Table 1: Statistics from molt model with data from 2016-2022. Mean dates, with 95% credibles intervals, are given as day of the year (since 1 Jan). The ranges are 2.5th-97.5th percentiles of every estimate over all 7 years. Sample sizes used in model: 838 molt sequences of adult females, 176 juvenile females, 164 juvenile males.

	Molt day		Molt duration	
Category	Mean (95% CI)	Range	Mean (95% CI)	Range
adult female	136.6 (135.6,137.6)	19Apr-13Jun	6.0 (5.5,6.3)	3.5-8.9
juvenile female	129.3 (127.7,131.0)	20Apr-04Jun	10.8 (9.8,11.6)	8.1-15.1
juvenile male	122.9 (121.2,124.5)	13Apr-26May	10.3 (9.1,11.6)	5.1-23.5

Table 2: Days of arrival, mid-molt (when 50% fur replaced), and departure in elephant seals at Año Nuevo, 2016-2022, estimated from molt and tenure models. Mean and standard deviation are given as day of the year (since 1 Jan: 91 = 1 April, 130 = 10 May, 160 = 9 June), with 95% credibles intervals. The final column gives the same means as a date, along with the range of dates (5th and 95th precentiles across all years). Sample sizes used in tenure model: 455 haul-out sequences of adult females, 106 juvenile females, 102 juvenile males.

Group	Event	Mean day (95% CI)	SD (95% CI)	Mean date (range)
adult female	arrival	118.7 (117.3,120.2)	15.0 (14.0,16.1)	29Apr (27Mar-24May)
	molt	136.6 (135.6,137.6)	13.9 (13.3,14.7)	17May (19Apr-13Jun)
	departure	161.2 (160.1,162.3)	11.2 (10.4,12.2)	10Jun (21May-30Jun)
juvenile female	arrival	103.1 (100.0,106.1)	14.5 (12.4,16.8)	13Apr (21Mar-11May)
	molt	129.3 (127.7,131.0)	10.1 (9.4,10.8)	09May (20Apr-04Jun)
	departure	150.0 (147.5,152.3)	10.9 (9.3,12.9)	30May (13May-21Jun)
juvenile male	arrival	99.4 (97.1,102.1)	11.3 (9.6,13.4)	09Apr (24Mar-30Apr)
	molt	122.9 (121.2,124.5)	10.1 (9.4,10.8)	03May (13Apr-26May)
	departure	145.7 (143.1,147.9)	10.4 (8.8,12.2)	26May (12May-13Jun)

Table 3: Statistics for arrival-tenure regression, three age-sex categories, 2016-2022. Credible intervals (parentheses) were calculated using posterior distributions from Bayesian model of tenure and arrival, incorporating error in every individual estimate. Intercept is estimated tenure at arrival day = 0, slope is reduction in tenure for each day later arrival.

	Intercept	Slope	N
Adult-female	94.6 (93.3,103.2)	-0.44 (-0.51,-0.43)	455
Juvenile-female	100.7 (99.6,113.6)	-0.52 (-0.64,-0.51)	106
Juvenile-male	81.3 (78.0,102.8)	-0.35 (-0.56,-0.32)	102

Table 4: Statistics for breeding-non-breeding comparison among adult females, 2016-2022. Credible intervals (parentheses) were calculated using posterior distributions from Bayesian model of molt. Molt date is day of year, duration is number of days between 5% and 95% molt. Breeding were females observed the winter before, during the breeding season; non-breeding are those not observed (thus including any breeders that were not observed).

	Date	Duration	N
Non-breeding	128.2 (127.8,128.7)	6.0 (5.6,6.4)	165
Breeding	139.3 (139.2,139.5)	5.9 (5.6,6.2)	673

Appendices

Alternative logistic parameterization

We reparameterized the standard logistic function so that the two parameters are precisely what we seek. Define $F(t) \in (0, 1)$ as the fraction molted as a function of day t. The standard logistic function is

$$F(t) = \frac{e^{a+bt}}{1 + e^{a+bt}} = \frac{e^{t'}}{1 + e^{t'}}, \tag{1}$$

where a and b are the parameters and $t' = a + bt$ is written for convenience. First define one new parameter, c, as the day of mid-molt, ie the day when molt reaches 50%, $F(c) = 0.5$. That happens at $e^{t'} = 1$, when $t' = 0$ so

$$c = -\frac{b}{a}. \tag{2}$$

Next, define a parameter d as the time between 5% and 95% molt, ie the time it takes the animal to molt. Find t' at $F = 0.05$ and 0.95,

$$F(t') = \frac{e^{t'}}{1 + e^{t'}} = \begin{cases} 0.95 & \text{when } t' = \ln 0.95 - \ln 0.05 = \ln 19 \\ 0.05 & \text{when } t' = \ln 0.05 - \ln 0.95 = -\ln 19, \end{cases} \tag{3}$$

where ln is the natural logarithm. That means $t = -a/b \pm (\ln 19)/b$. The desired parameter d is the difference between those two values of t,

$$d = \frac{2 \ln 19}{b}. \tag{4}$$

The logistic function never reaches 0 or 1, and we chose 5% and 95% based on the limits of our observations. Had we chosen instead 1% to 99% as the definition of molt time, parameter d would be 1.56× higher ($2 \ln 99$).

The model was fitted using the new parameters c and d, and all results are presented with those parameters. Within the model, an algorithm in a subroutine converted c and d back to a and b (Eqs. 2, 4) to make use of the standard logistic formula (Eq. 1). It was therefore not necessary to rewrite Equation 1 using c and d.

Modeling molt date

Our goal here was to estimate the mean molt date and its variance. We used data from 2016-2022 because we had detailed observations of many individuals in each of those years,

and preliminary calculations indicated there was no year-to-year variation in molt date over that period. To assure valid estimates, however, we used a model including both a year term and a term for individual animals. That avoided concerns about repeated measures from individuals whose molt was observed in more than one year. The terms for year and individual required fitting the logistic curve to molt progress in an hierarchical framework, with two levels: individual and year.

For each individual i in year j, the model included a pair of molt parameters (c_{ij}, d_{ij}), which we write θ_{ij} for brevity. There were hyper-means $\widehat{\theta_i}$ for each individual and $\widehat{\theta_j}$ for each year, along with a grand hyper-mean $\boldsymbol{\theta}$, the mean molt across all individuals and years. Within each group (individual or year), we assumed parameters followed a Gaussian distribution, so there were corresponding hyper-standard-deviations σ_a, σ_y. There was a single σ_a for all animals, assuming all had the same year-to-year variation (a standard assumption in multi-level models), and one σ_y across years.

Fitting individual parameters required an error term for molt observations, ϵ, which was assumed to be constant for all individuals in every year; ϵ was estimated along with the molt parameters. The probability of one observation of a molt fraction, M_{ijt}, on day t for individual i in year j, given the parameters, is

$$P_{ijt} = \mathcal{N}(M_{ijt}, Mean = F(t, \theta_{ij}), SD = \epsilon), \tag{5}$$

where $F(t, \theta_{ij})$ is the logistic prediction on day j given parameters θ_{ij} (Eqs. 1, 2, 4). $\mathcal{N}$ means the normal probability of observing $M_{i,j,t}$ given the mean and standard deviation ϵ. A Gaussian error for the observed fraction molted was not our first choice, since M is constrained to $[0, 1]$. We tested alternative errors (beta, logit, half-normal), and the Gaussian worked best, leading to strong parameter estimates quickly. The fact that M is never < 0 though the Gaussian error would accept it does not cause errors. Overall, we found an estimate of $\epsilon = 0.10$, showing that observations of percent molt were $\pm 10\%$.

There were additional likelihood functions for the hyper-parameters, for example,

$$H_i = \mathcal{N}(\theta_{ij}, Mean = \widehat{\theta_i}, SD = \sigma_a) \tag{6}$$

is the probability of the individual's estimated mean $\widehat{\theta_i}$ given its annual estimates θ_{ij} and the within-animal standard deviation σ_a. There were also likelihood functions for the year means $\widehat{\theta_j}$ and the grand mean $\boldsymbol{\theta}$. The only prior probabilities for any parameters were the trivial requirements that standard deviations be > 0.

The full likelihood for observations of one individual included both the probability of observations given the logistic model (Eq. 5) and the probability of the hyper-mean (Eq. 6). The likelihood of hyper-parameters, however, did not depend on individual observations, only the estimates of all individual means. The same applied to observations within and across years. This is the key to the multi-level approach, because some individuals had too few observations to produce a useful fit of the logistic model on their own, while others with many observations throughout the molt produced strong estimates of logistic parameters. By including the hyper-parameters, those with many observations supported

those with few . This worked well with the molt data, because parameter d, governing how fast they molted, varied little among females, so in animals with poor data, the population-wide $\hat{d}$ helped shape the curve. But c, the date of molt, varied widely between animals, meaning that molt day for animals with poor data was poorly constrained.

Parameter fitting

We used a Bayesian, Monte-Carlo parameter-fitting method, sampling the posterior distributions by repeated Metropolis updates. The model for adult females included 383 individuals over 7 years, with a total of 837 female-year combinations, meaning 837 logistic parameters, 390 hyper-means, plus a grand mean and 3 standard deviations. At each step of the Monte Carlo chain, one of those parameters was updated by a random draw, and a new likelihood was calculated (Eq. 5, 6). The Metropolis algorithm explores parameter space, accepting new parameter combinations close to the maximum likelihood but not at the maximum. Models for adult females, juvenile males (164 animal-years), and juvenile females (178 animal years) were run separately.

The completed Markov chains from each model provided the posterior distributions for all parameters and any statistics derived from parameters. Chains were run 20000 steps, and examined visually for mixing; they converged quickly. The initial 16000 steps were discarded as burn-in. We report the mean of post-burn-in chains as best estimates, and quartiles 0.025 and 0.975 for 95% credible intervals. Hypotheses were tested by checking overlap of credible intervals.

Modeling arrival and departure

A model for the tenure of every individual throughout the spring haul-out was separate from the molt model because it is an independent topic. We decided, however to take advantage of estimates from the molt model in several ways that both strengthened and simplified the tenure estimates. First, most of the adults carried dye marks on their unmolted fur from the winter breeding season, then lost the mark upon molting. Animals were thus harder to detect after molting. Arrival and departure models were thus separated, the former using all observations prior to an individual's estimated molt day (parameter c in the molt model), the latter using observations after the molt day. We also used a subset of all animals having molt date estimated with high precision, those with 95% credible intervals of $c < 6$ days wide. This is a well-observed subset and thus leads to stronger estimates of arrival and departure dates.

A second way we took advantage of the molt results arose because we found no year-to-year variation in molt date. For this reason, we omitted a year term from the arrival and departure models. Moreover, we simplified the model by omitting a hierarchy for individuals across years. The single multi-level feature was the animal-year combination. Thus, the estimate for each individual was separate in every year. In well-observed animals,

arrival and departure dates were strongly constrained by observations, and in our current analysis, we are not interested in variation among individuals.

Both arrival and departure estimates arose directly from observations in a straightforward way. If an animal was first seen on 1 May, the arrival date must be $\leq$ 1 May. If that animal was then observed most days until molting, arrival was probably close to 1 May, but if the animal was only seen every fifth day, there would be a good chance it arrived several days earlier. The delay between true arrival and observed arrival thus depends on detection probability, which is a simple calculation. After the first observation, we counted all days an individual was observed divided by all days observers were in the field. It was important to exclude the first day from this calculation, otherwise the detection estimate would be biased upward. The departure estimate is exactly the same in reverse.

The parameters needed are A_k, the arrival date, and δ_{k1} detection probability, both referring to individual-year combination k. The 1 indicates detection before the molt. The likelihood of δ was estimated as

$$P(\delta_{k1}) = \mathcal{B}(T, O), \tag{7}$$

where T is the total number of days with observations and O the number on which animal k was observed, with $\mathcal{B}$ meaning the binomial probability. Given δ, the probability of a date A was

$$P(A_{k1}) = \mathbf{G}(F - A, \delta_{k1}). \tag{8}$$

F is the first date observed and $\mathbf{G}$ is a geometric distribution with probability δ. It is the probability of failing to observe the animal $F - A$ times before the first success. Since there was a single hierarchy for arrival date across all female-year combinations (ie no year term), there was just a single hyper-mean and hyper-standard-deviation (as in Eq. 6). The likelihood functions for the model of departure D were equivalent, given post-molt detection δ_{k2}, a last day L of observation, and departure hyper-parameters. Arrival and departure parameters were fitted using the same Monte Carlo procedure described for the molt model. A tenure in every case was calculated as $D - A$ from every step of the Monte Carlo parameter chain.

Model verification

We graphed the fitted logistic curve for every individual's molt sequence in the years 2020-2021. These are included at the end of the Supplement. This allowed a visual check for cases where the curve missed data points. An example is animal 2020-49700, where the animal was recorded as unmolted, then fully molted once, unmolted once again, and finally fully molted; at least one must be an error. The model accommodated by fitting a gradual molt. Indeed, our visual screening revealed that poor fits such as this one were nearly always due to an error mistaking 100% molt for 0%, or vice versa, with the error usually producing an unusually gradual or unusually abrupt molt.

We thus screened all cases in adult females where the molt duration exceeded 9 days, and in

juveniles where it exceeded 12 days, over all years, 2016-2022. This led us to conclude that any molt duration > 10 days in adults and > 15 days in juveniles were caused by errors.

The tenure chart (main text, Fig. 2) highlights other outliers, and we thoroughly screened the most extreme. One obvious outlier appears at the top left of Figure 2, apparently arriving 70 days before molting. She was an interesting exception, because she had an horrendous and recent shark scar when she arrived to breed in January, probably losing her fetus in the attack. After departing in late February, she returned in early April for 6 days, was not seen for 66 days, and finally returned in June to go through a normal molt sequence. She broke the rule that animals always come ashore continuously during the molt, but she was still healing in March and likely could not migrate normally. The second extreme outlier (down Figure 2) also arrived 70 days before molting, but her early observation was easy to discount as a mis-identification. Other outliers in arrival might be valid, but can also be attributed to errors in molt score. We also checked two cases in Figure 2 in which females appeared to start molting before they arrived. Both are most likely due to a single mistaken molt score. There were few such outliers, we did not remove any from the data presented.

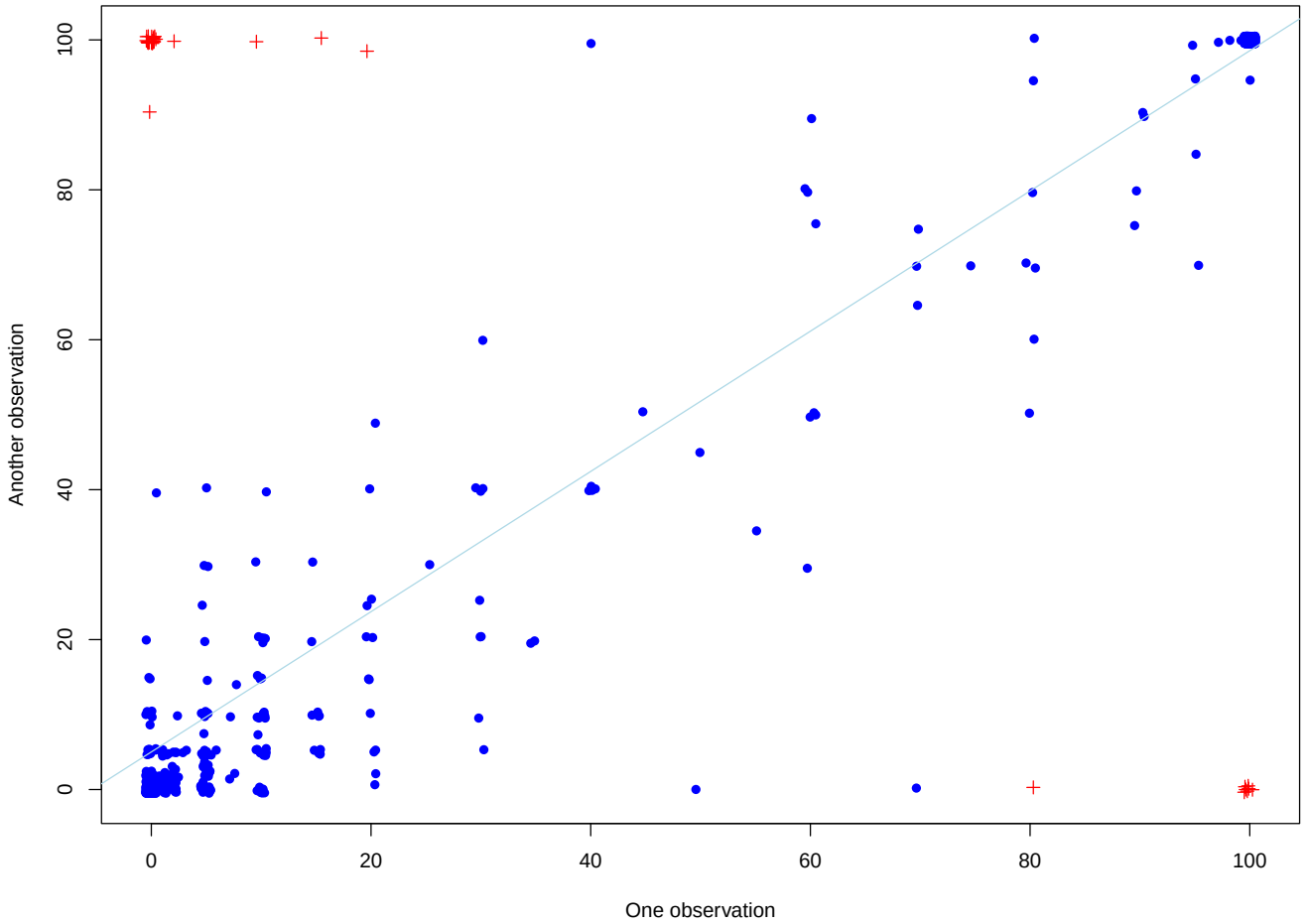
Post-hoc tests of molt date versus age and breeding status

To test whether molt timing (date and duration) varied with breeding status, we took advantage of posterior distributions for every molt-sequence (animal-year) in the Bayesian model, since these reflect statistical confidence. Statistics were recalculated using 200 randomly-selected sets of post-burn-in parameters from the Monte Carlo chains. Credible intervals were then calculated as 95^{th} percentiles of those 200 replicates; statistical significance was inferred from non-overlapping intervals.

Consistency of molt scores

Observations were frequent, and two or more observers worked together on most days, so there were numerous cases where two different people recorded a molt score for the same animal on the same day. There were occasions where one observer recorded data for the same animal twice, but we discarded those from this analysis in case they were duplicates. That left 1220 replicate estimates of molt, including 1079 with two observations, 135 with three, and six in which four different observers noted the same animal on a day. For the 1079 pairs, the two estimates were highly correlated, and in the vast majority of unmolted or fully molted animals, the two observers agreed exactly (Fig. A1). Among the 141 with > 2 observations, there were 117 where the entire set was identical; the average standard deviation across scores within a set was 1.06% molt.

Figure 1: Consistency of molt score using 1220 cases in which two or more different observers scored an animal on the same day over 2016-2022. The x-axis is one of the two scores, the y-axis the other. At the top right, there were 645 cases where both observations were 100% molt, and the bottom left includes 278 where both were 0% (points are jittered slightly, otherwise those would all appear as a single point). There were 32 cases, the red crosses, where observers were opposite, including 26 where one observation was 0% and the other 100%. The line is the regression ($r^2 = 0.986$). Removing all points at exactly 0% or 100%, scores were still consistent ($r^2 = 0.815$).



Supplemental References

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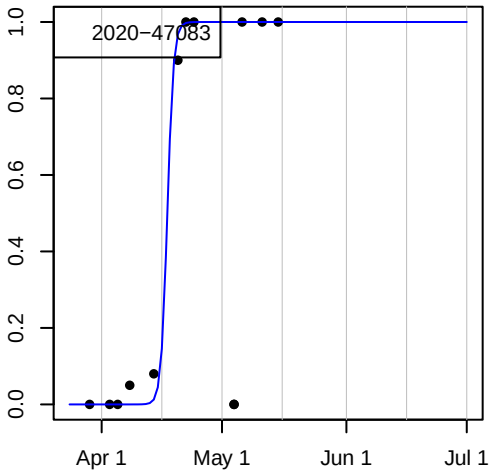
Complete model fits

