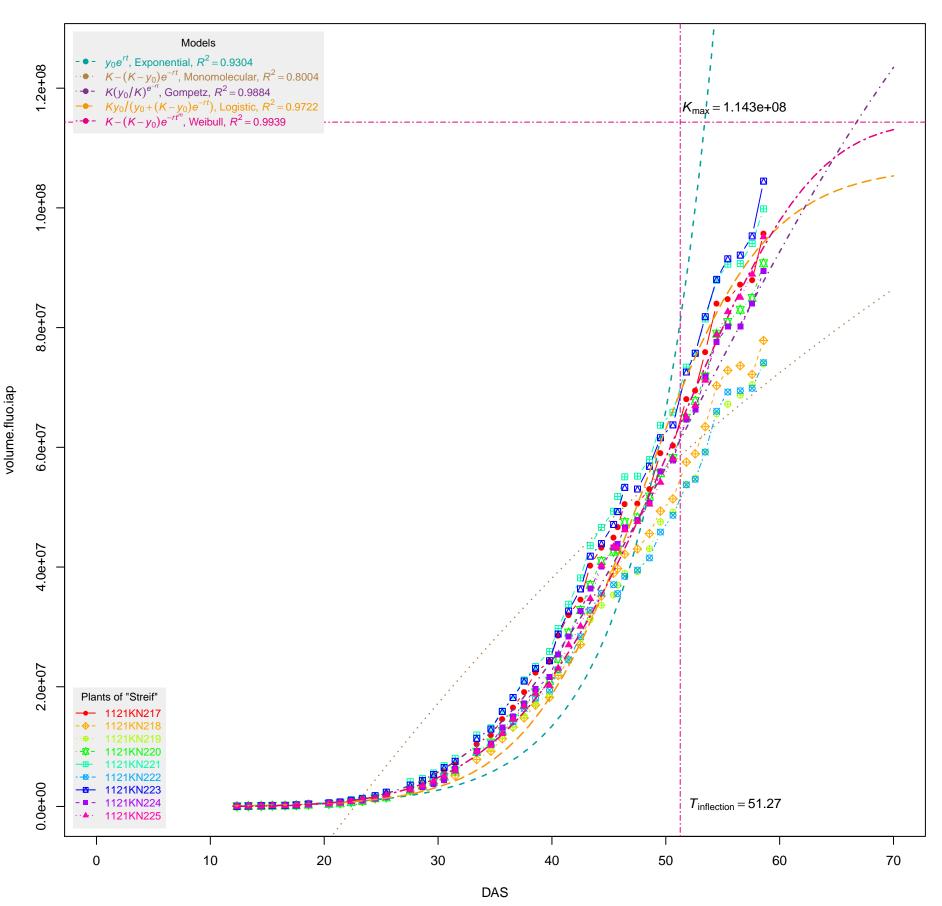
DAS

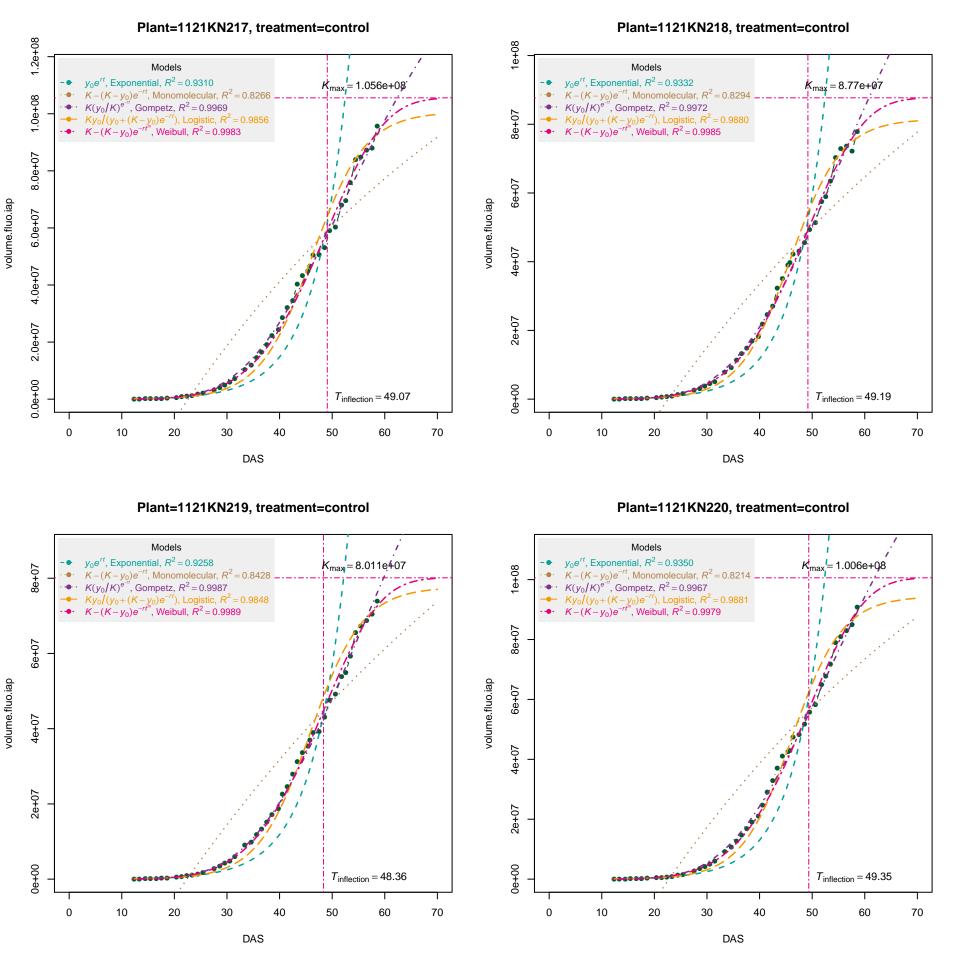
DAS



#### Plant=1121KN063, treatment=control







0e+00

10

20

 $T_{\text{inflection}} = 49.28$ 

60

70

50

30

DAS

40

 $T_{\text{inflection}} = 49.67$ 