Following are the logistic fits to every adult female's molt sequence in 2020 and 2021.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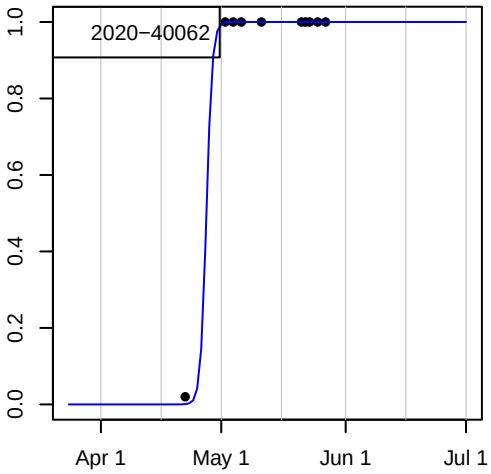
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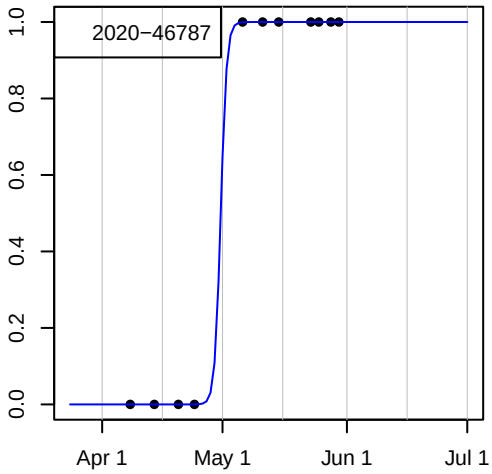
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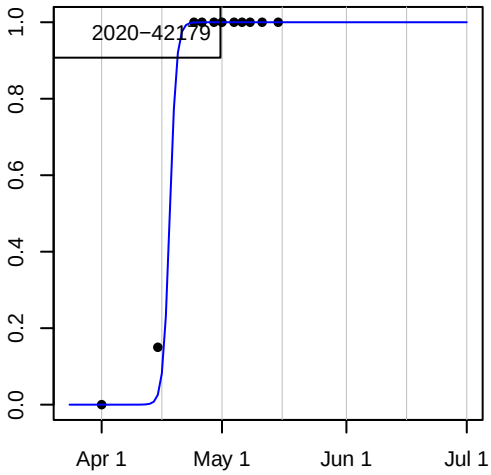
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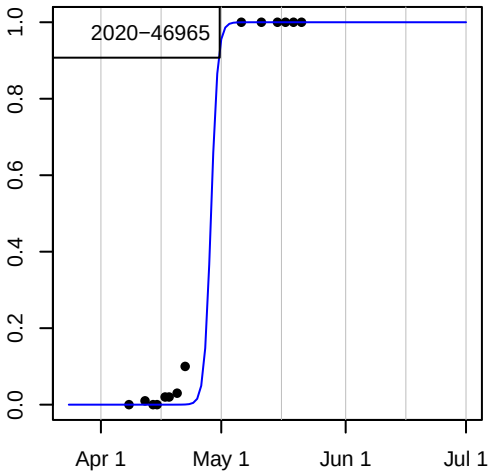
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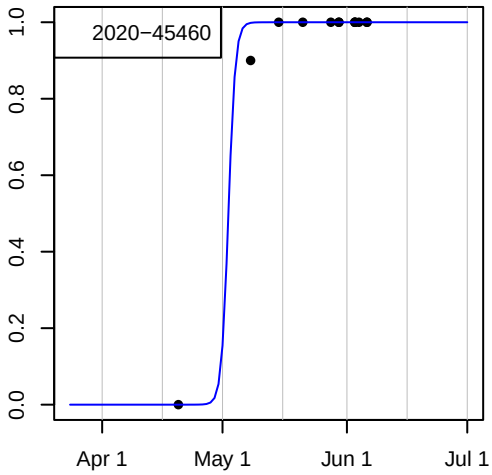
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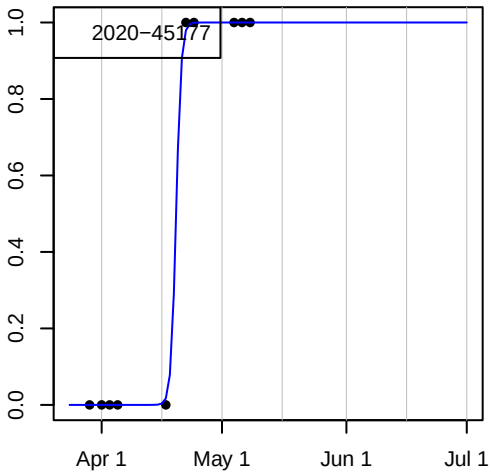
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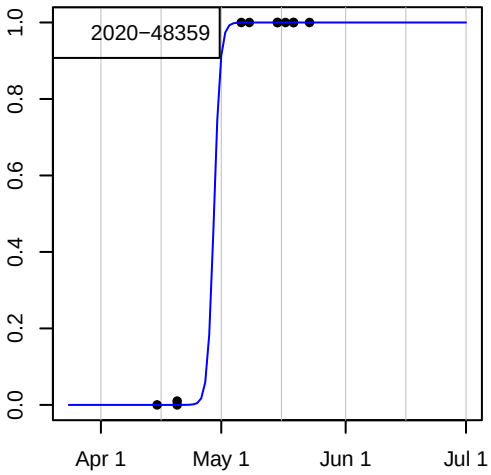
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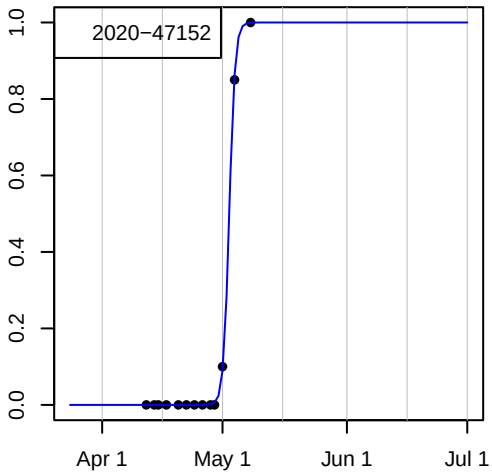
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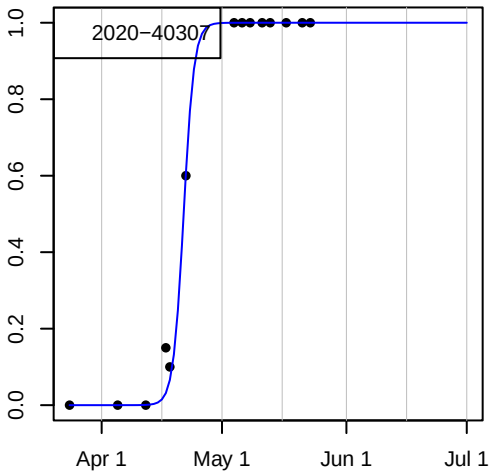
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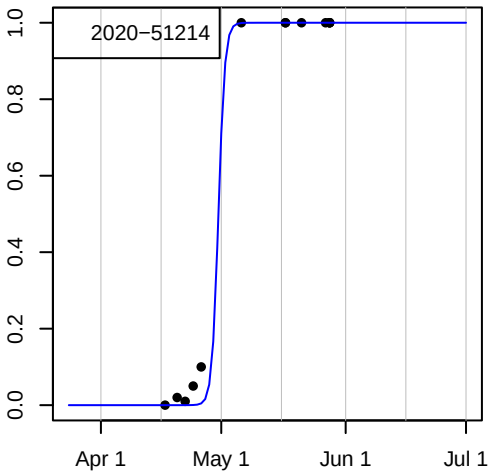
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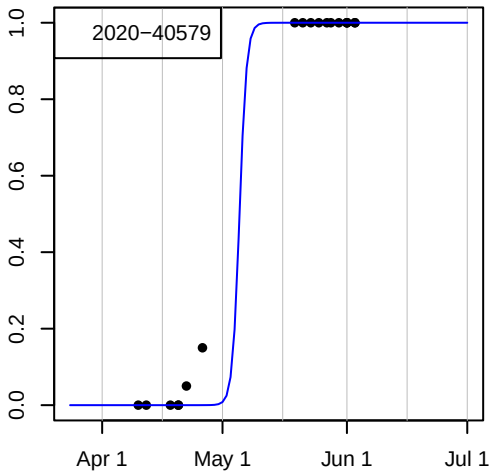
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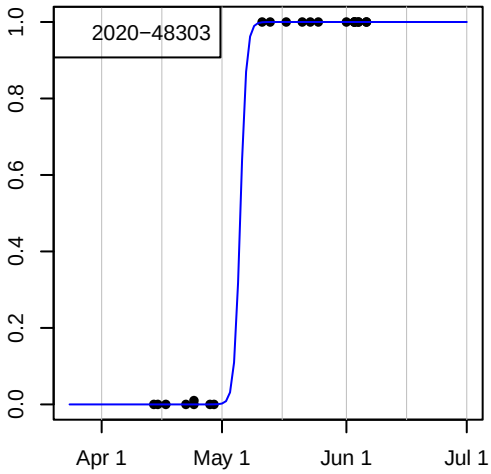
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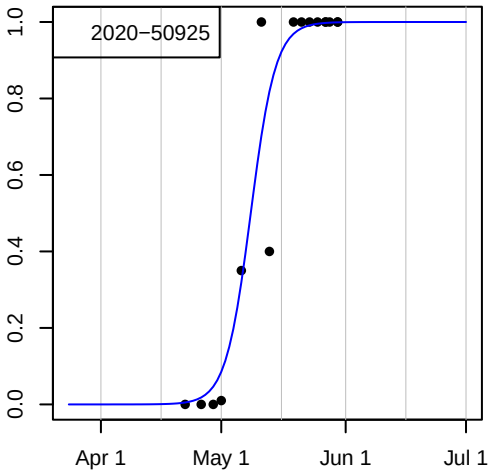
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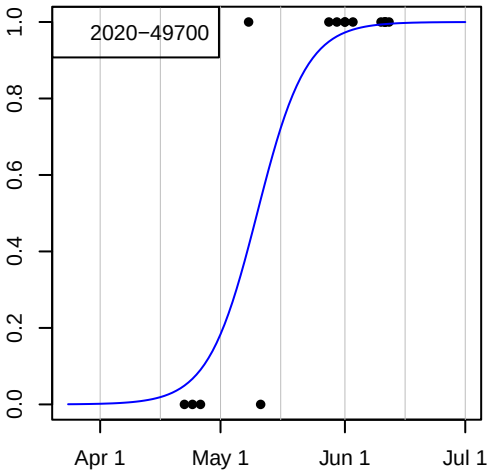
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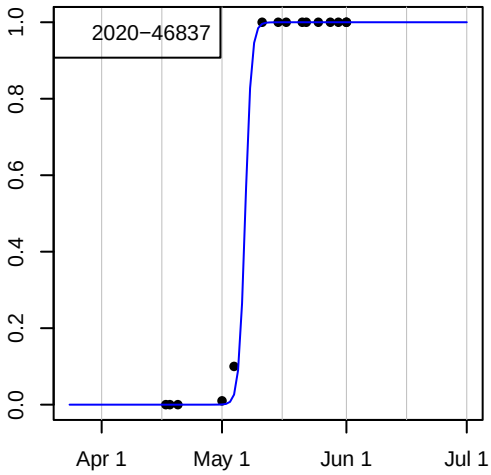
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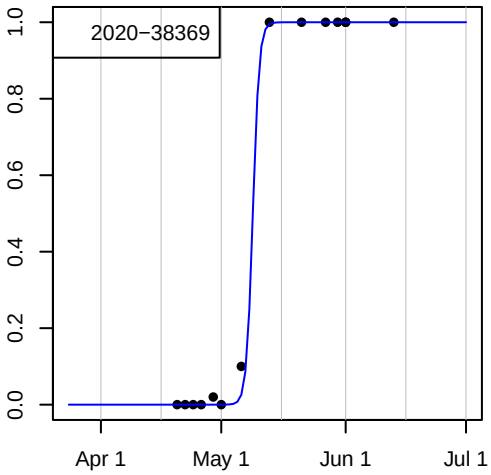
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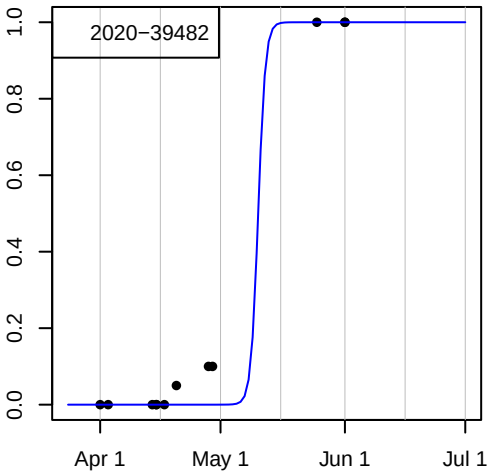
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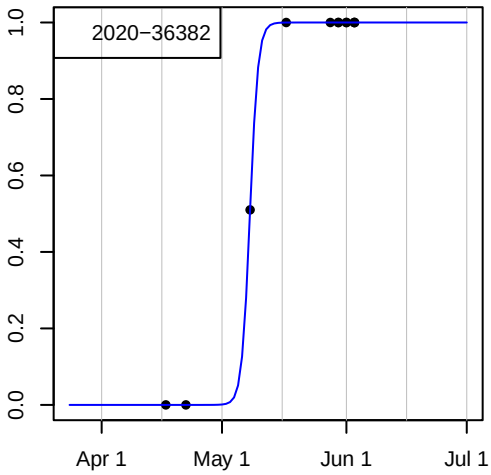
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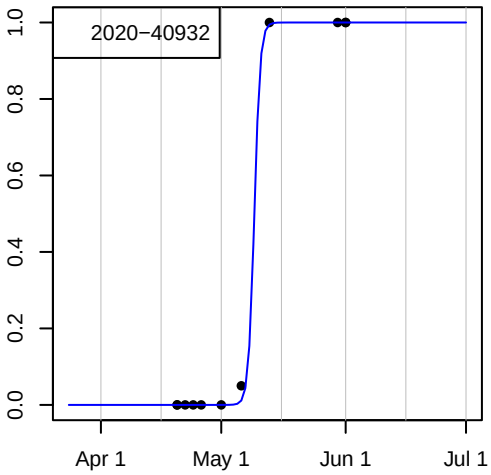
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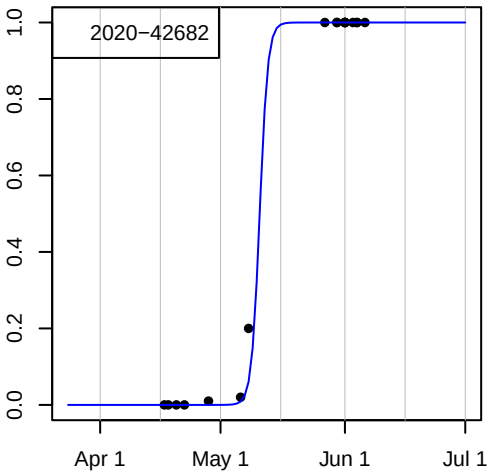
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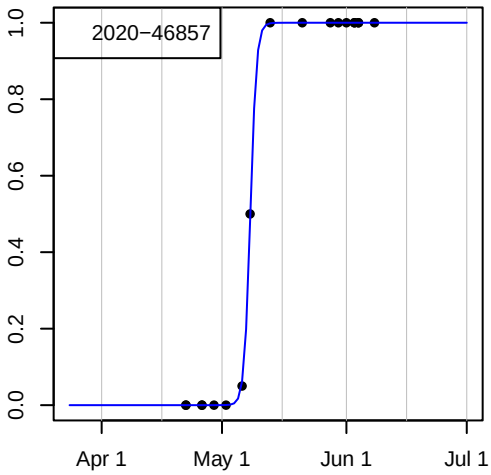
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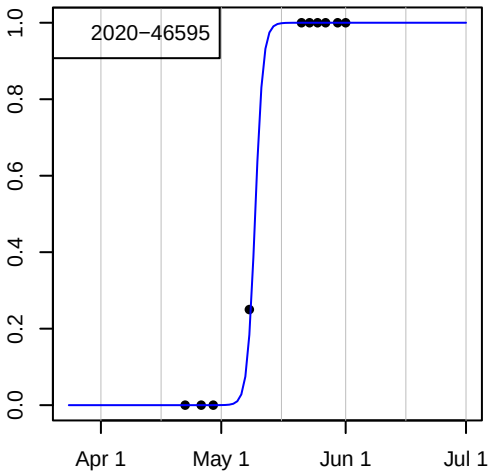
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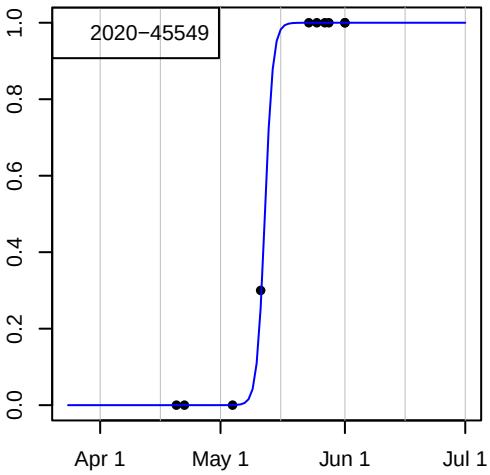
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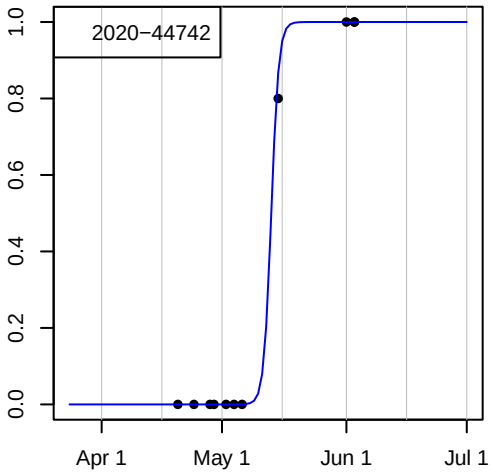
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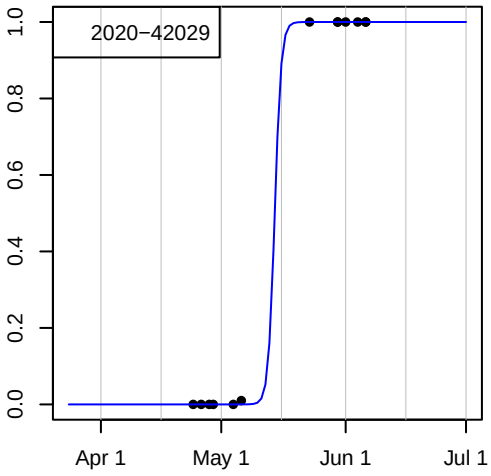
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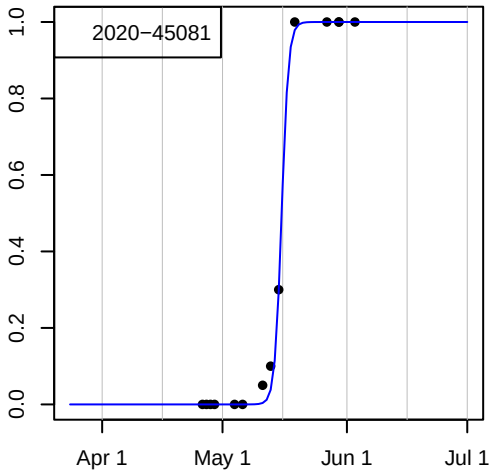
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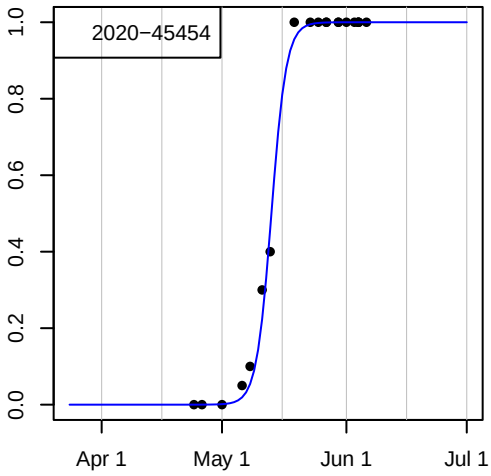
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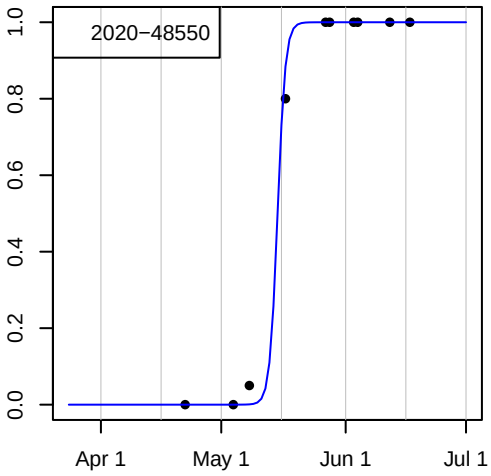
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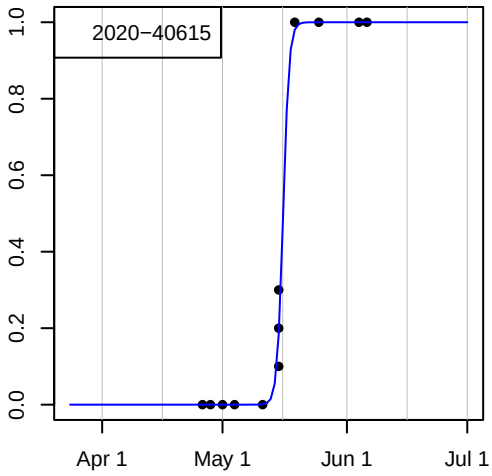
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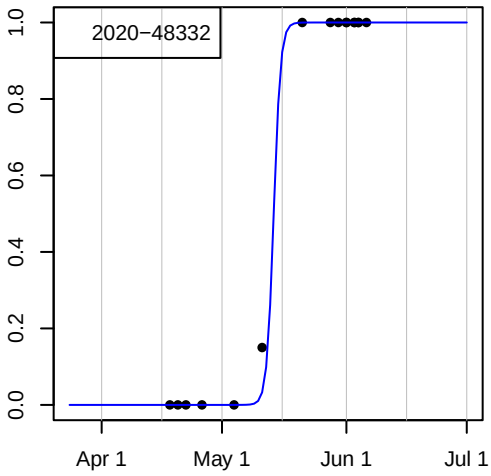
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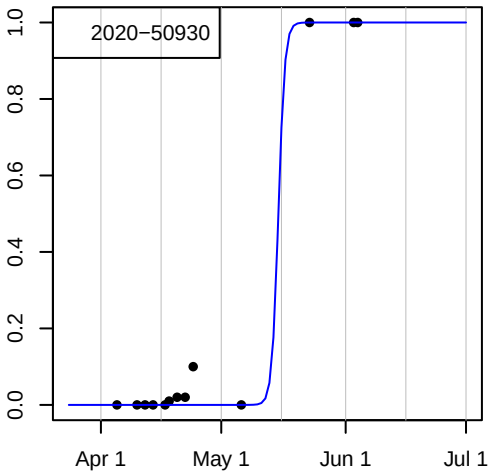
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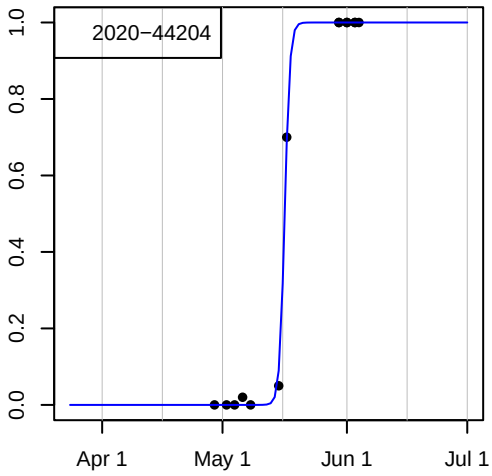
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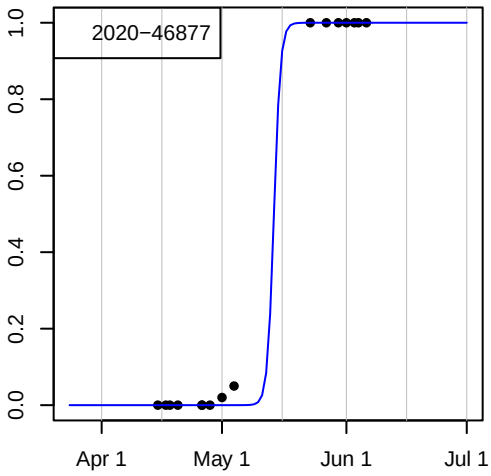
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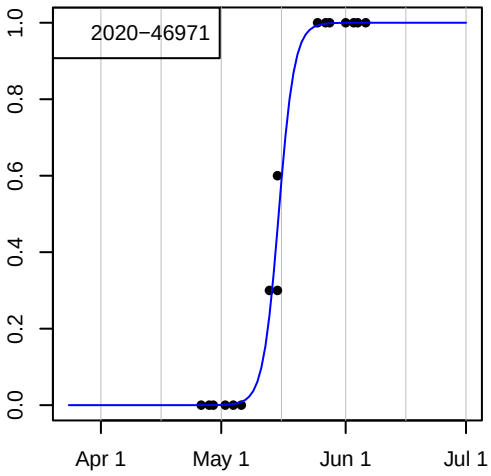
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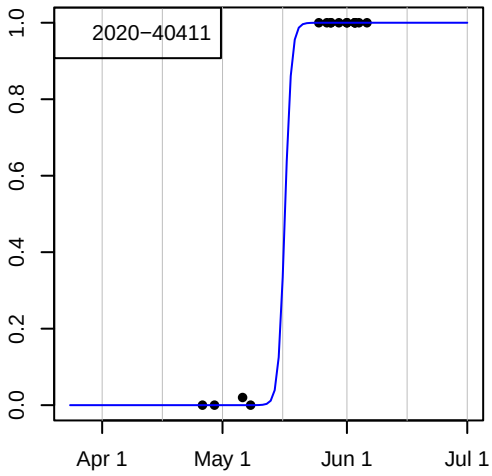
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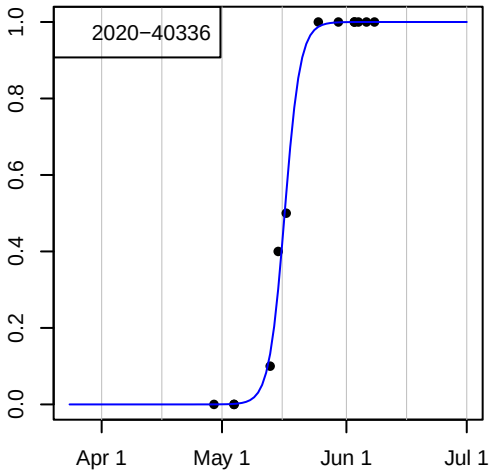
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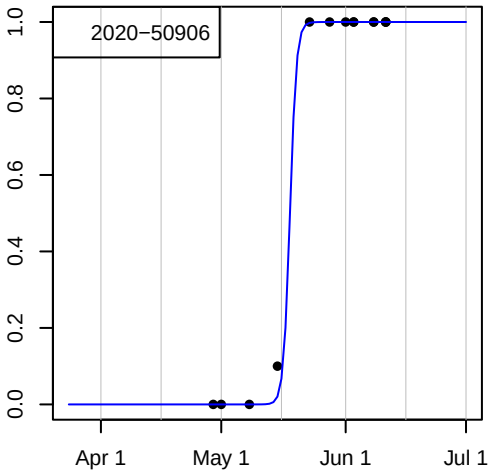
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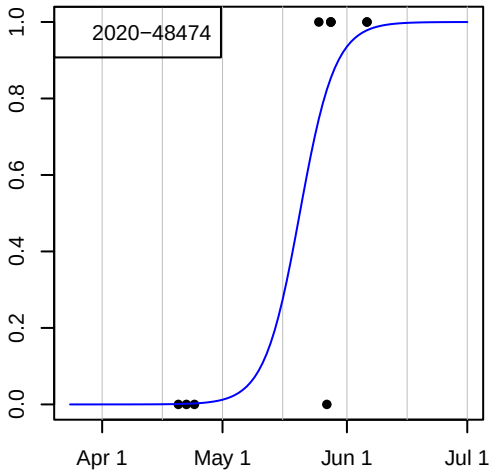
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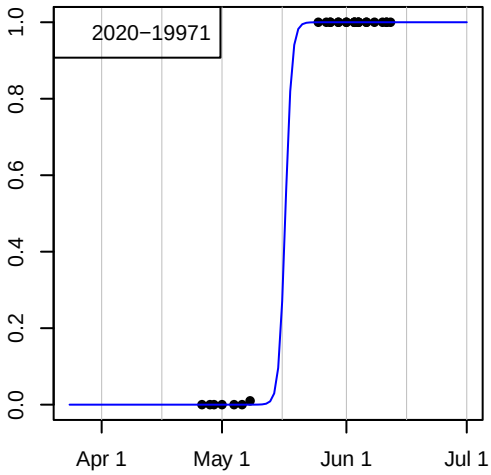
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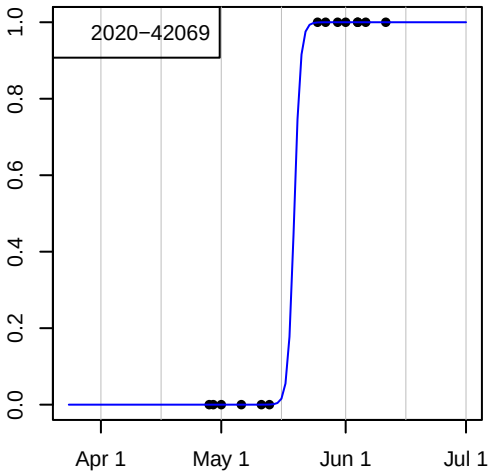
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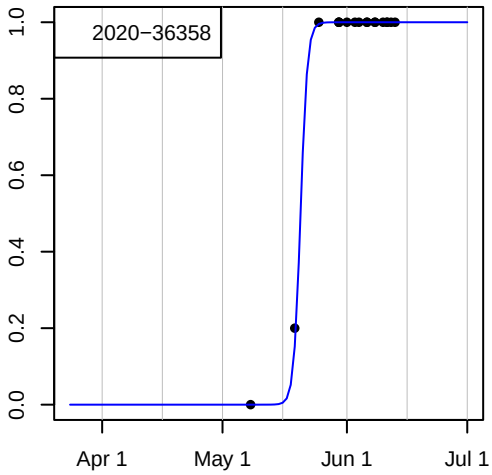
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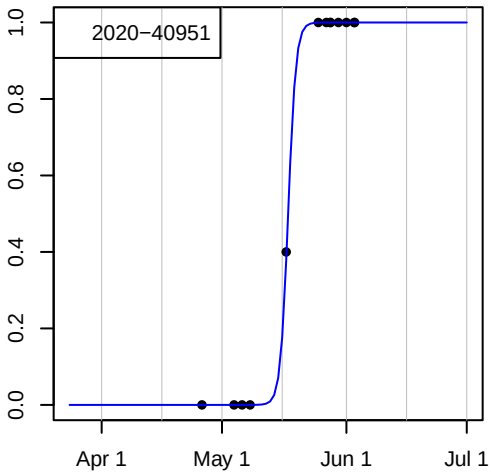
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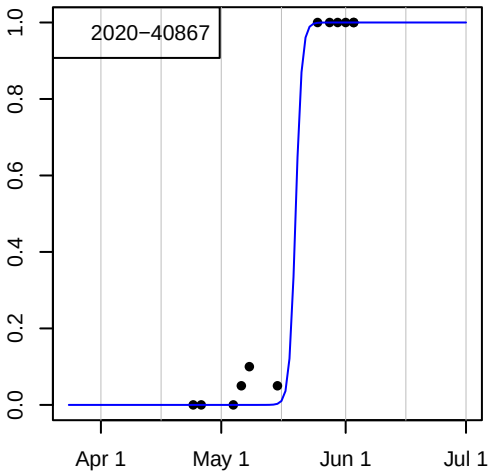
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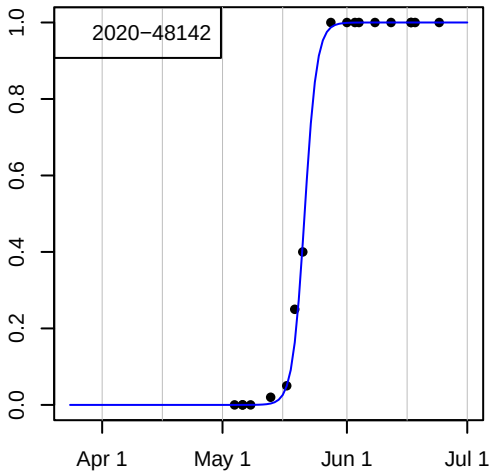
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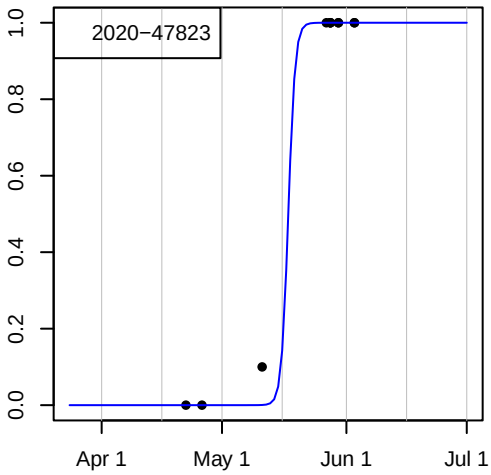
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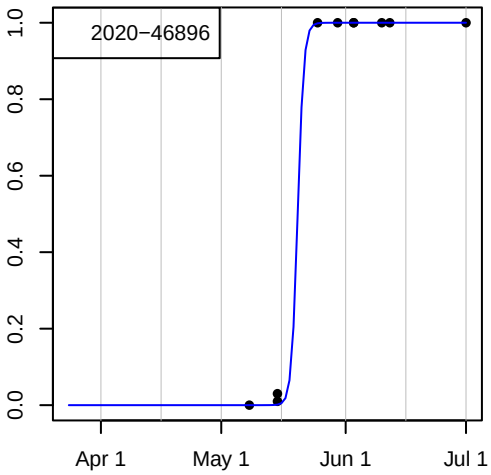
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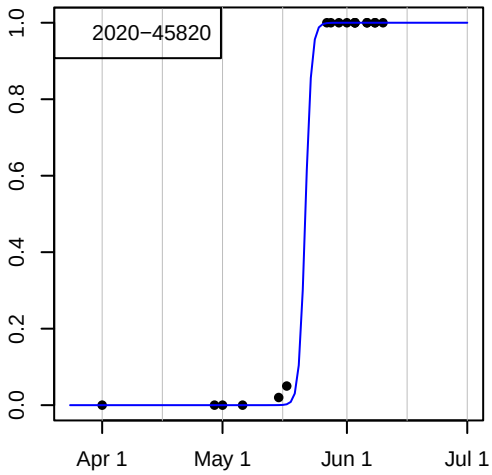
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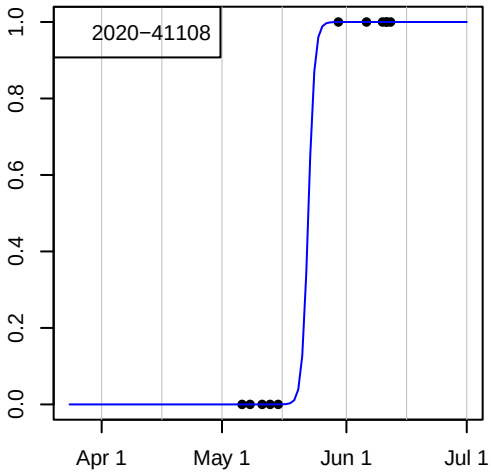
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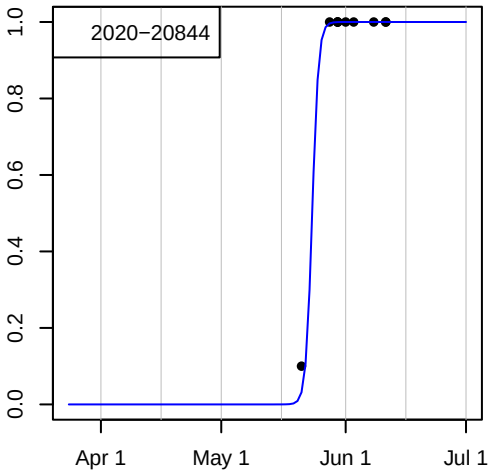
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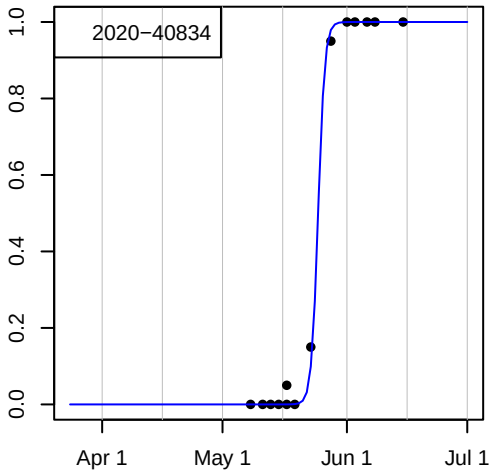
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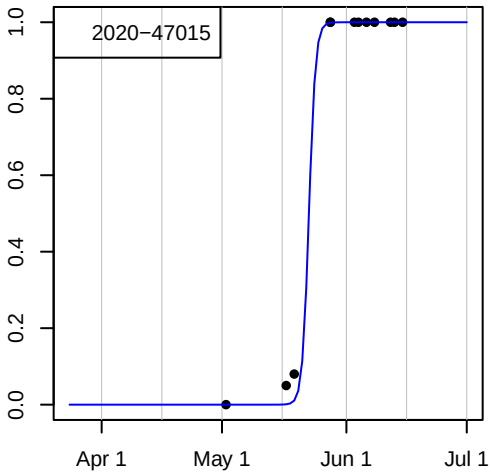
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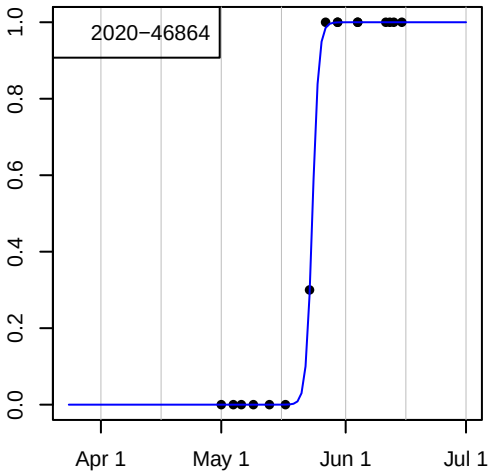
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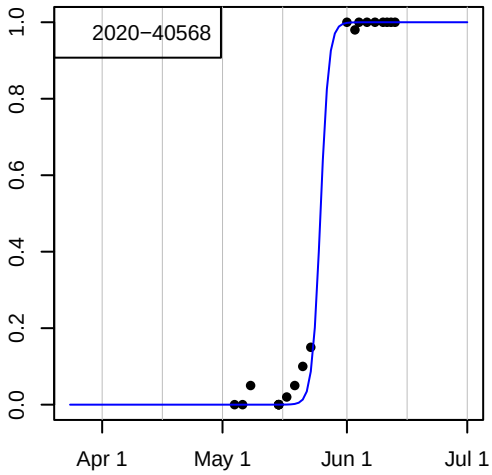
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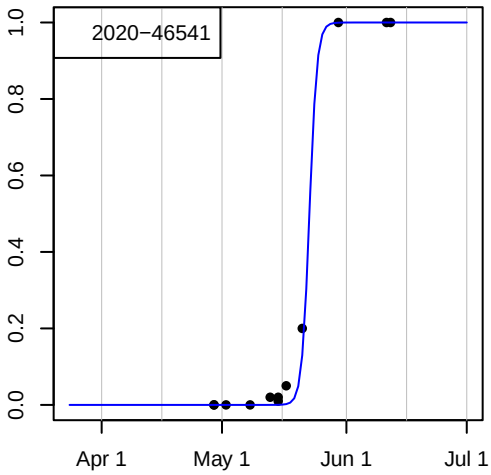
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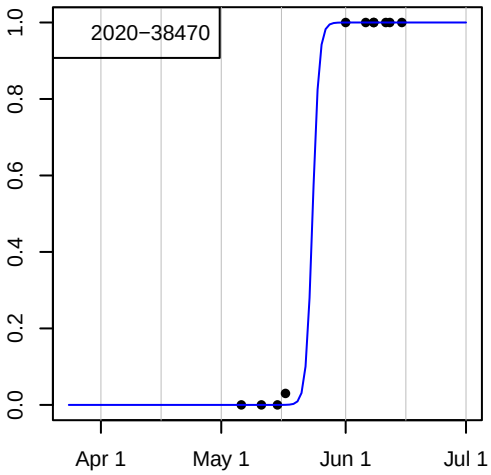
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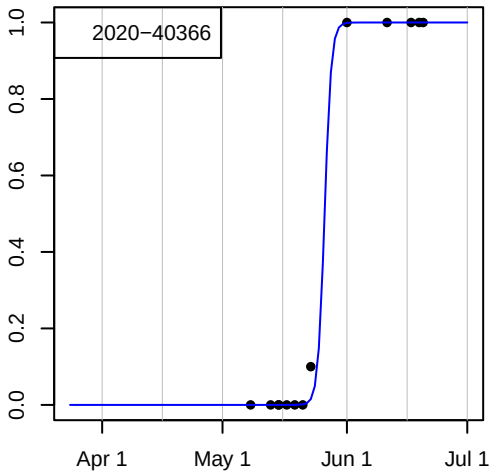
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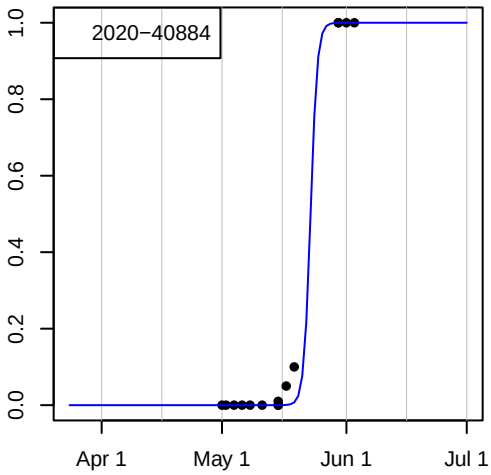
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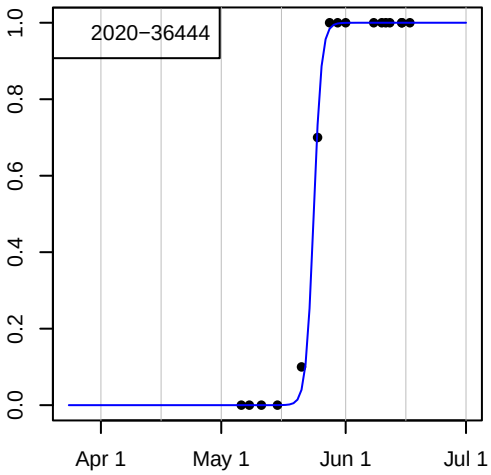
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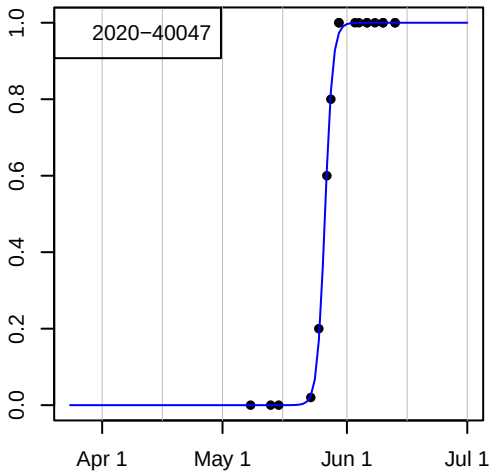
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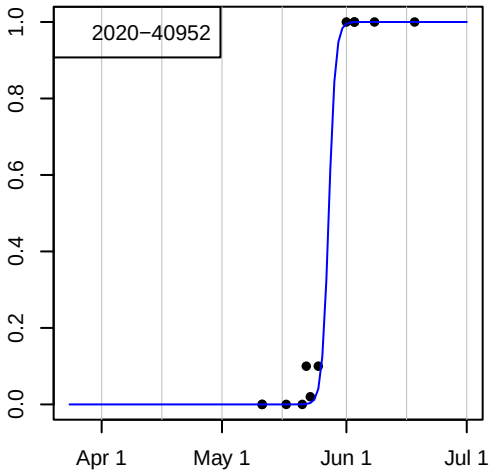
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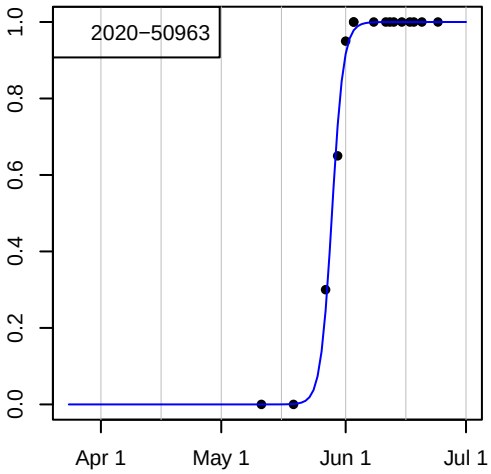
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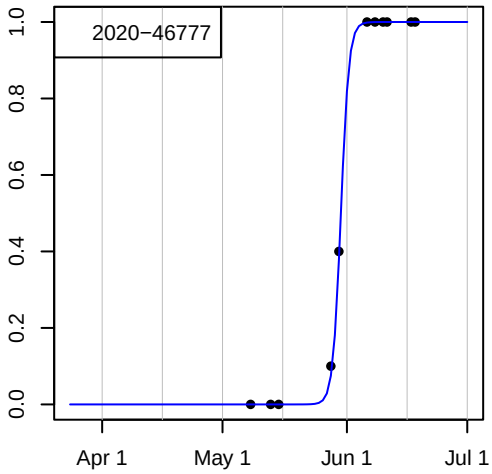