50

60

70

30

DAS

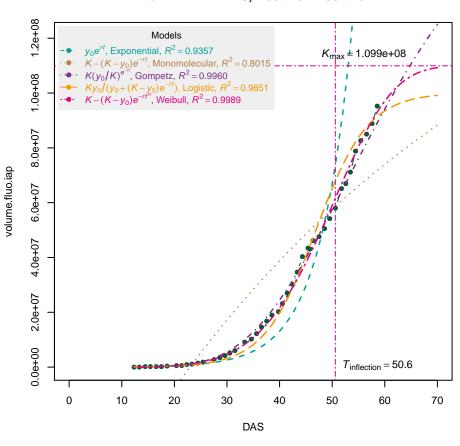
40

0.0e+00

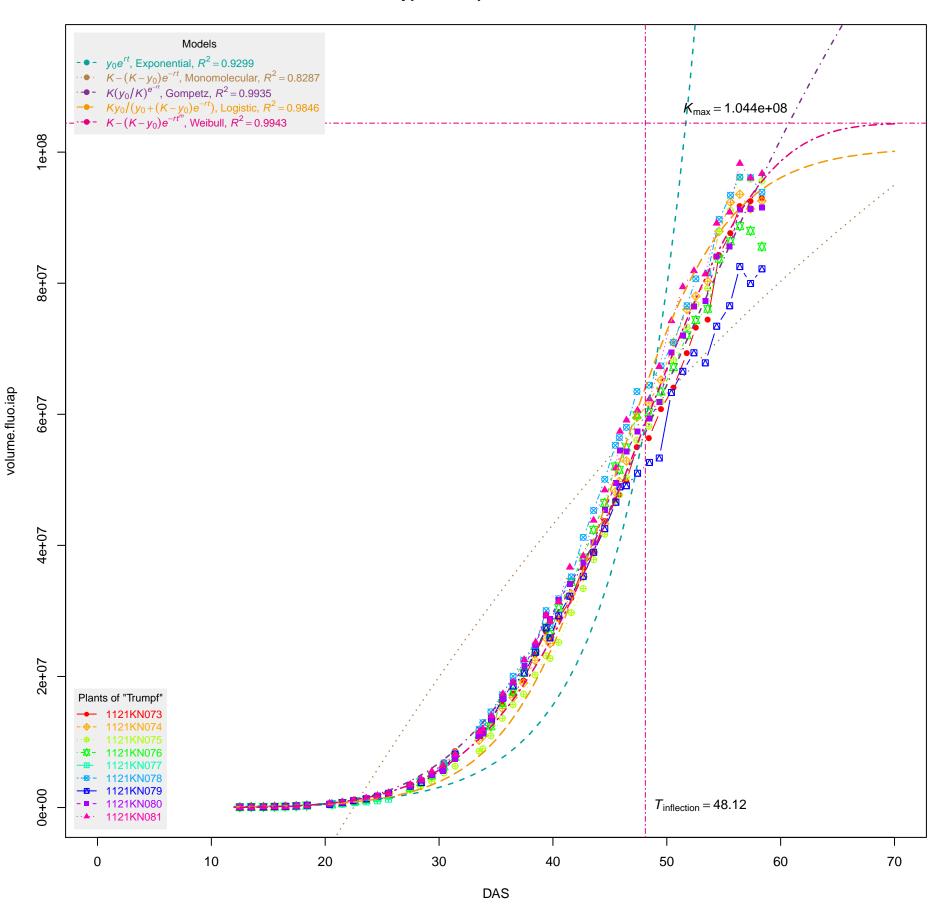
0

10

#### Plant=1121KN225, treatment=control



# **Genotype=Trumpf**, treatment=control



0

10

20

30

DAS

40

60

70

50

10