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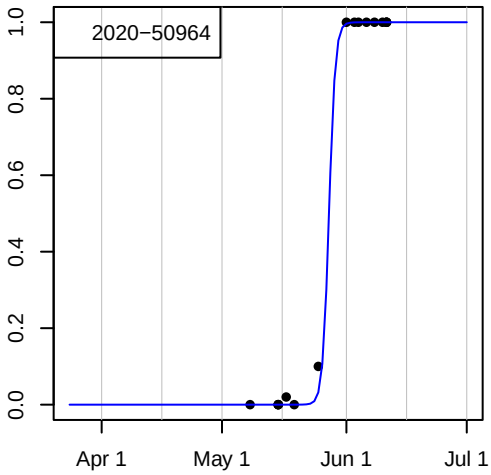
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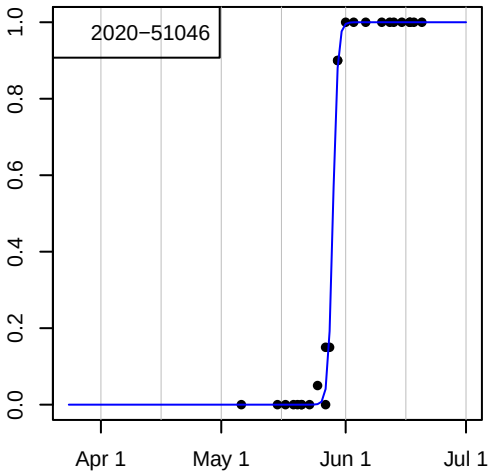
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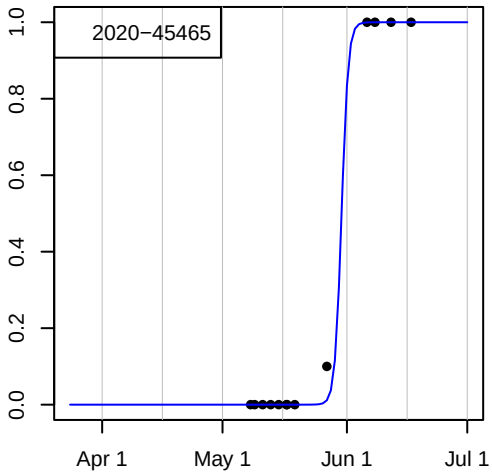
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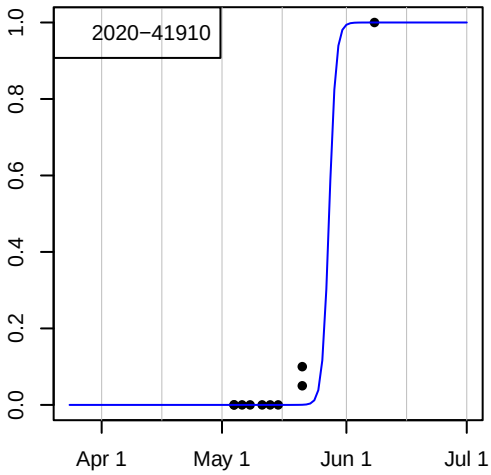
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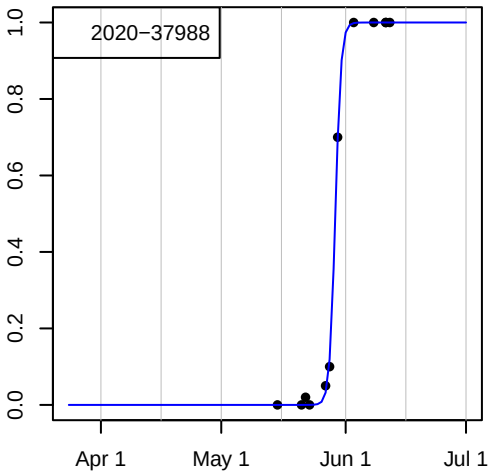
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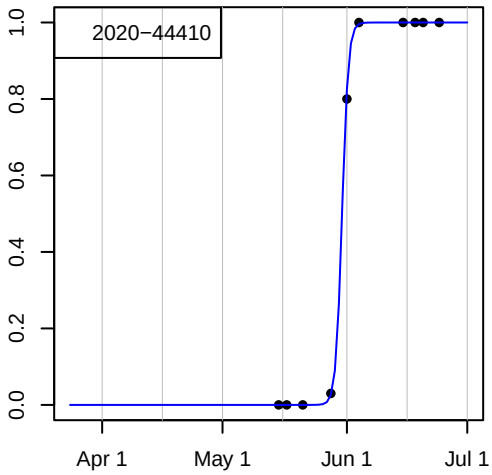
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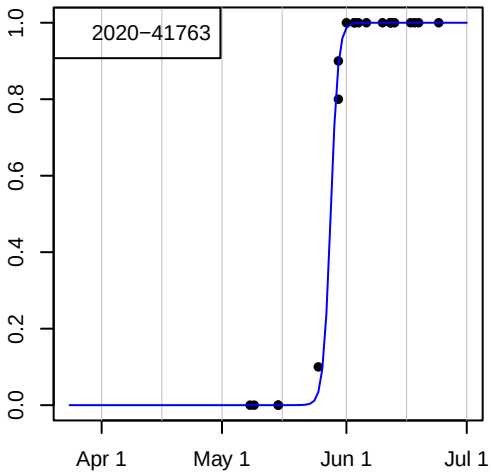
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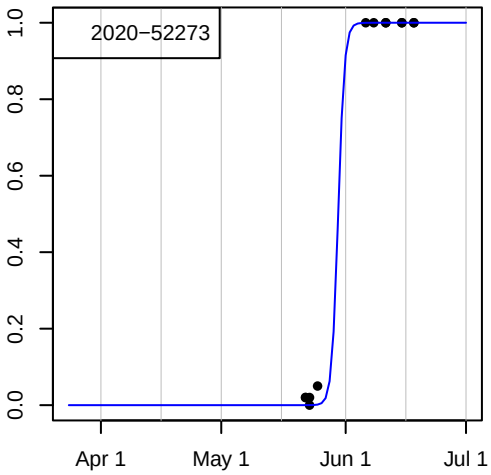
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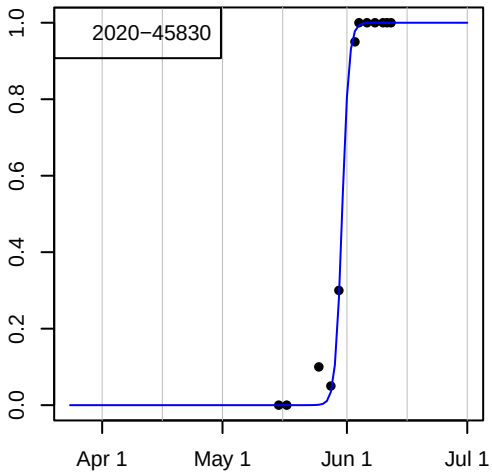
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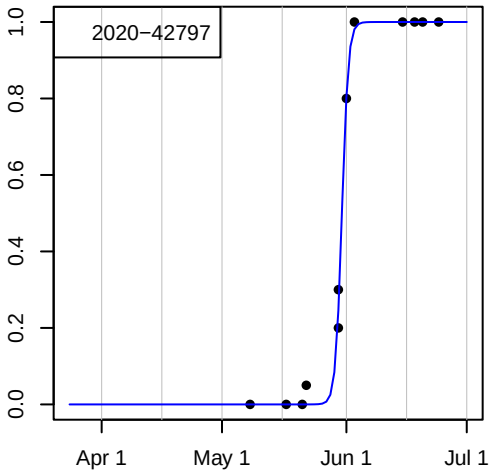
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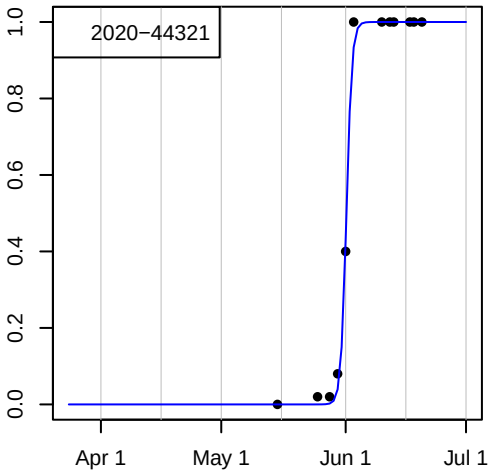
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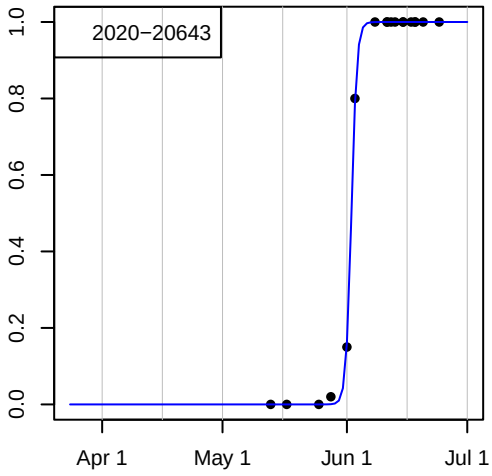
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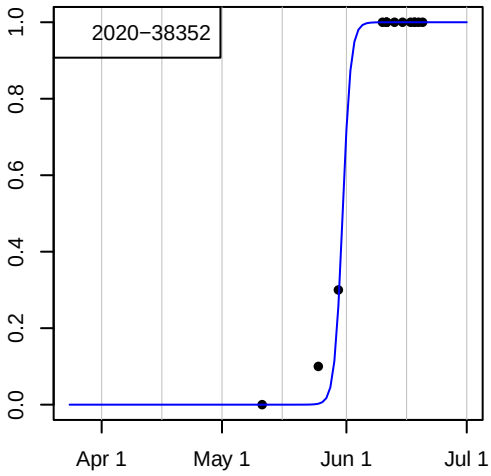
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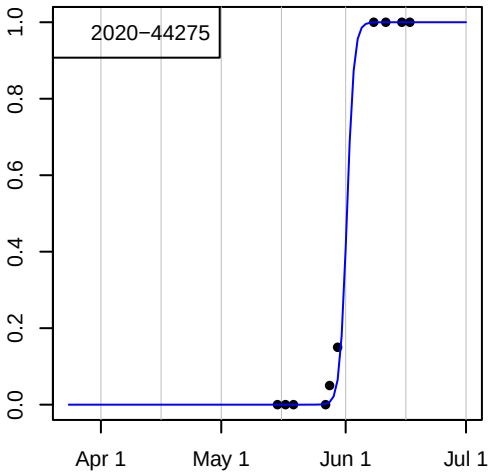
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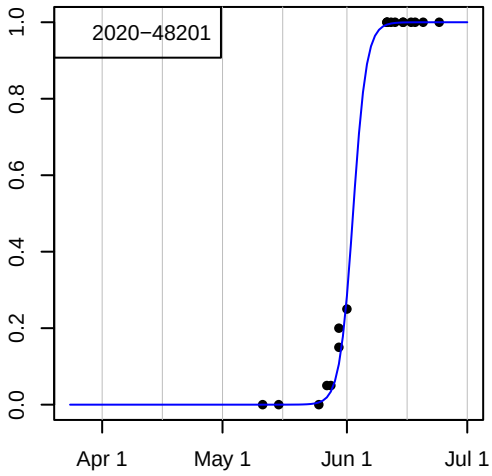
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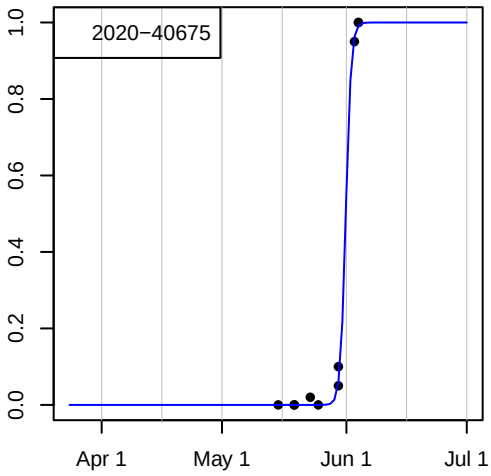
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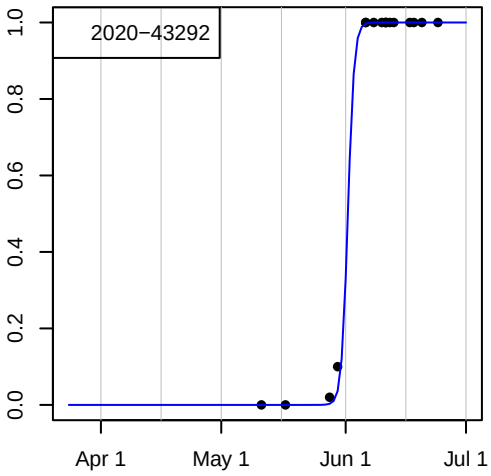
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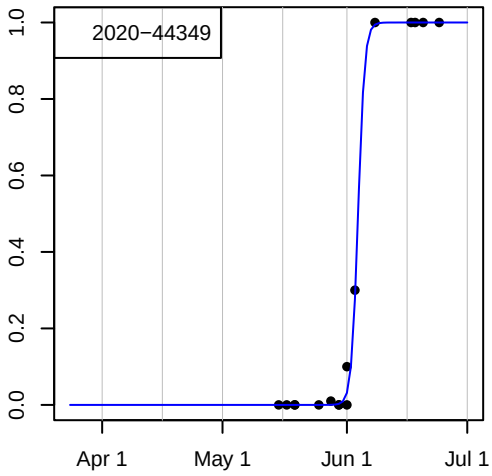
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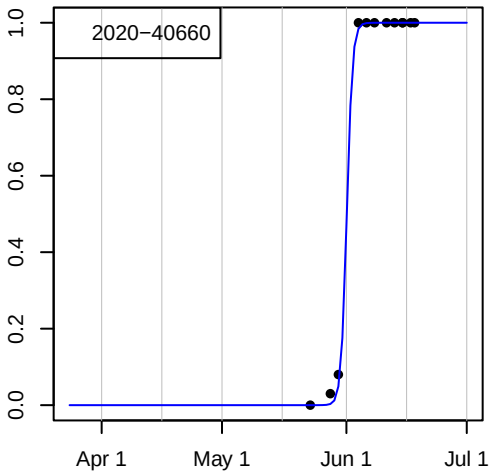
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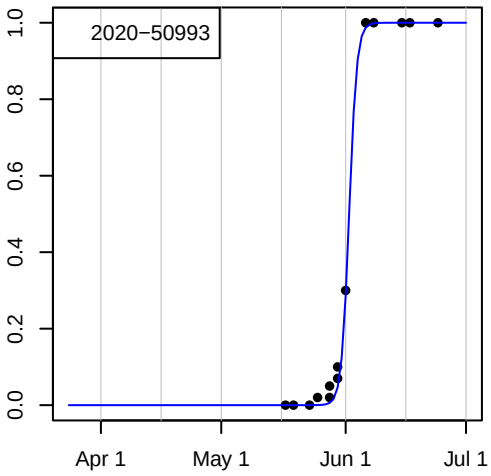
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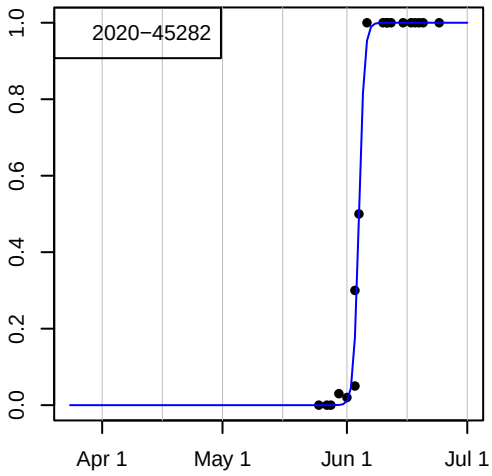
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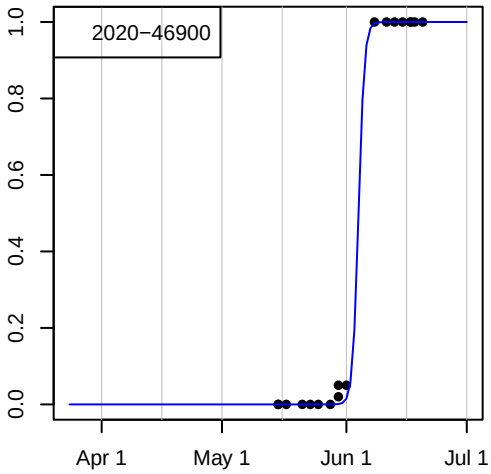
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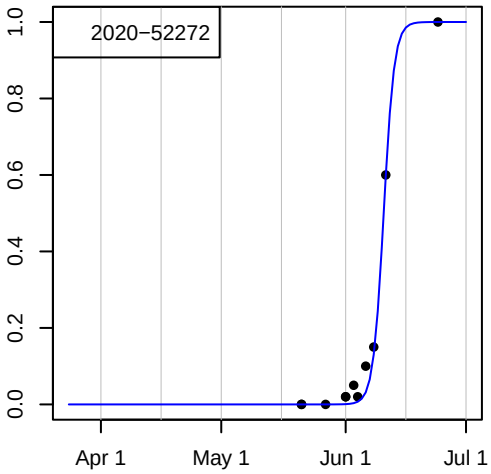
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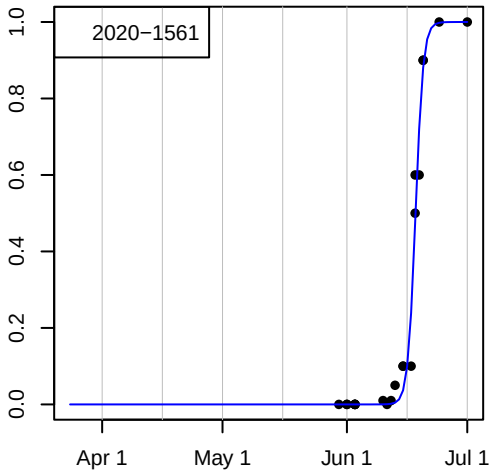
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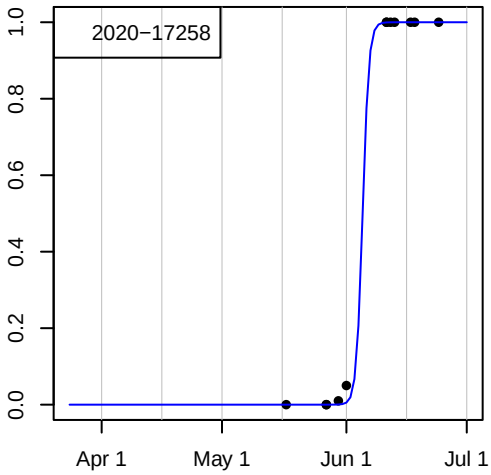
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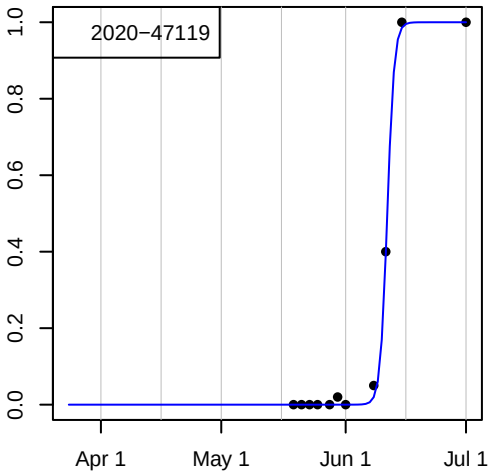
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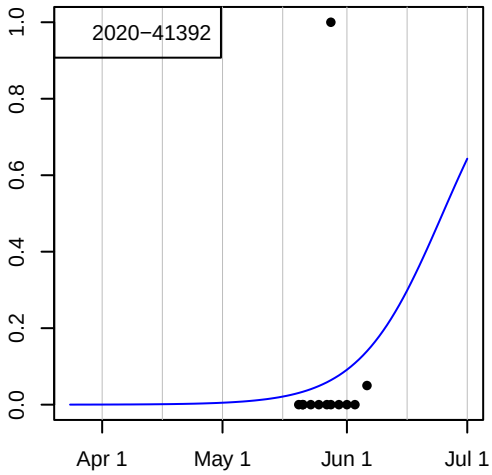
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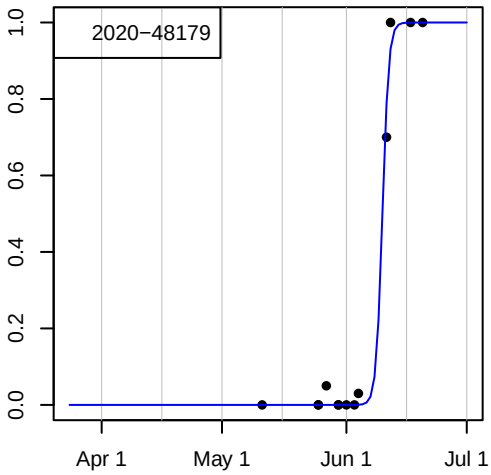
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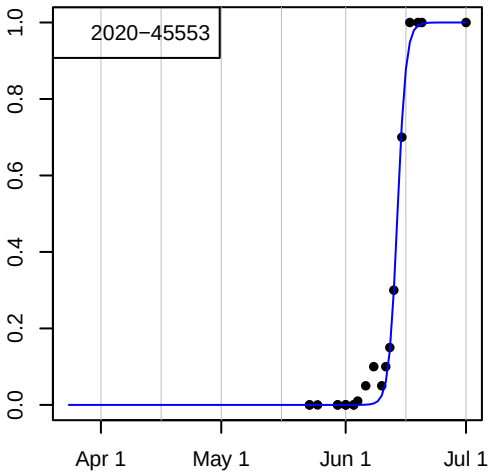
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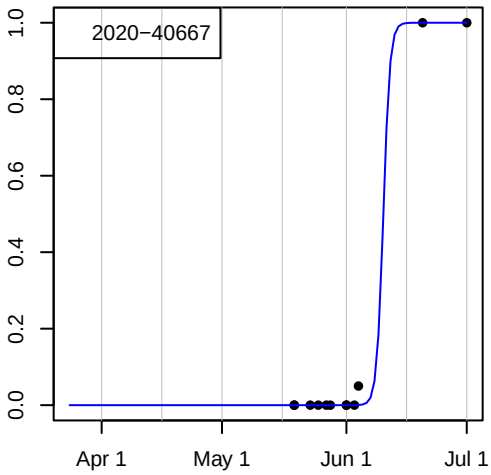
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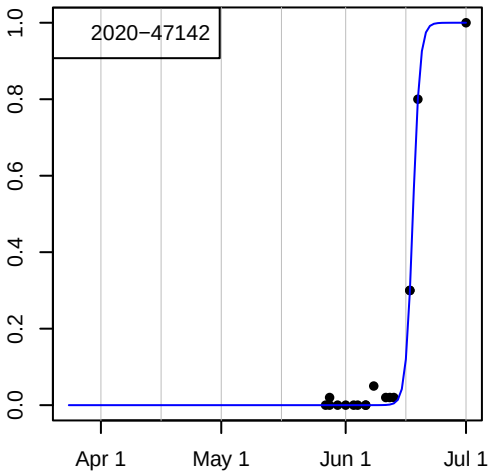
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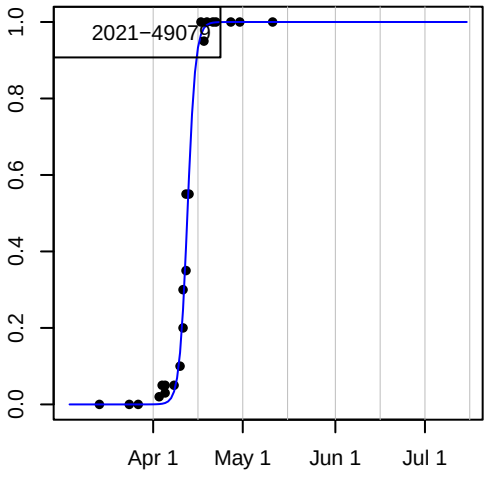
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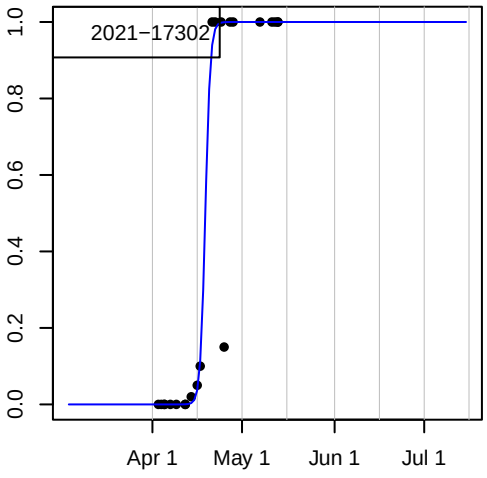
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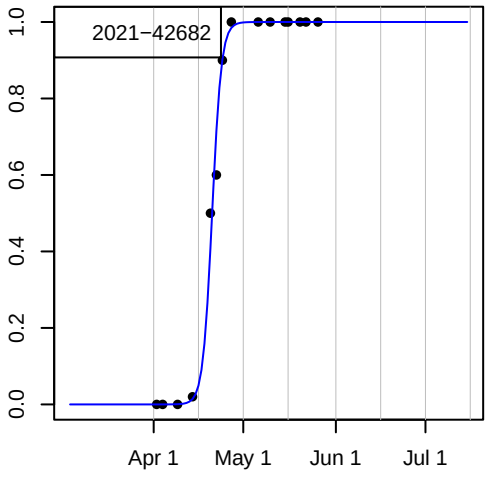
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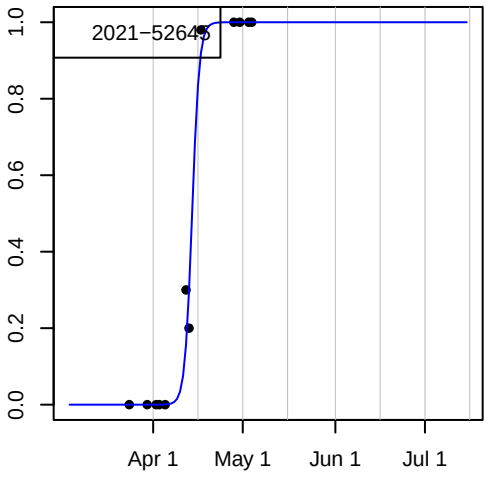
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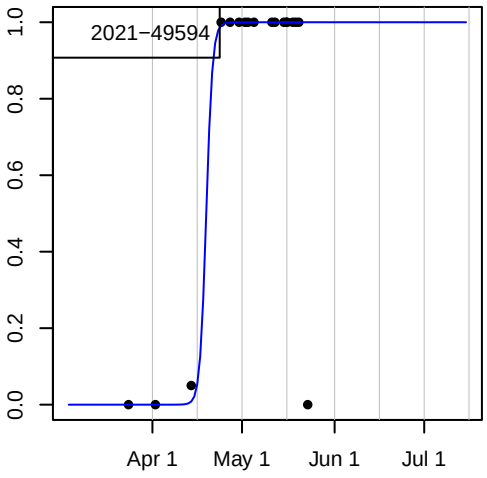
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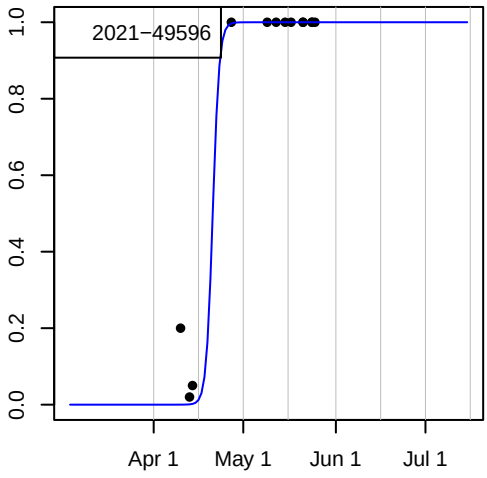
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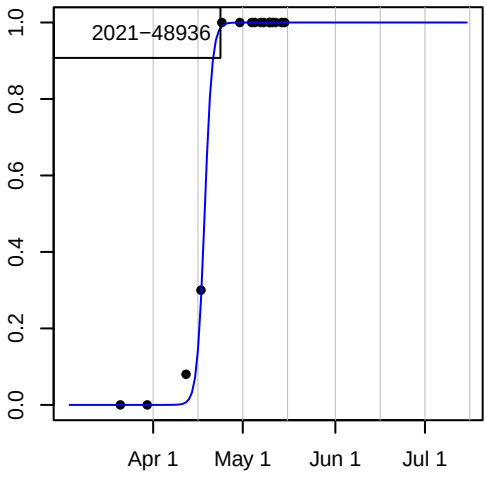
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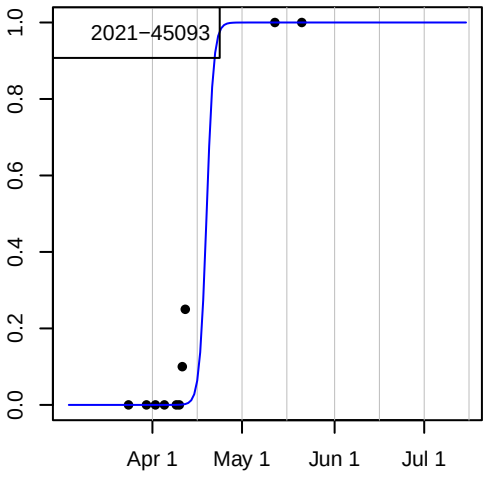
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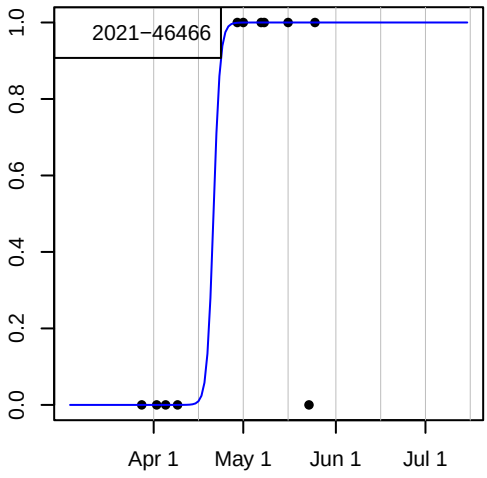
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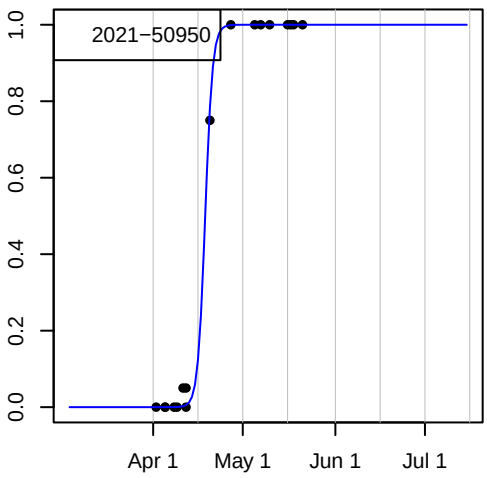
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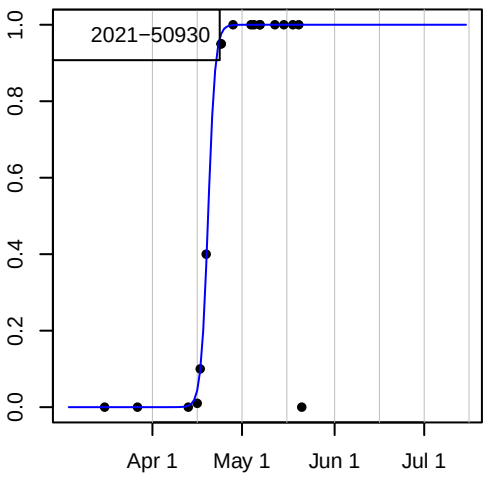
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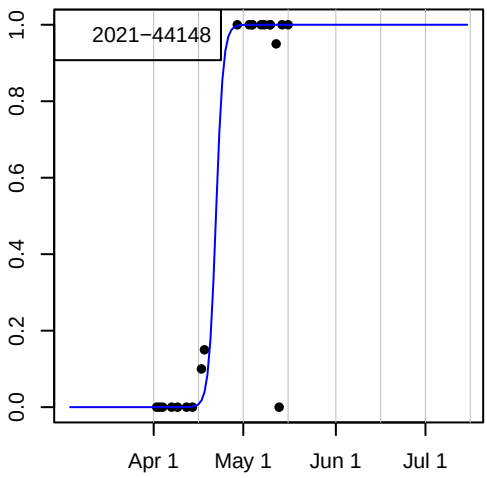
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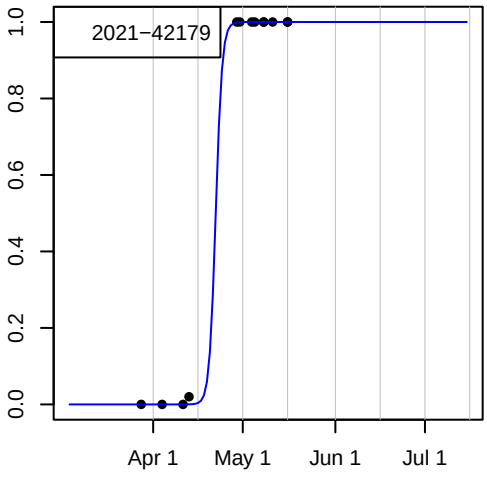
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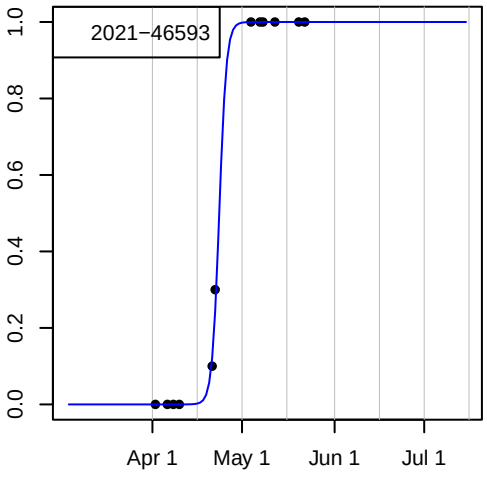
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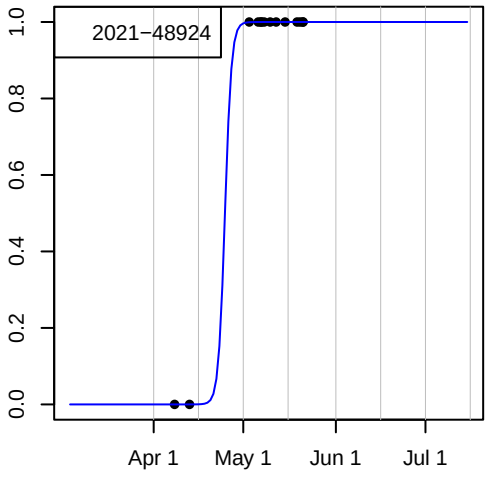
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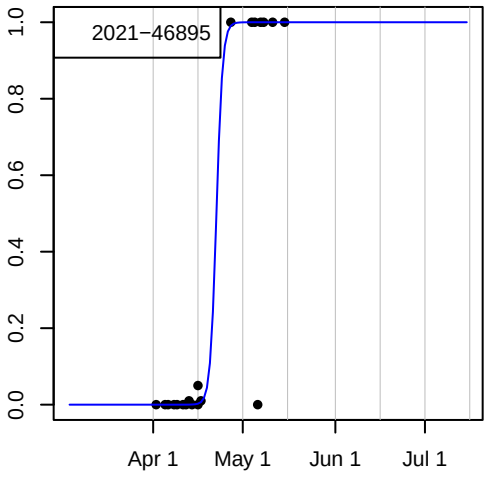
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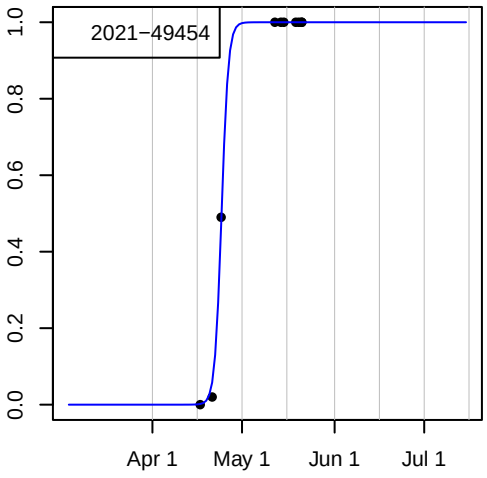
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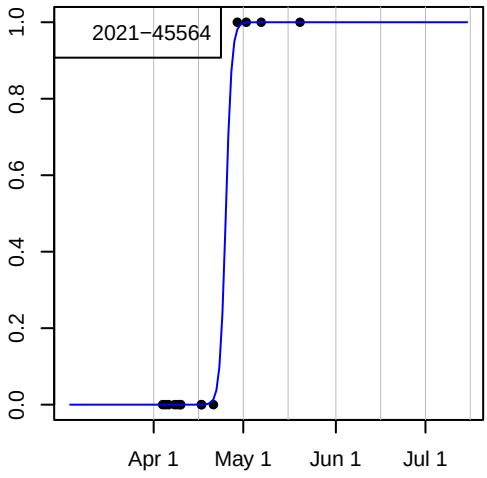
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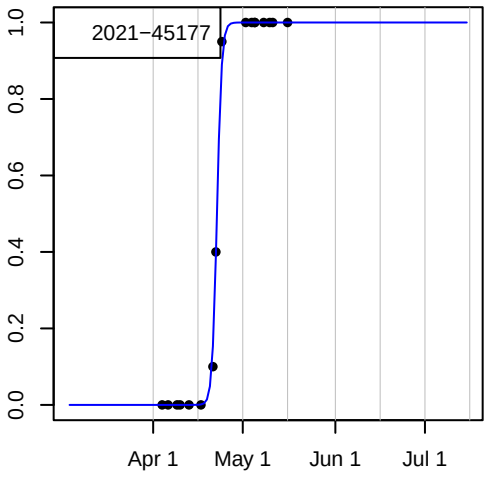
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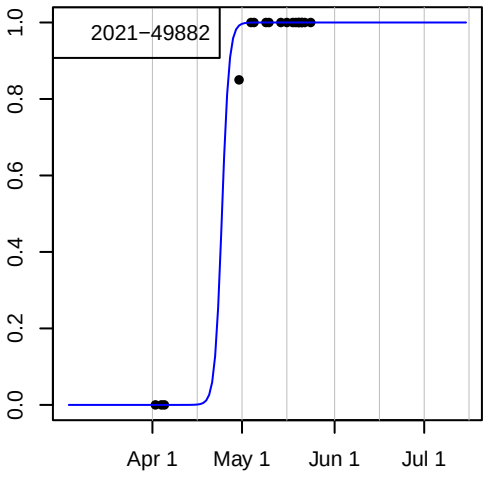
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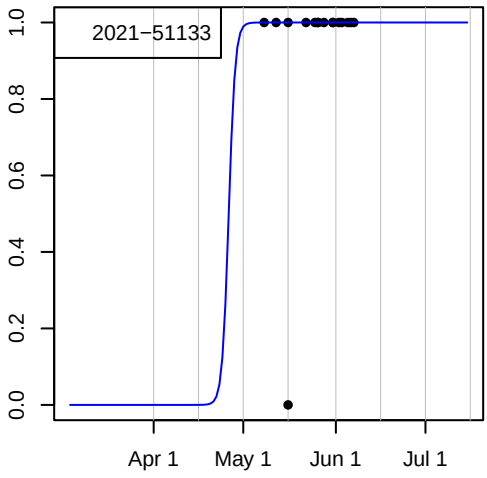
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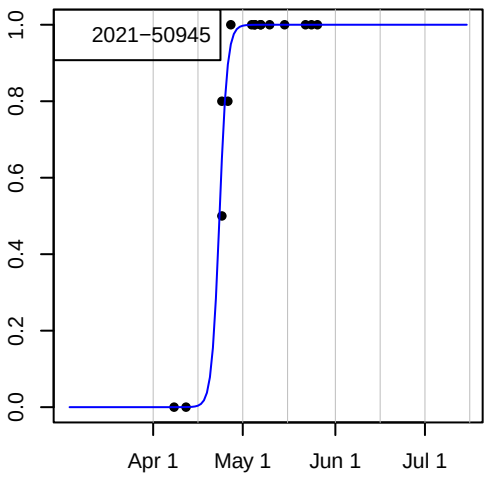
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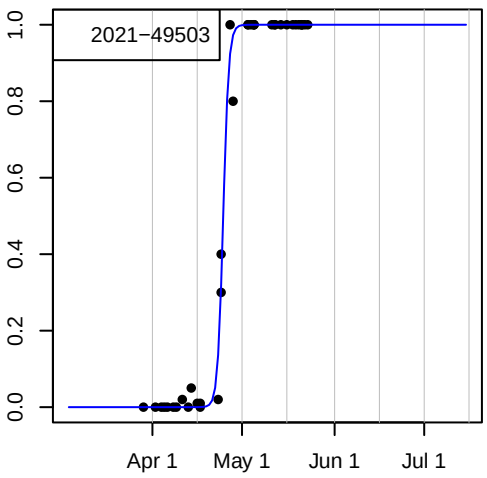
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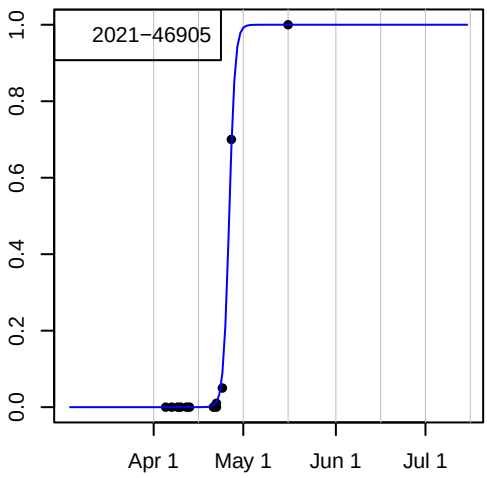
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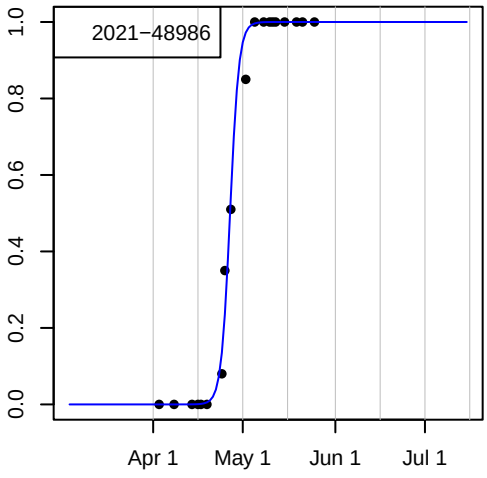
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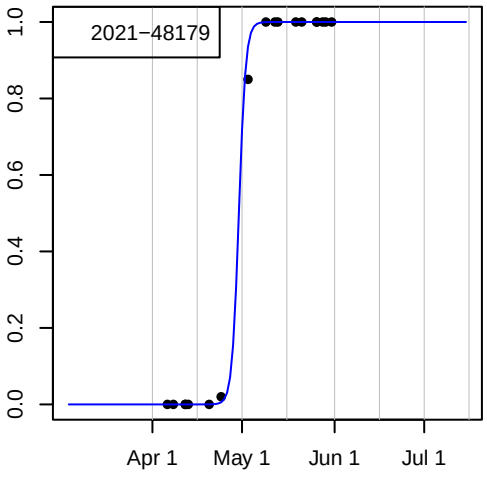
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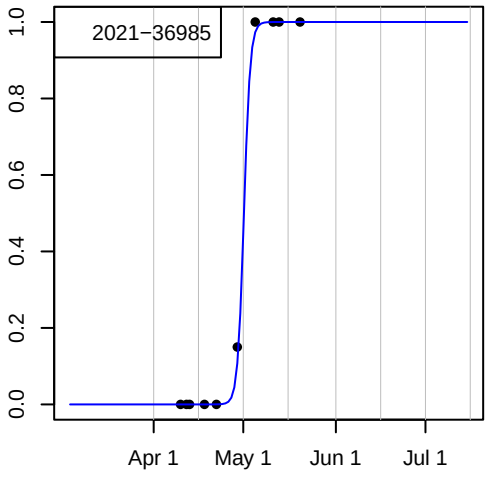
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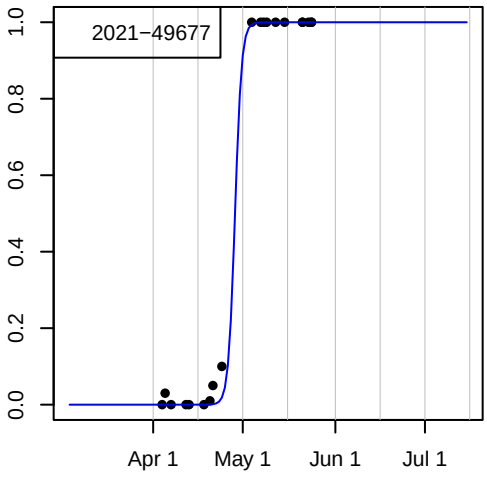
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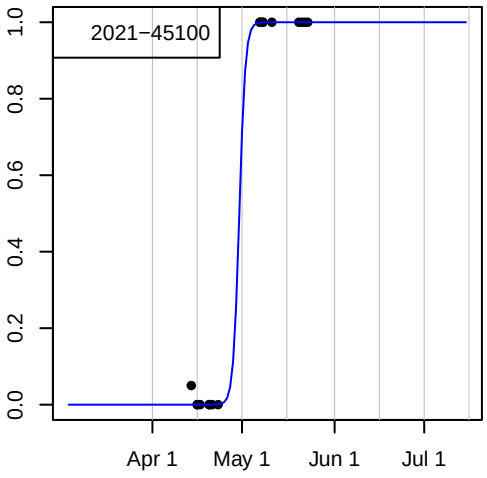
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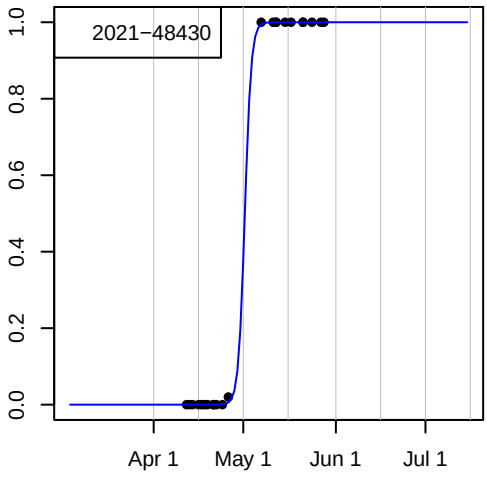
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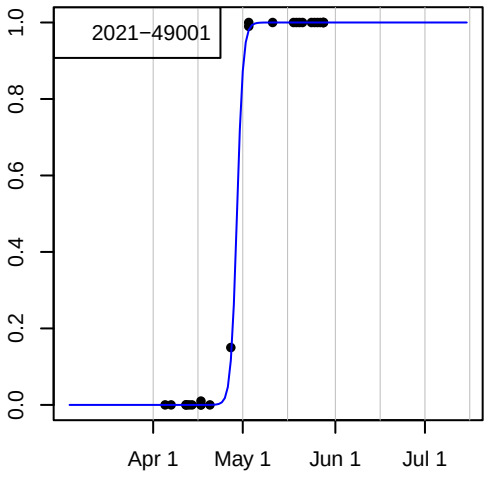