20

30

DAS

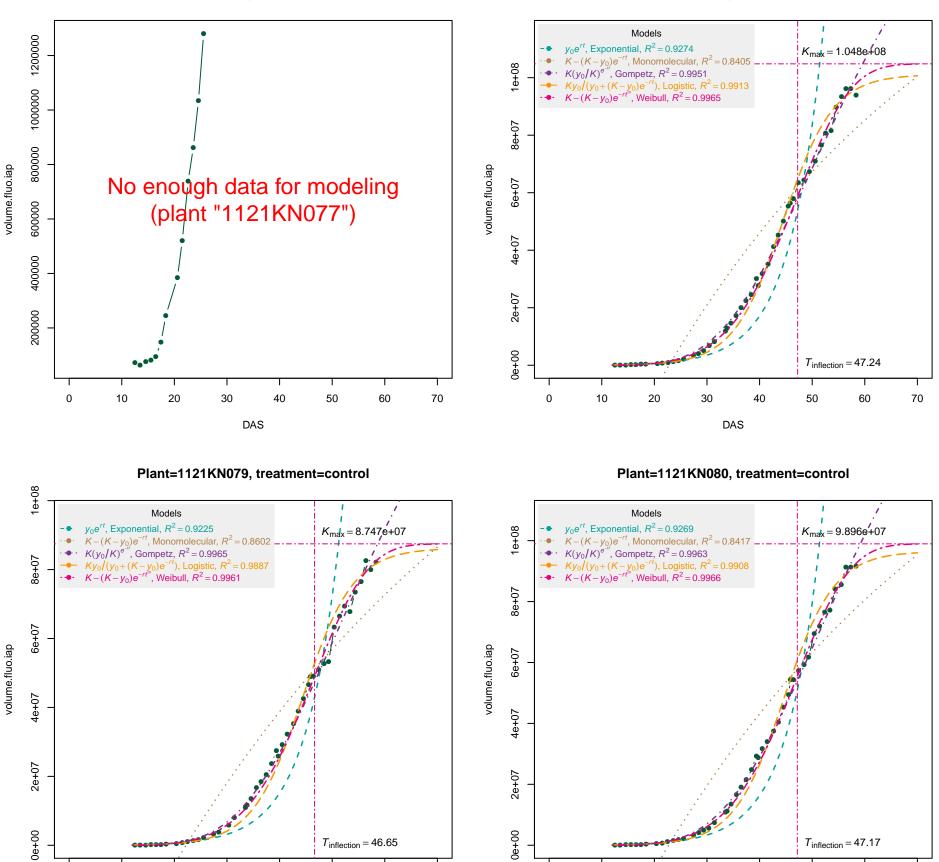
40

50

60

 $T_{\text{inflection}} = 47.17$ 

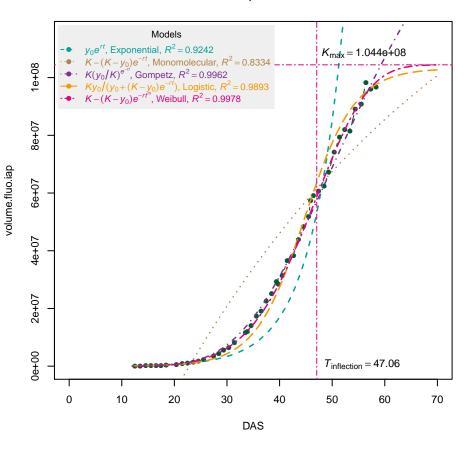
DAS



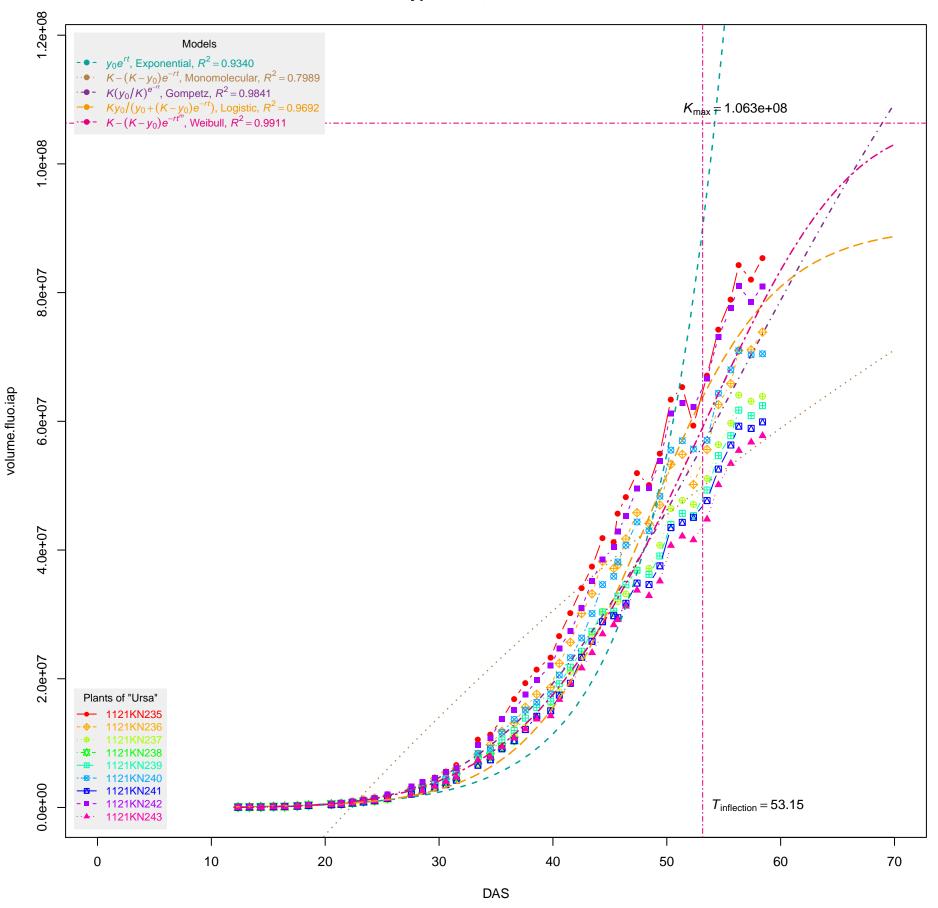
 $T_{\text{inflection}} = 46.65$ 

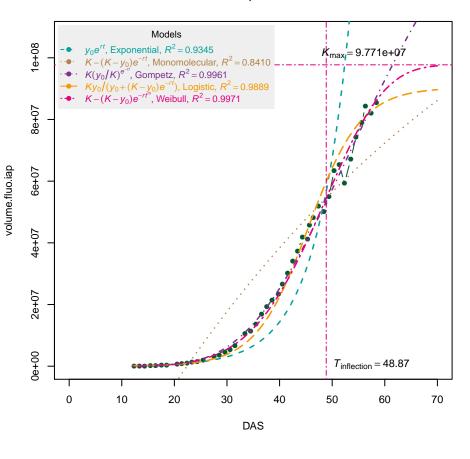
DAS

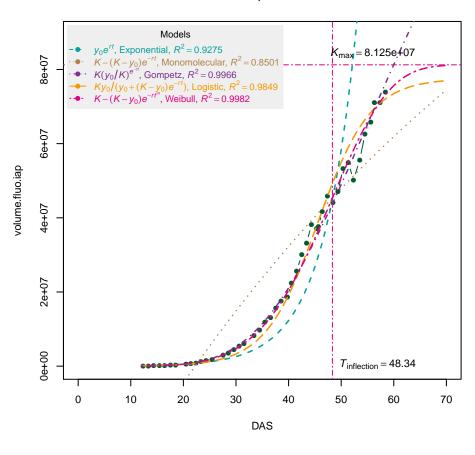
### Plant=1121KN081, treatment=control



# Genotype=Ursa, treatment=control

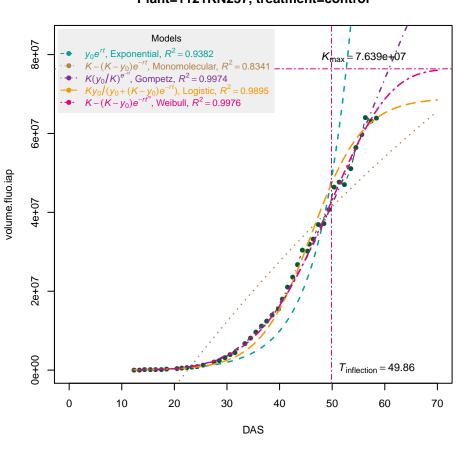


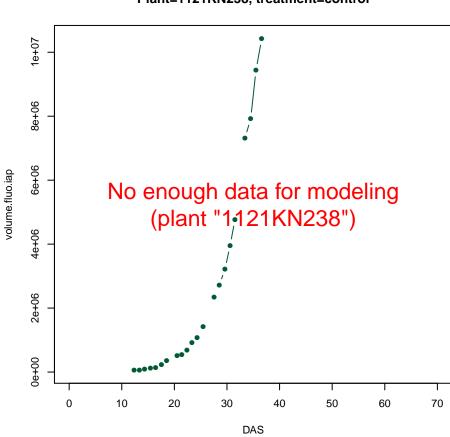




Plant=1121KN237, treatment=control