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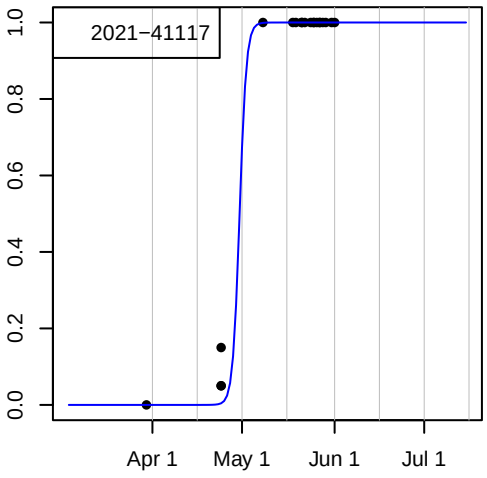
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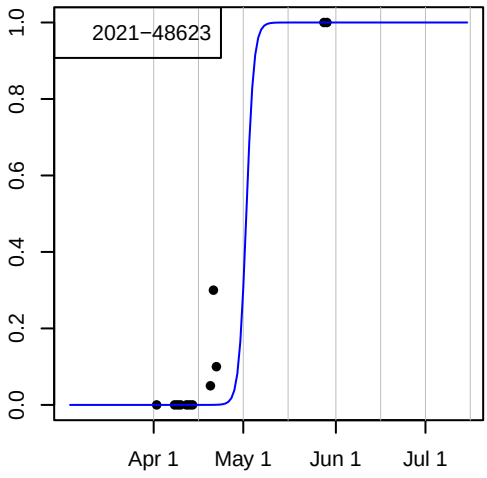
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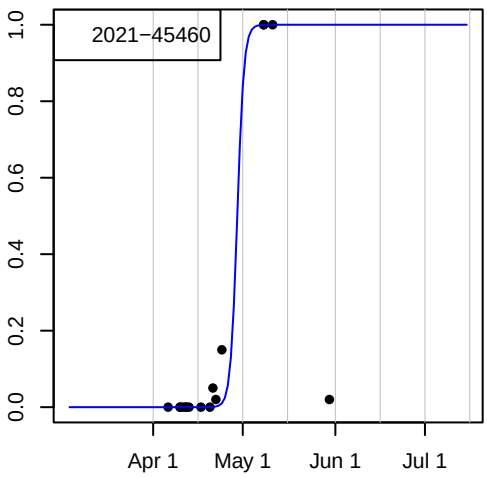
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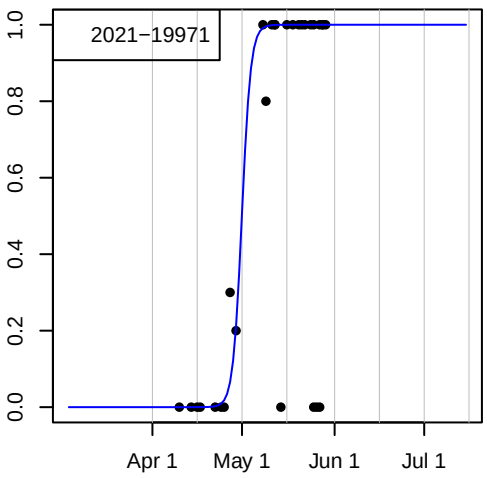
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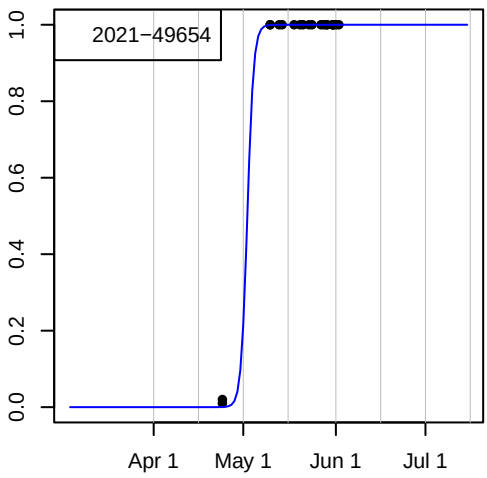
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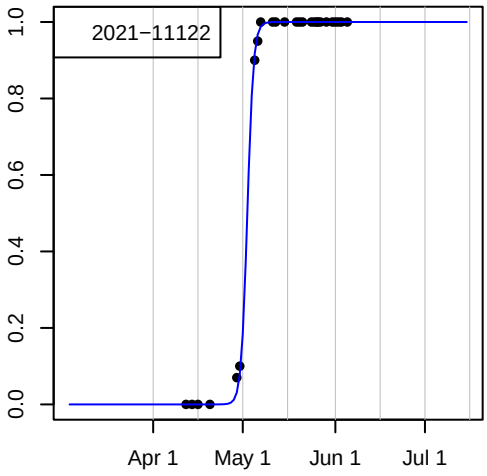
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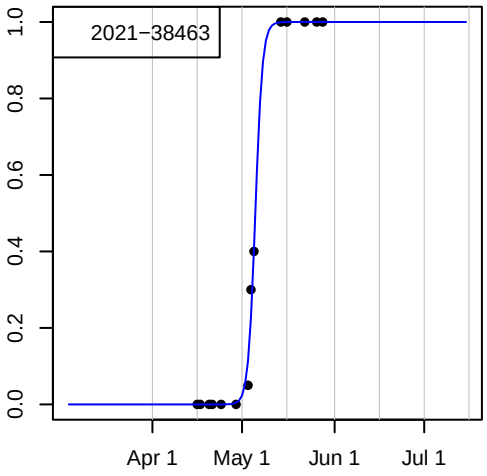
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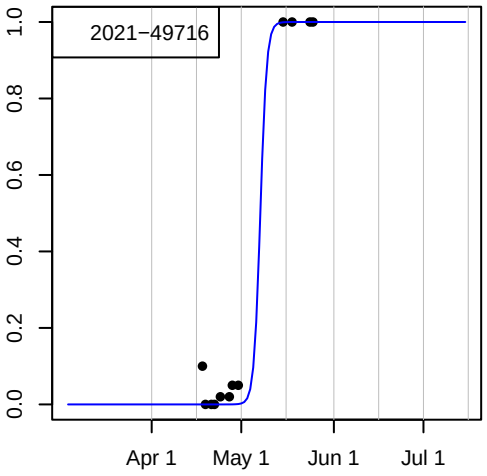
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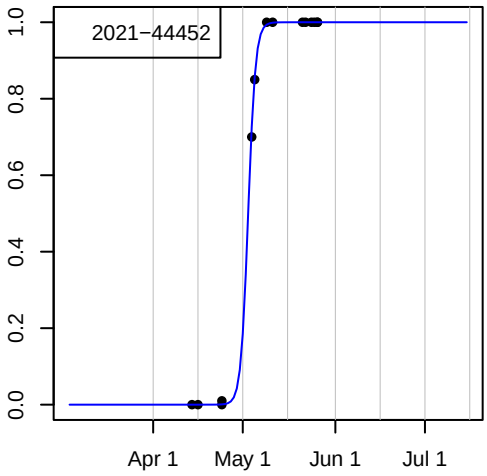
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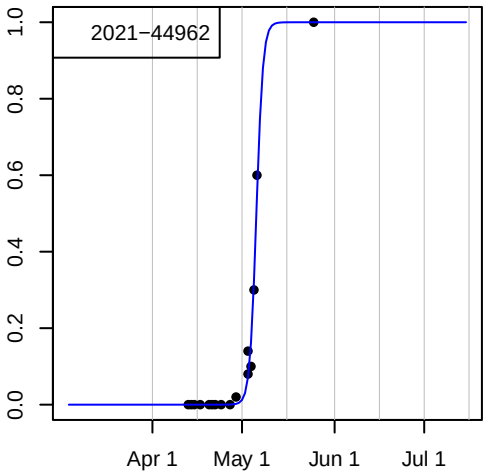
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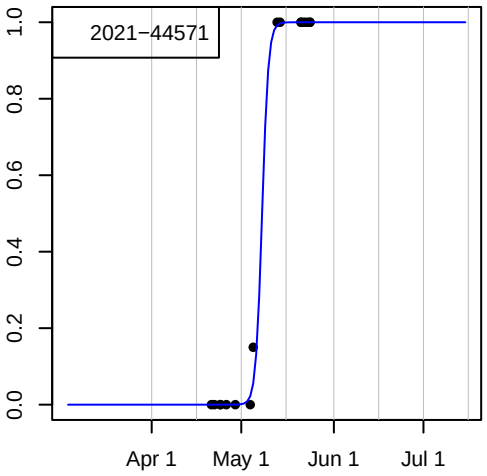
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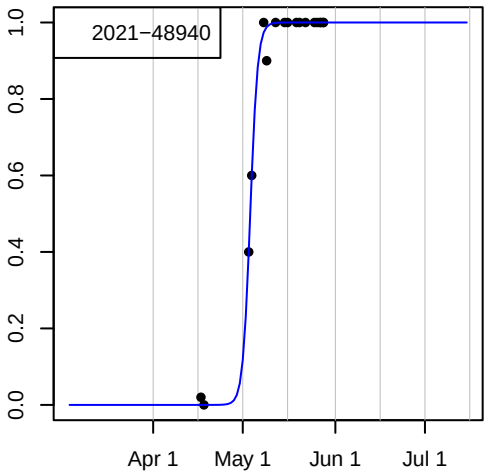
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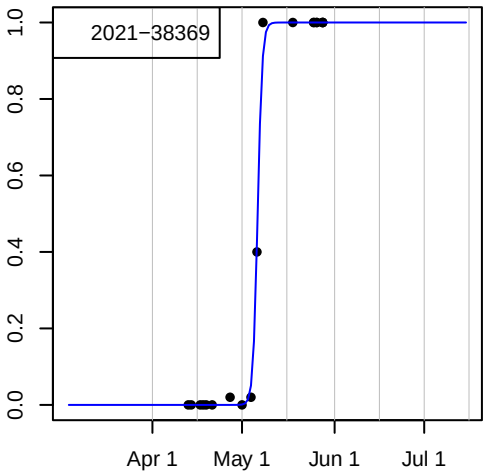
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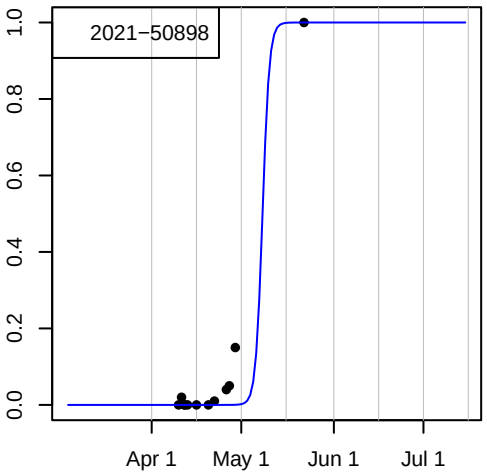
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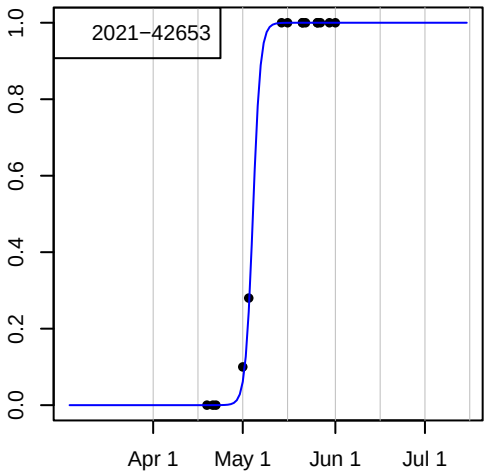
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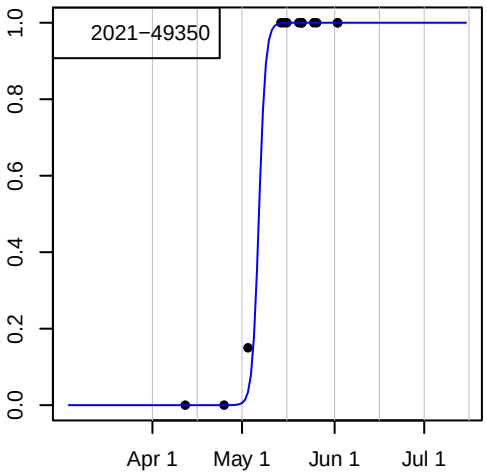
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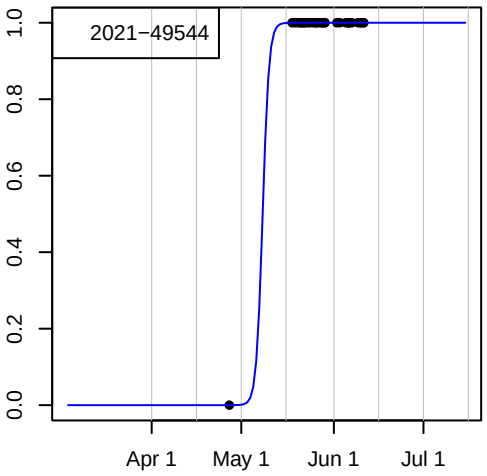
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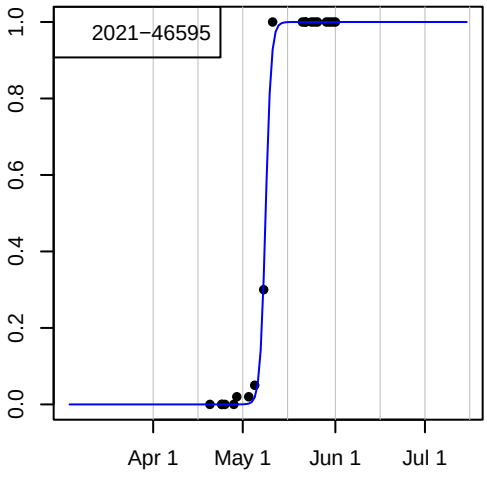
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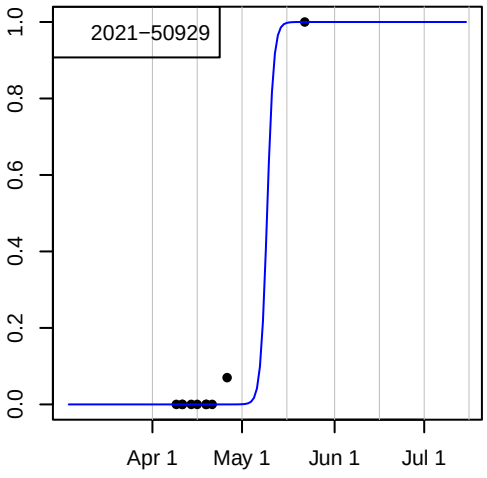
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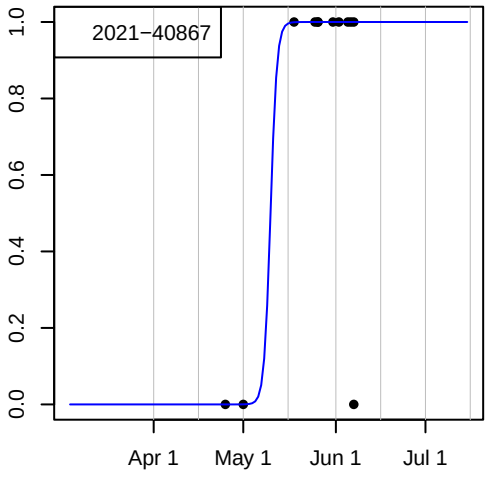
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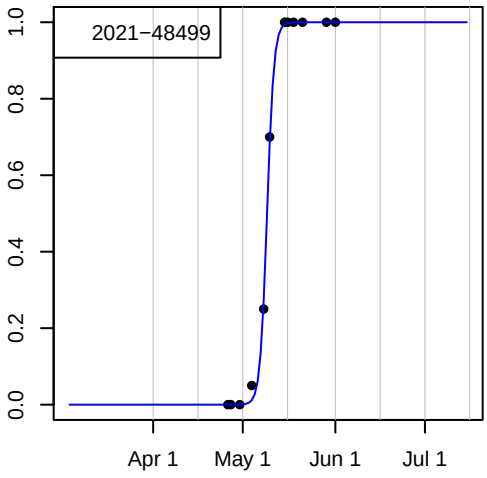
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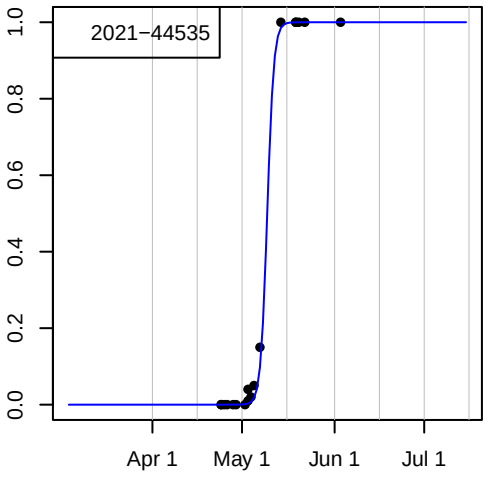
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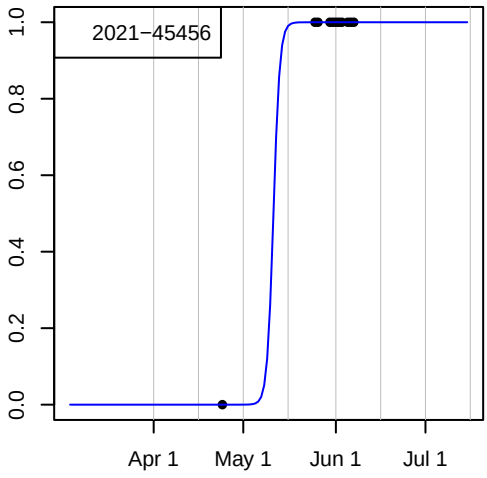
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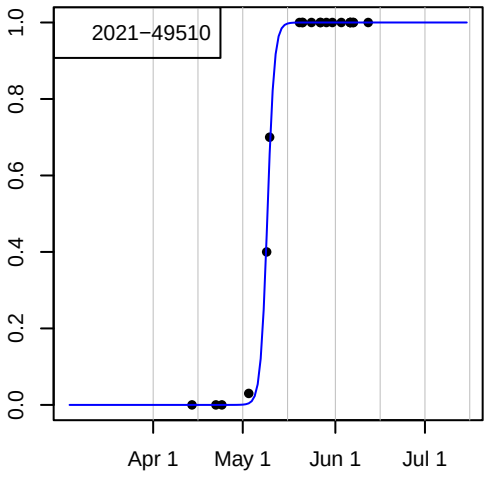
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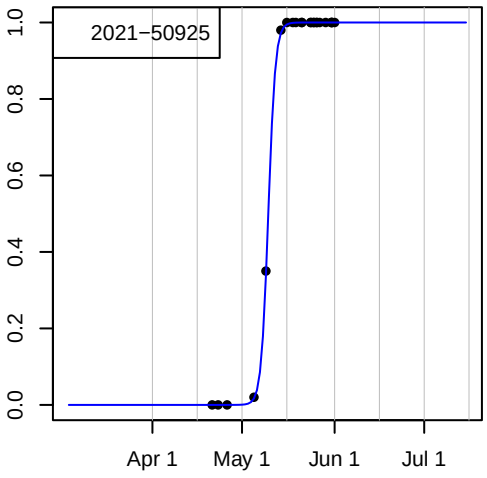
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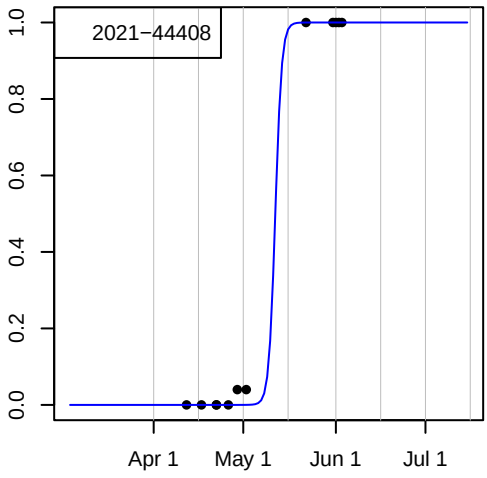
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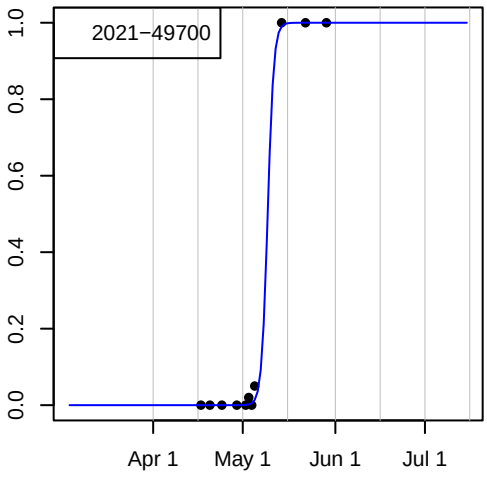
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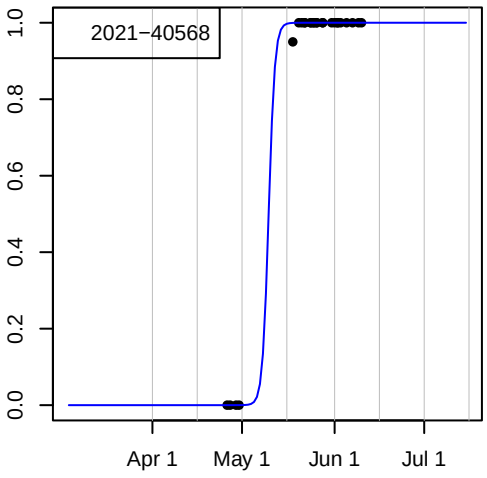
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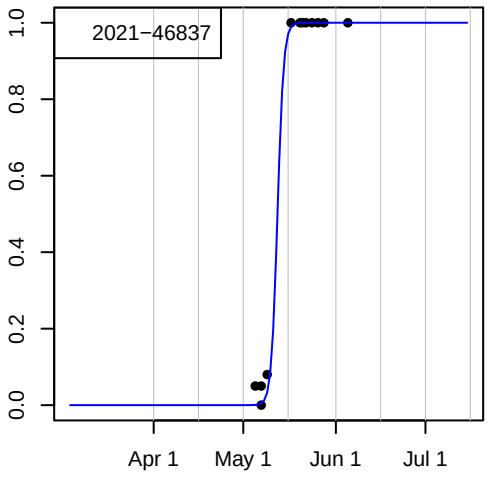
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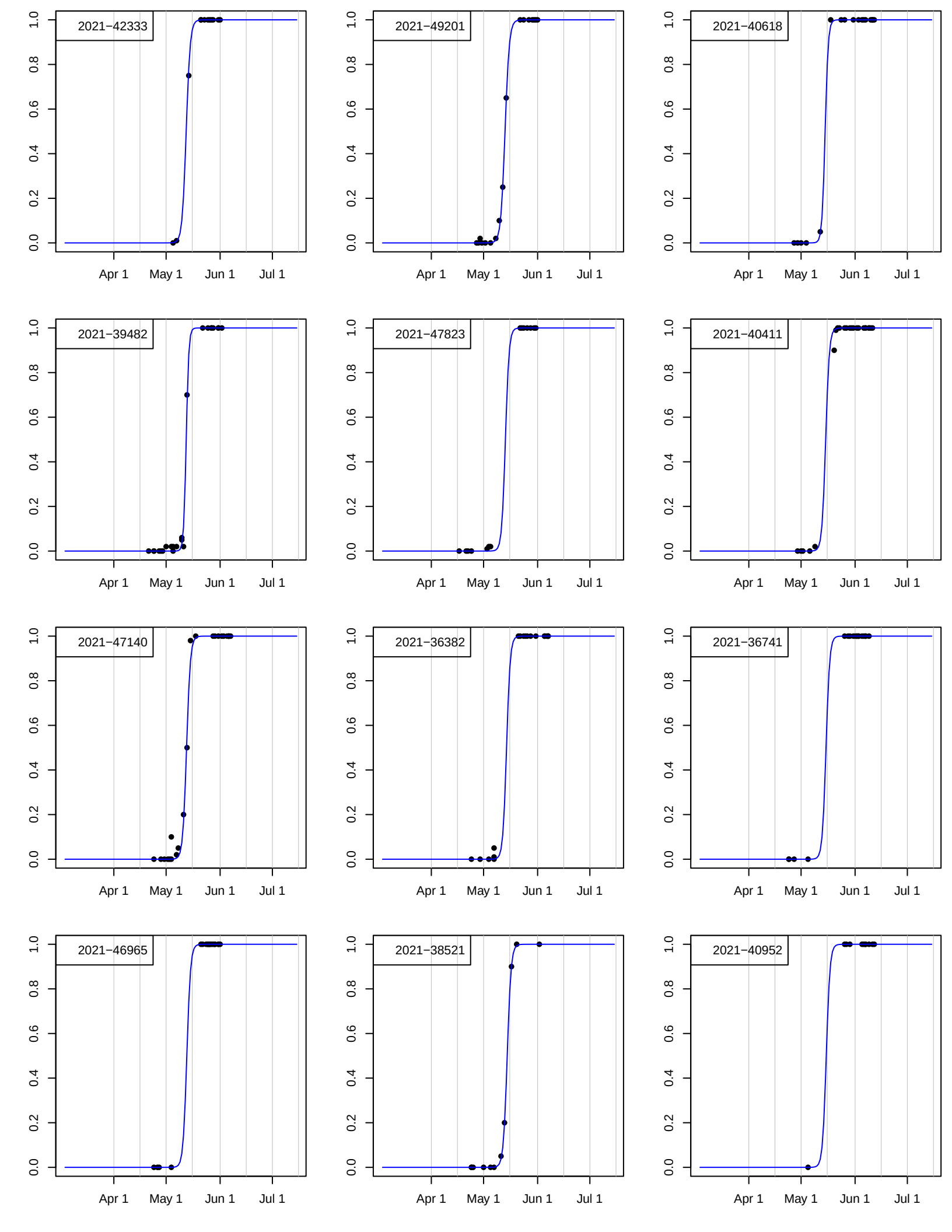
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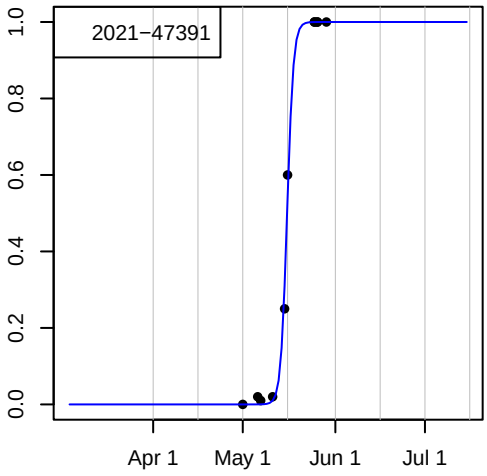
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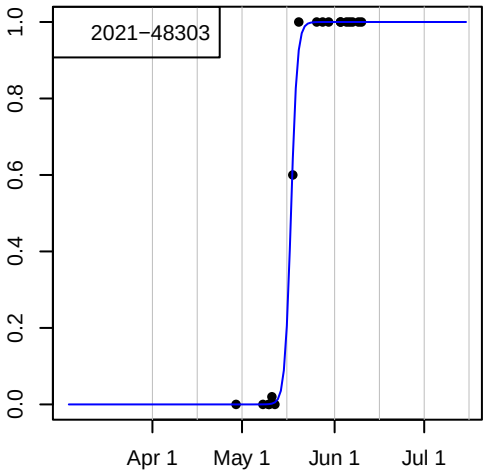