Plant=1121KN238, treatment=control





 $T_{\text{inflection}} = 48.76$ 

60

50

70

 $T_{\text{inflection}} = 50.49$ 

60

70

50

10

20

30

DAS

40

0

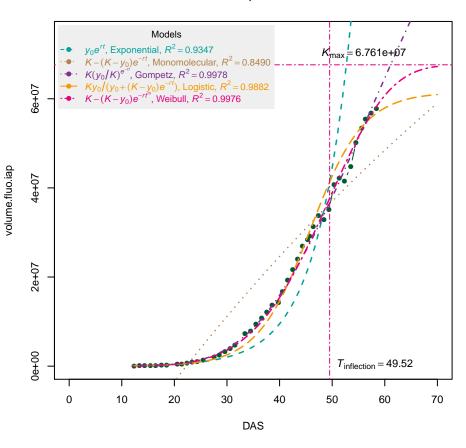
10

20

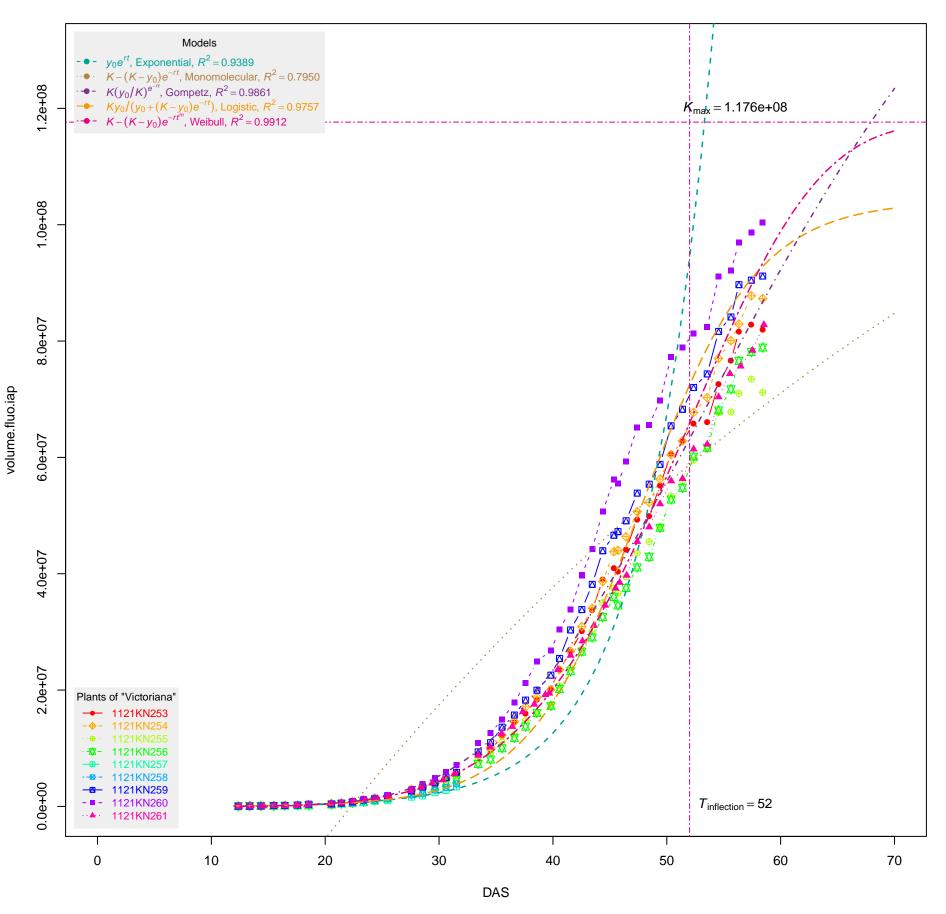
30

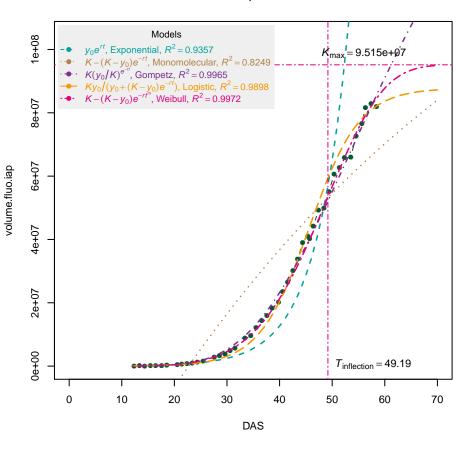
DAS

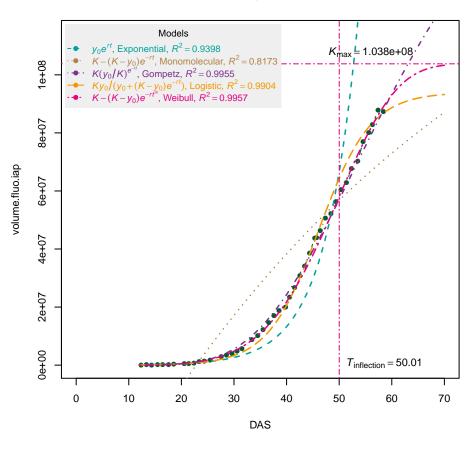
### Plant=1121KN243, treatment=control



# **Genotype=Victoriana**, treatment=control

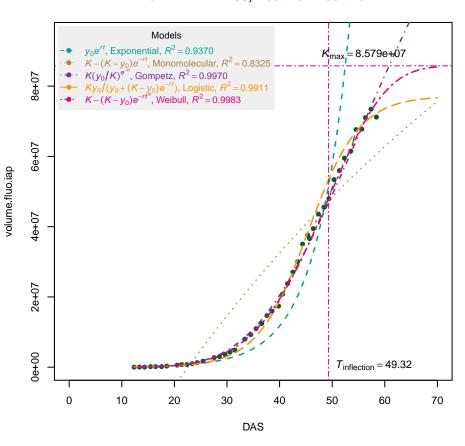