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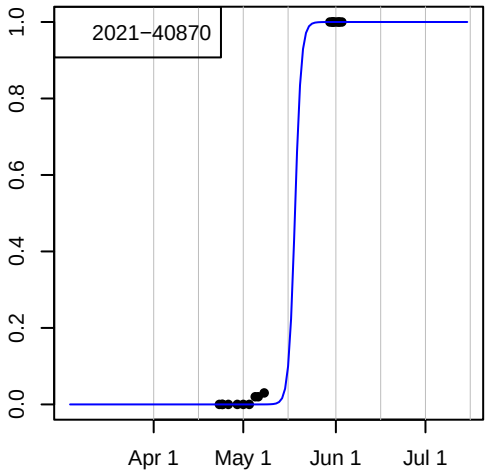
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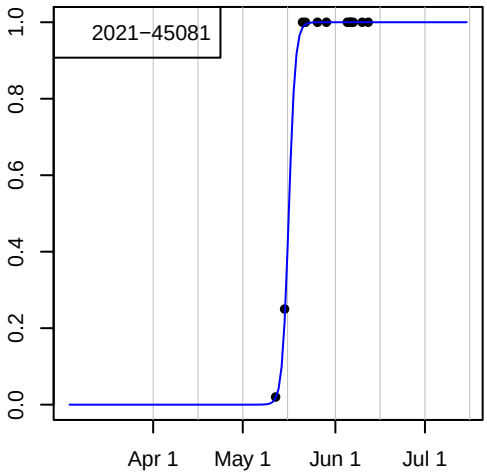
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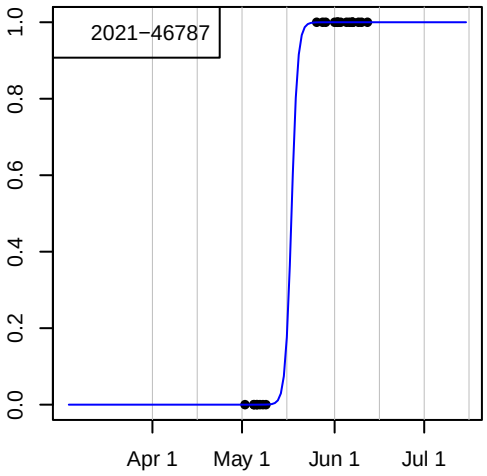
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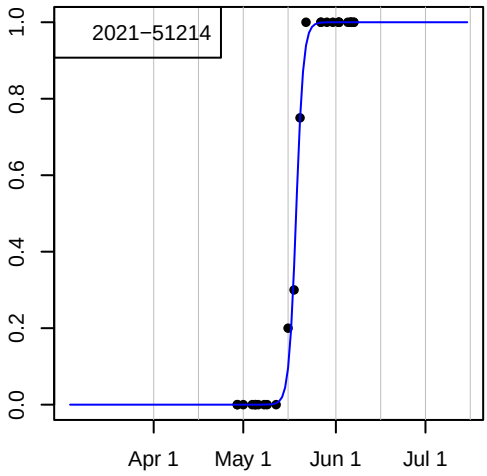
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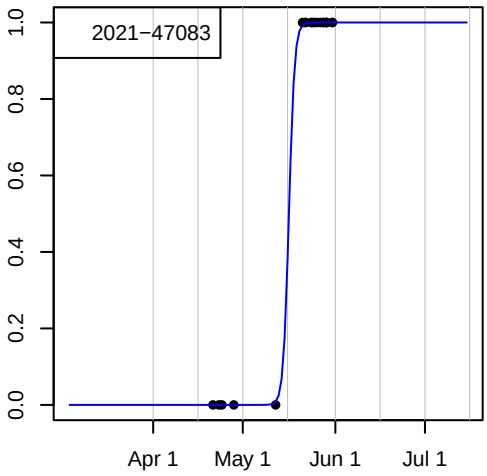
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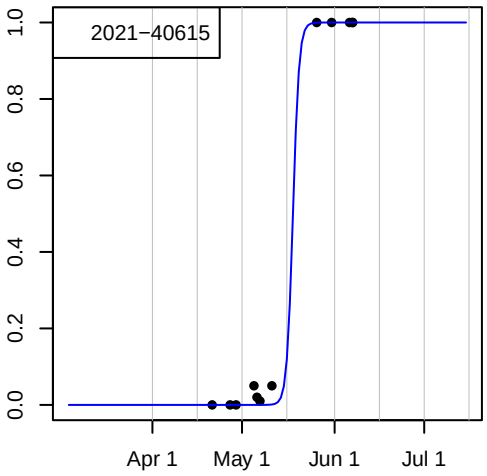
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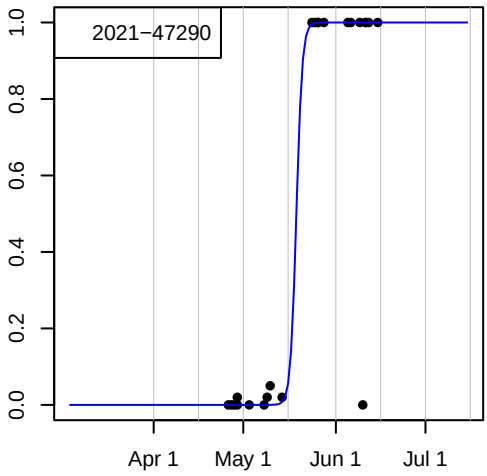
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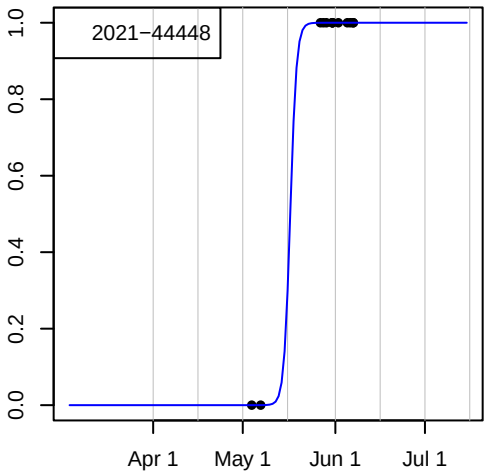
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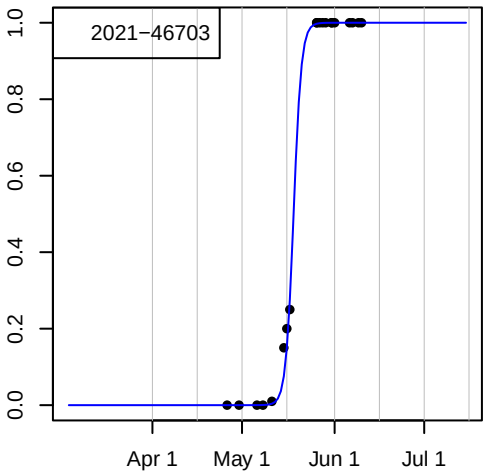
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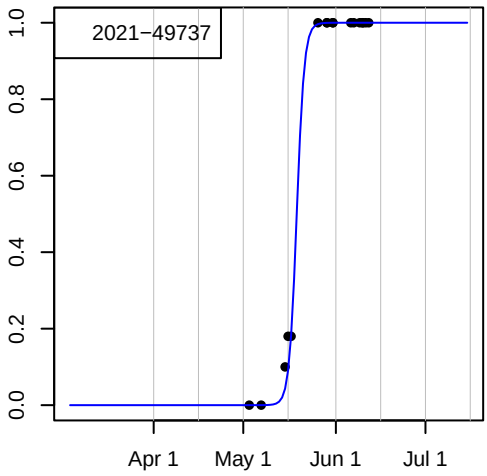
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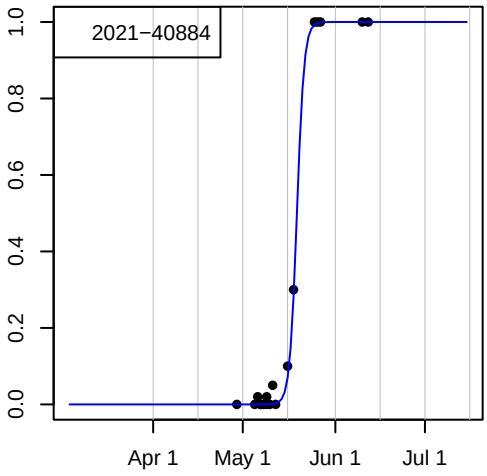
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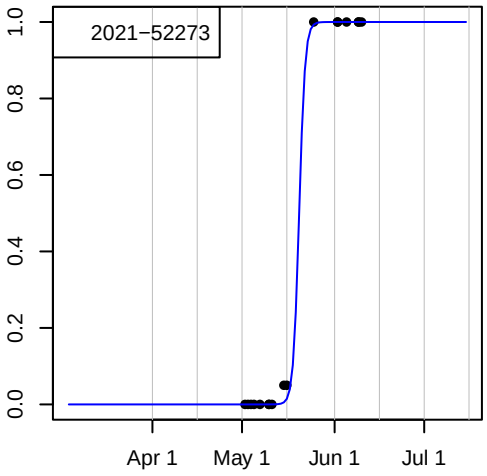
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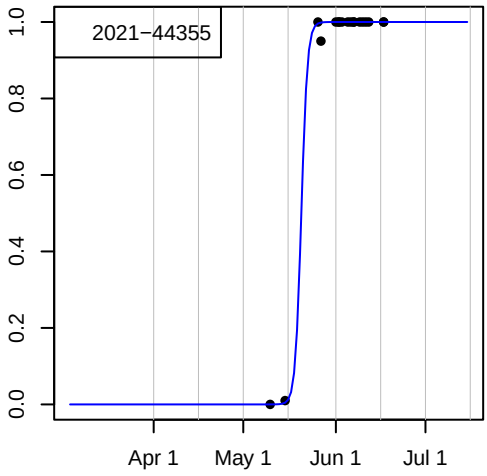
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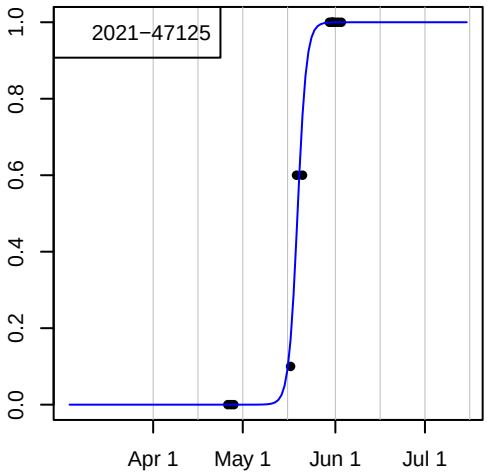
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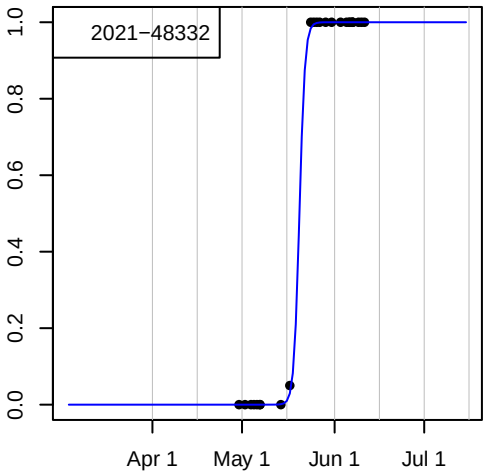
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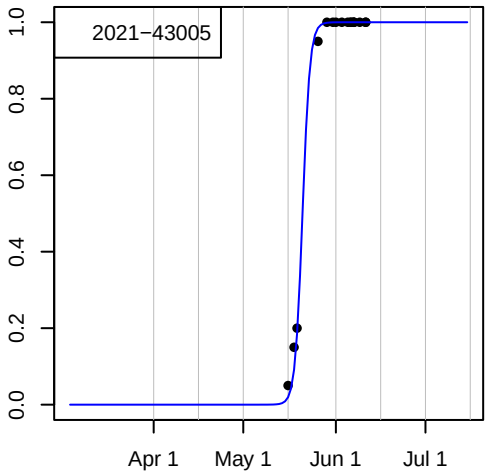
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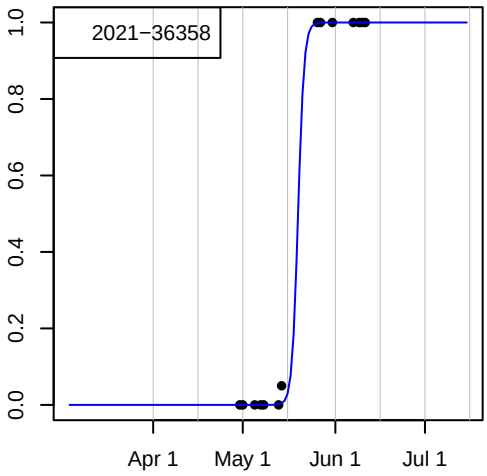
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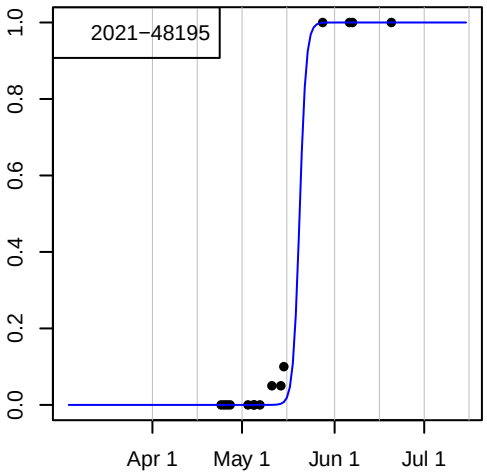
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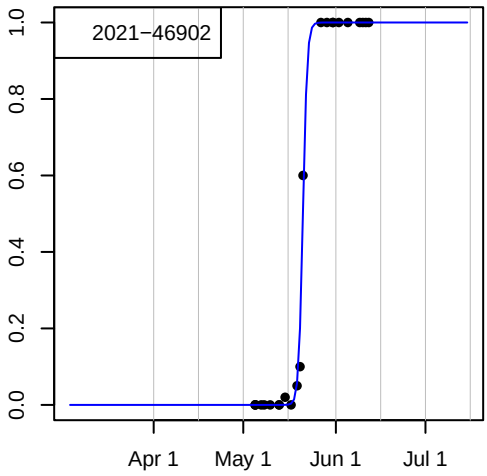
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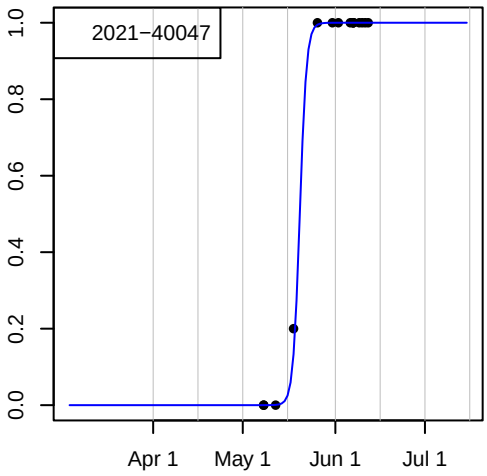
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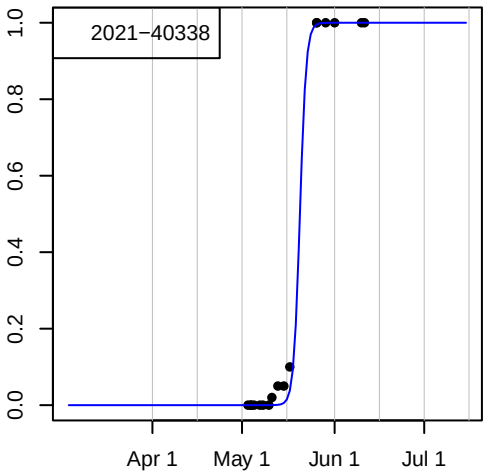
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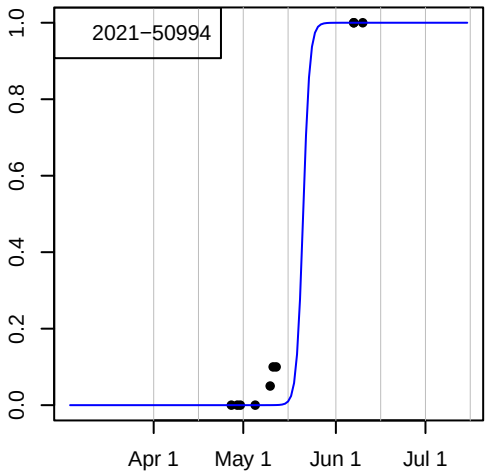
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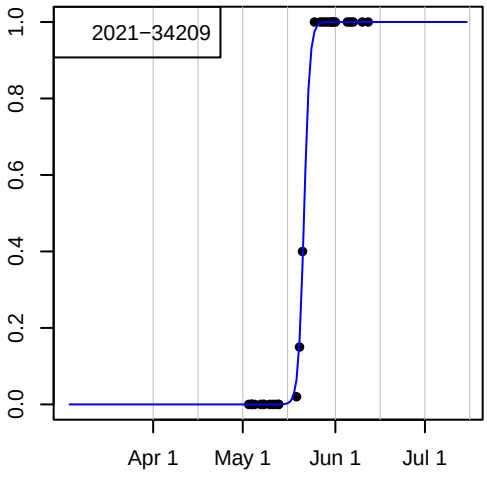
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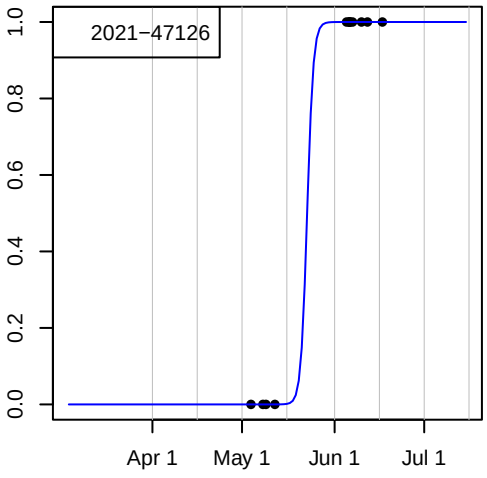
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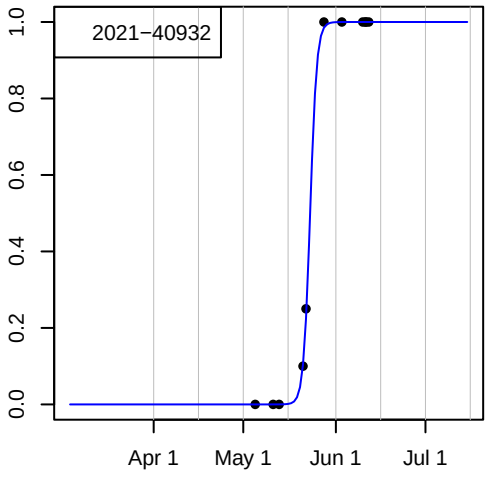
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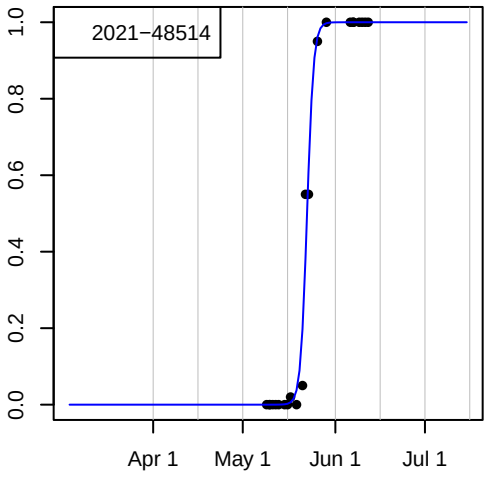
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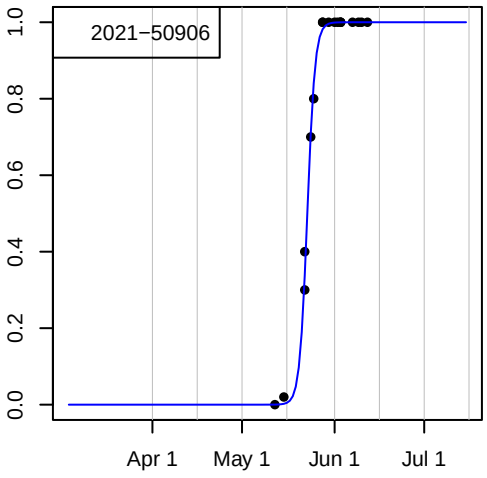
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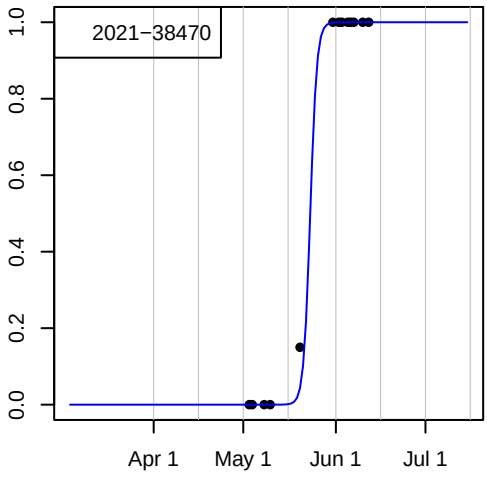
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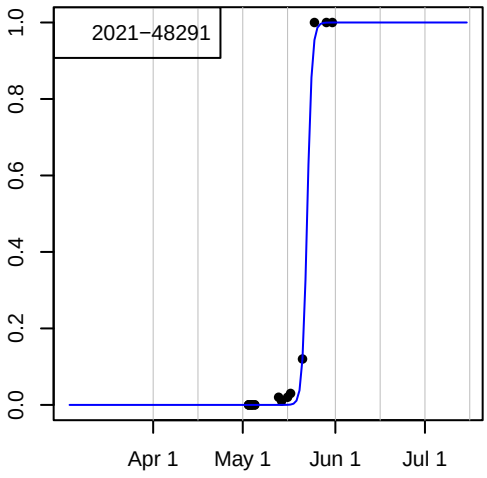
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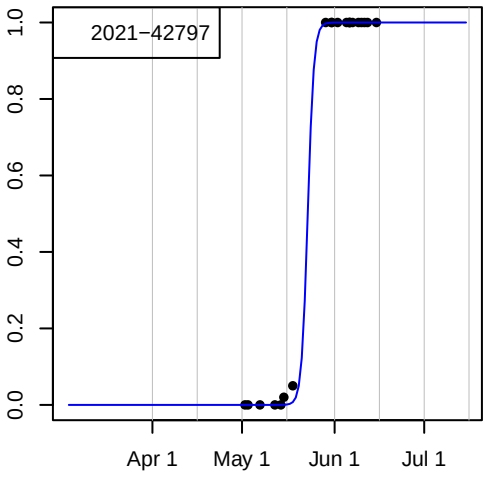
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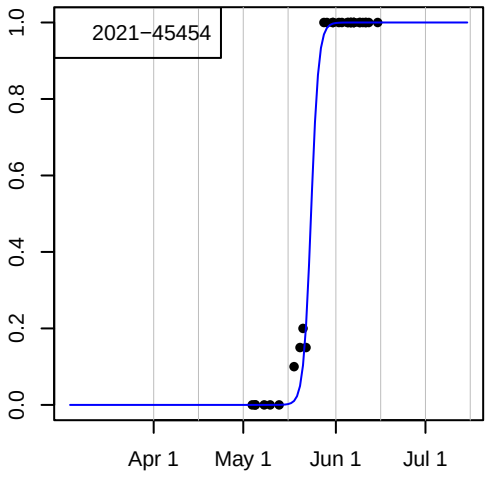