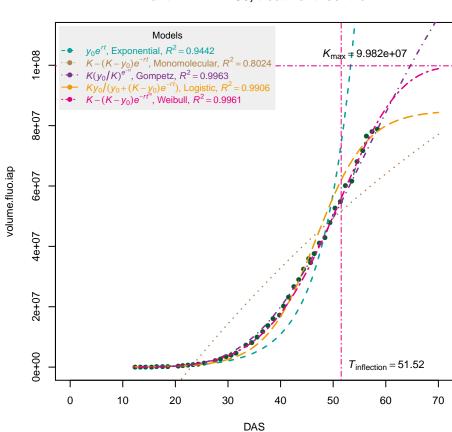


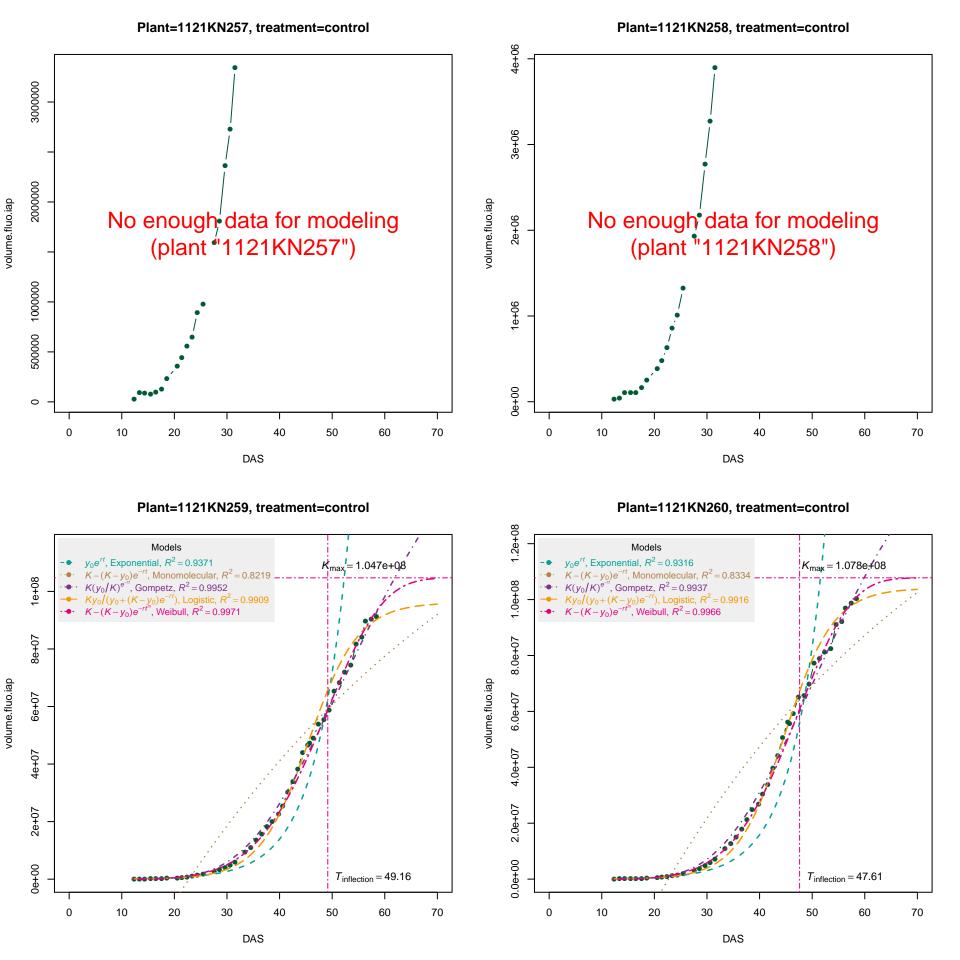


Plant=1121KN255, treatment=control

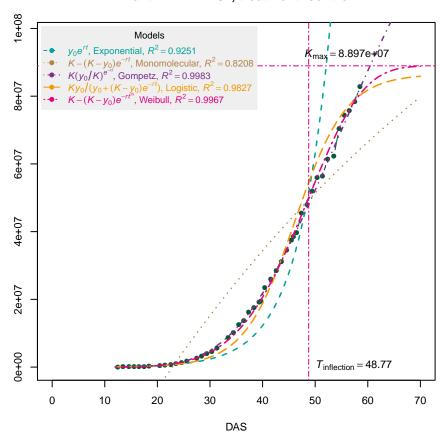
Plant=1121KN256, treatment=control





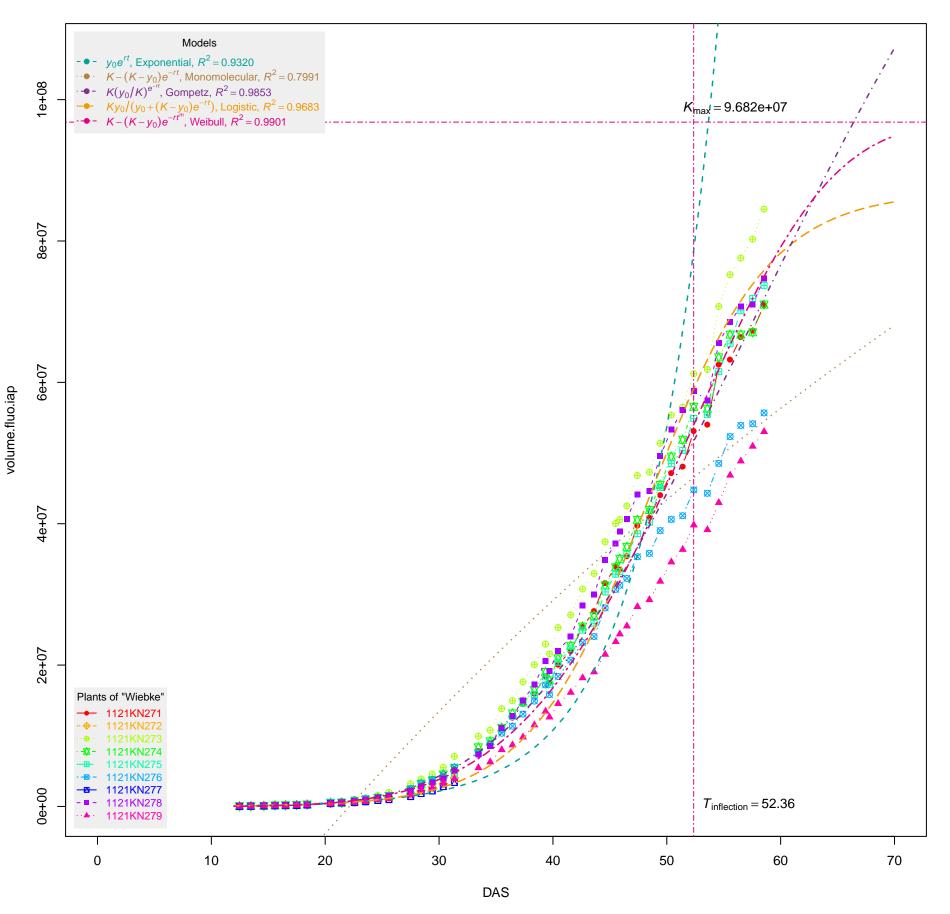


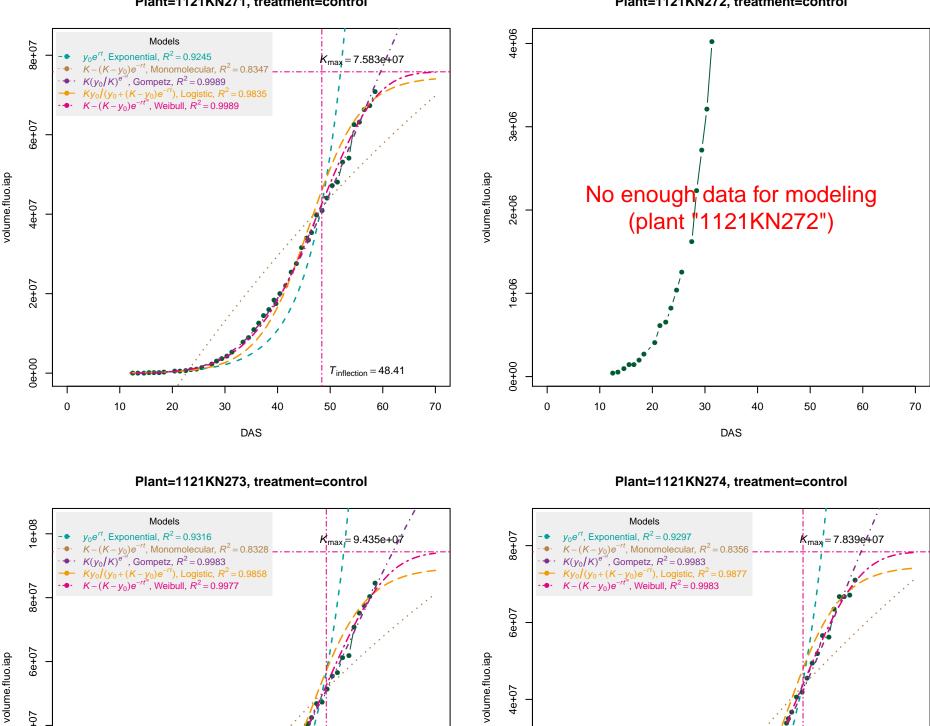
### Plant=1121KN261, treatment=control

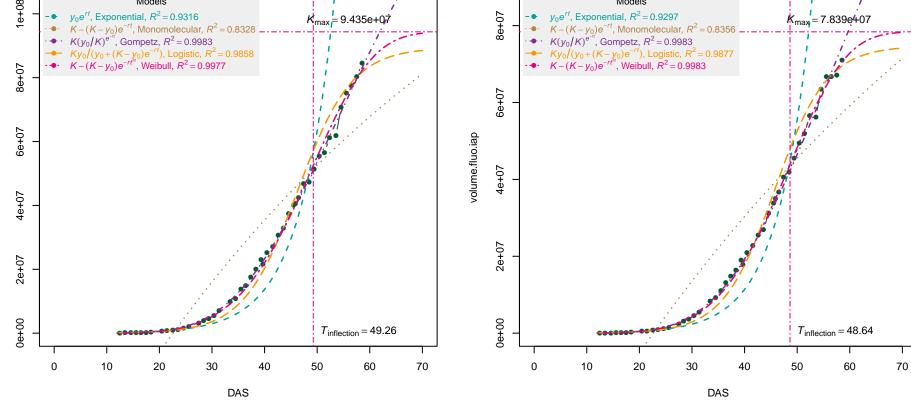


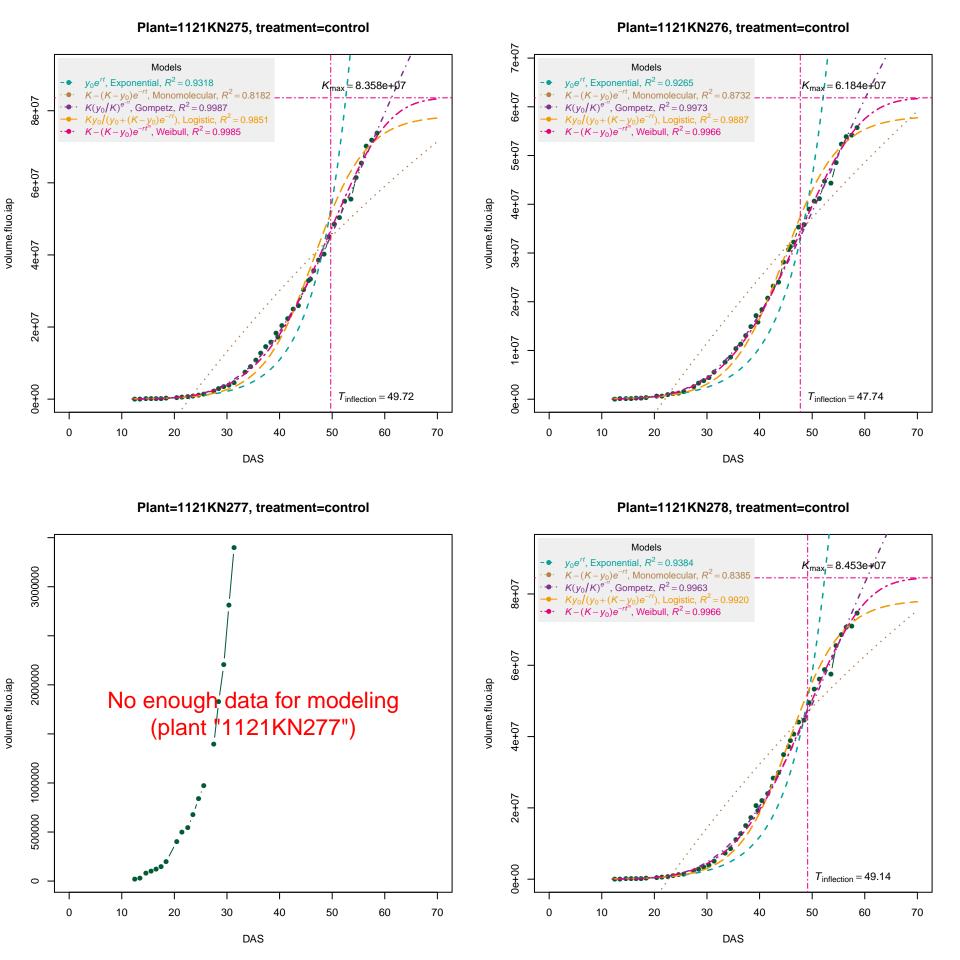
volume.fluo.iap

# **Genotype=Wiebke**, treatment=control









#### Plant=1121KN279, treatment=control