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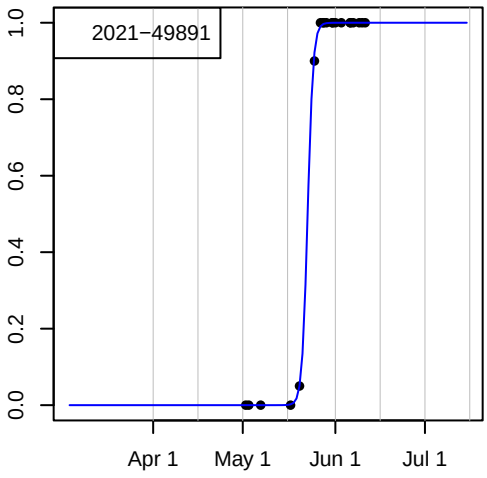
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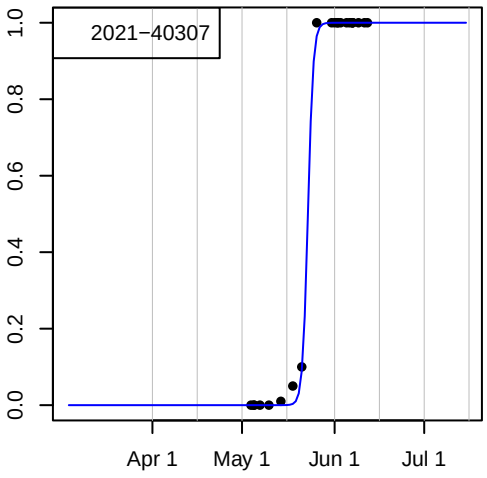
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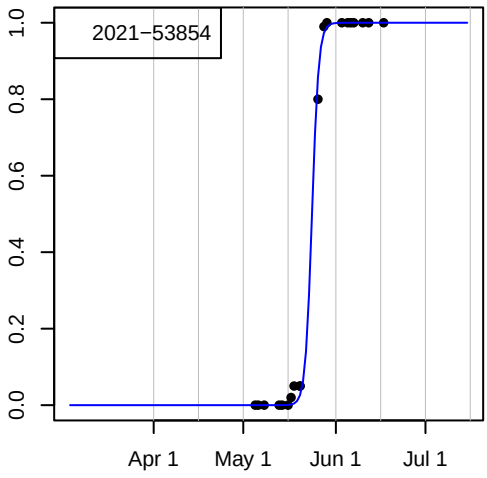
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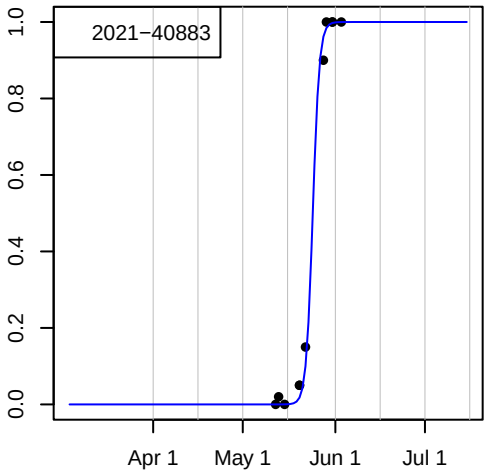
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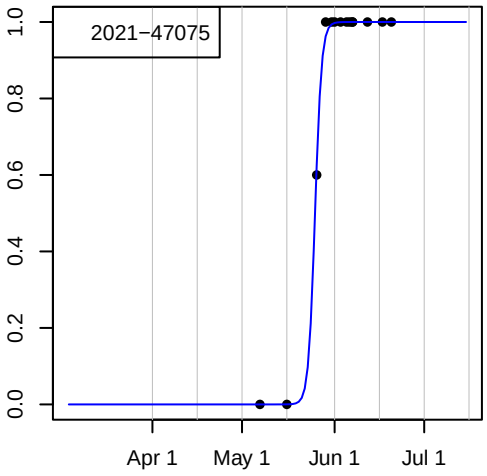
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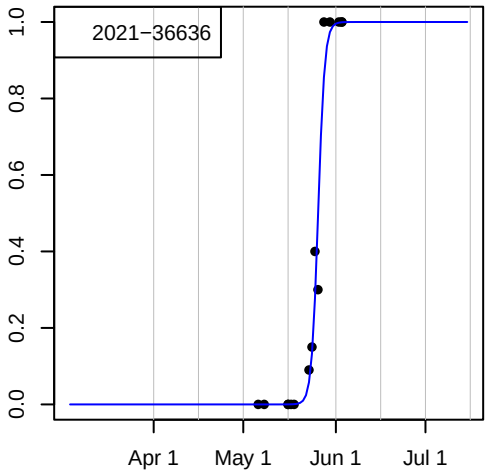
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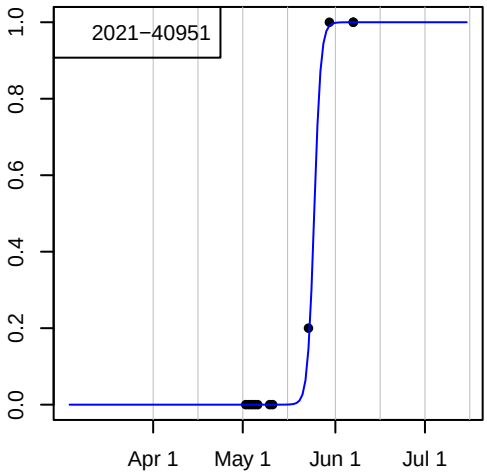
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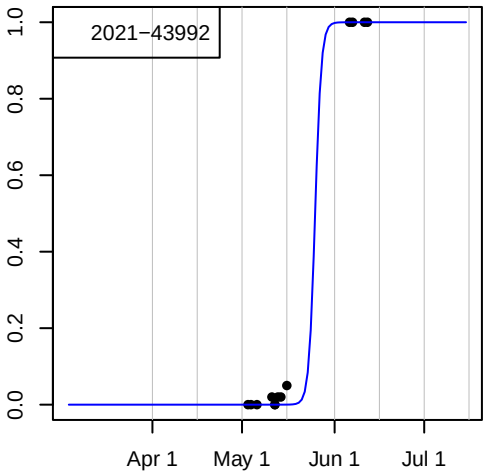
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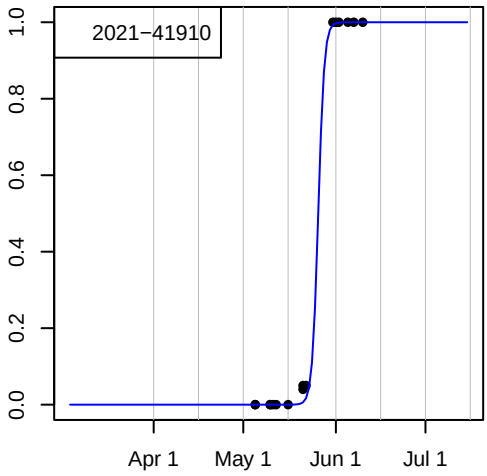
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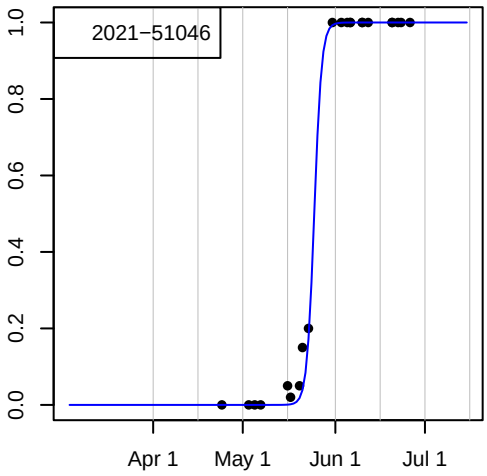
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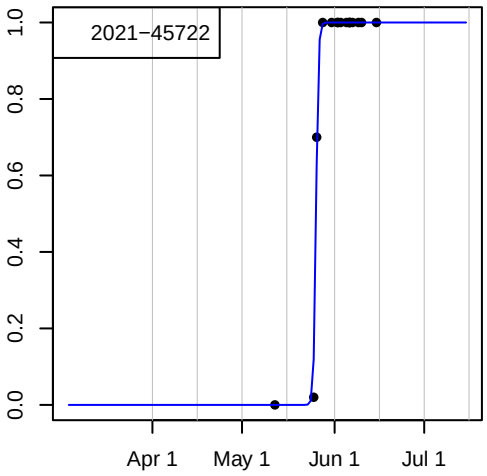
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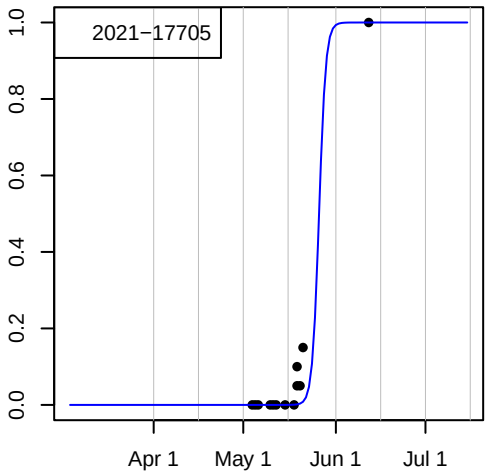
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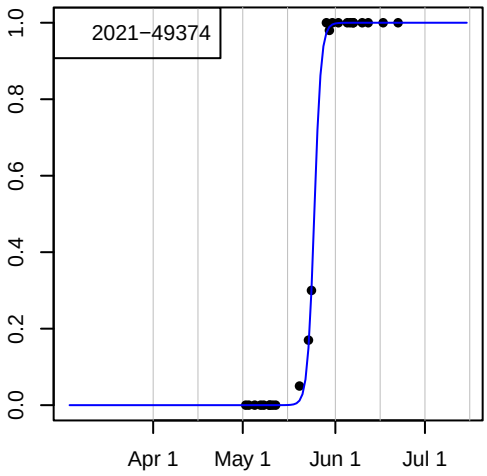
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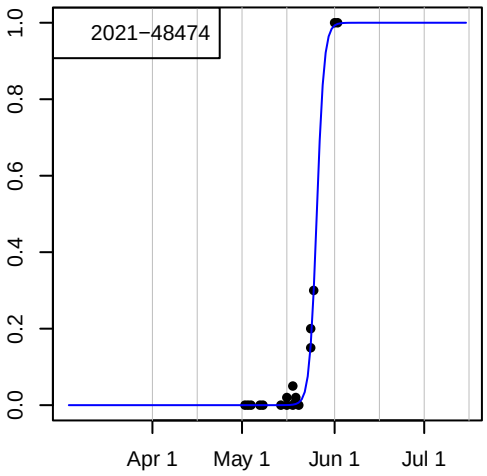
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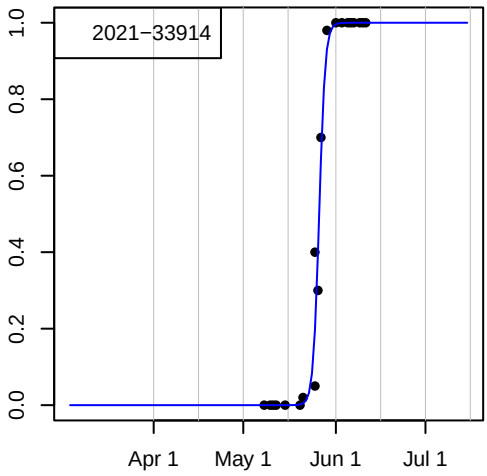
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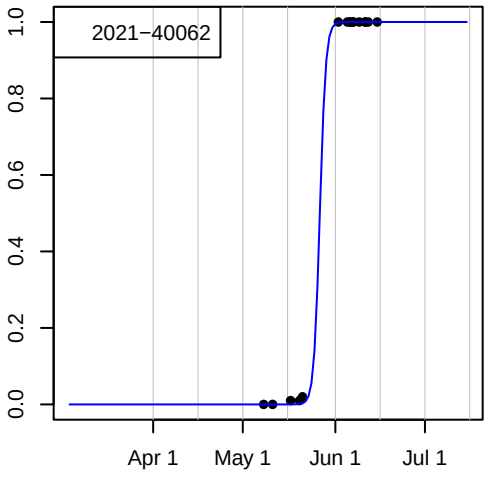
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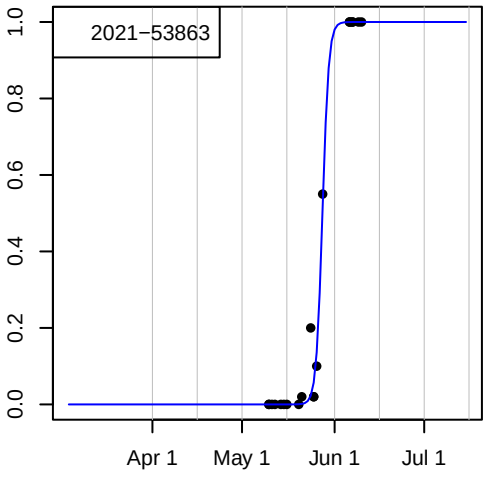
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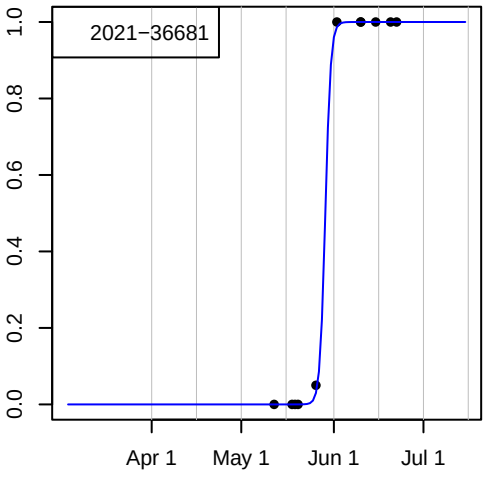
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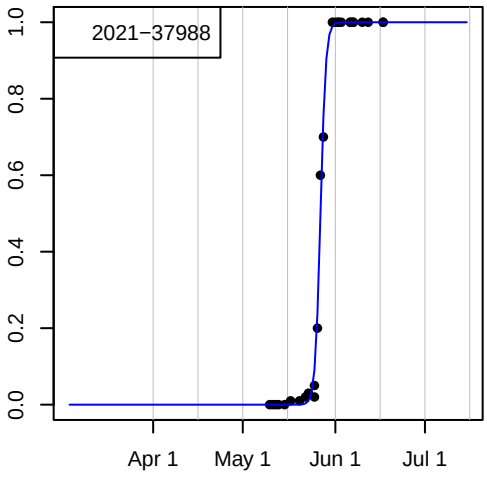
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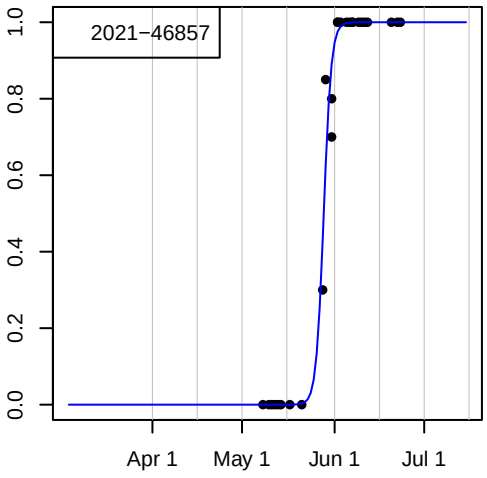
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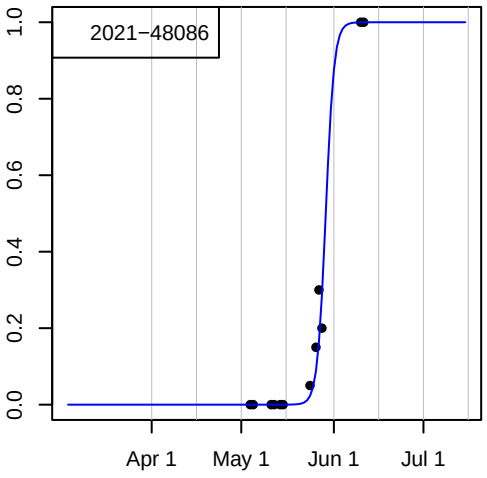
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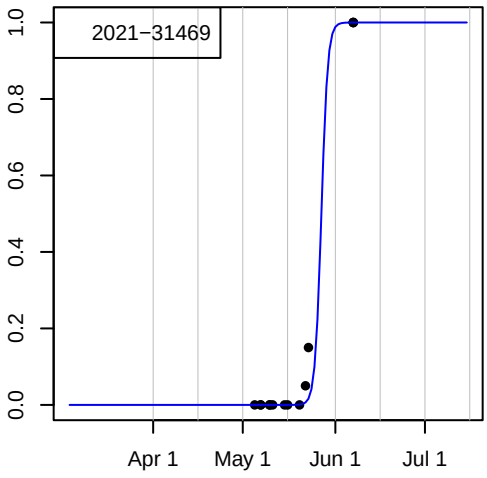
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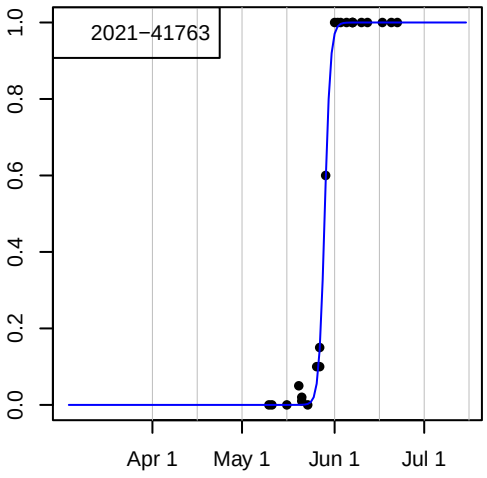
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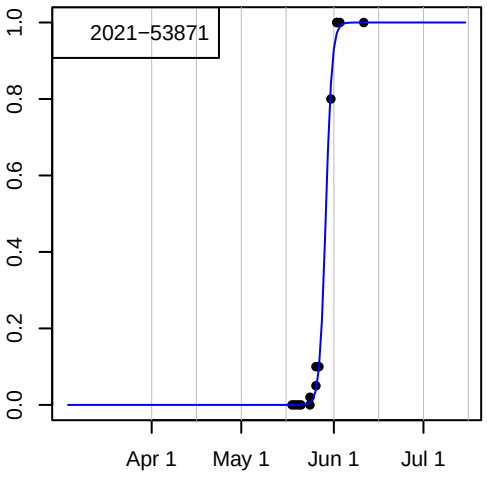
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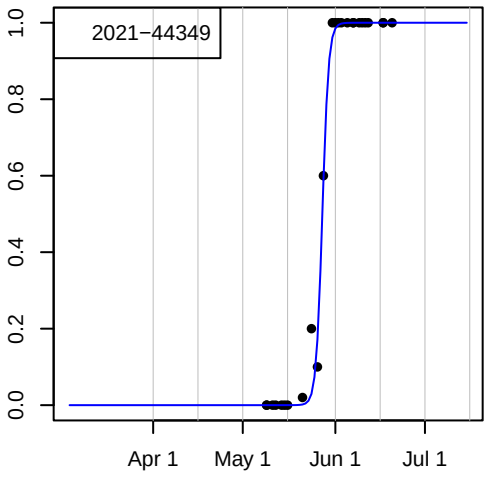
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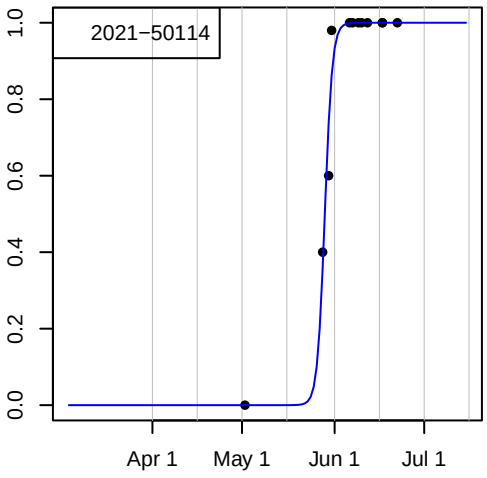
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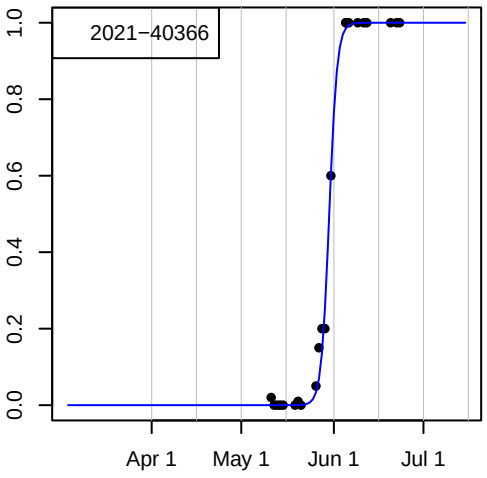
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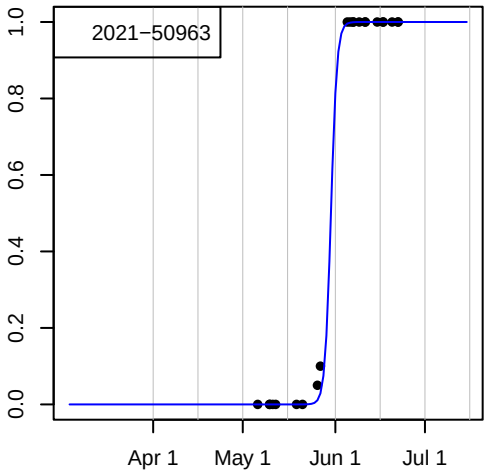
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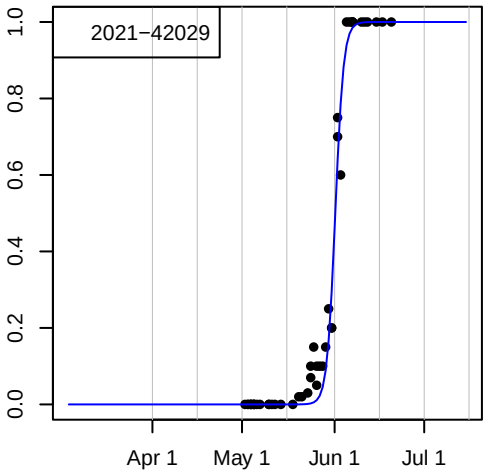
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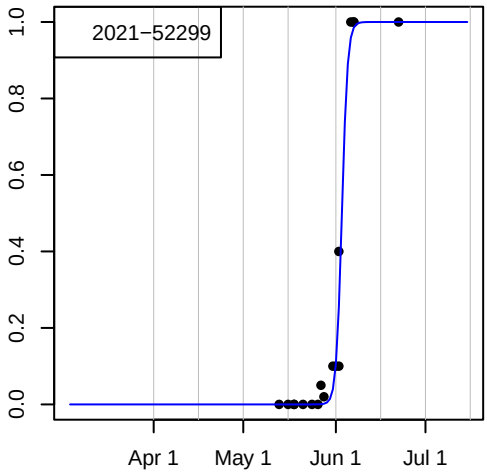
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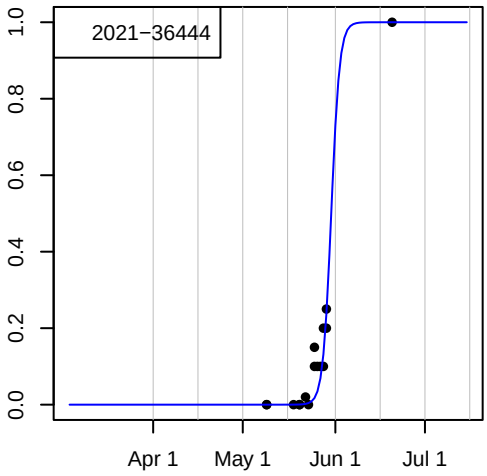
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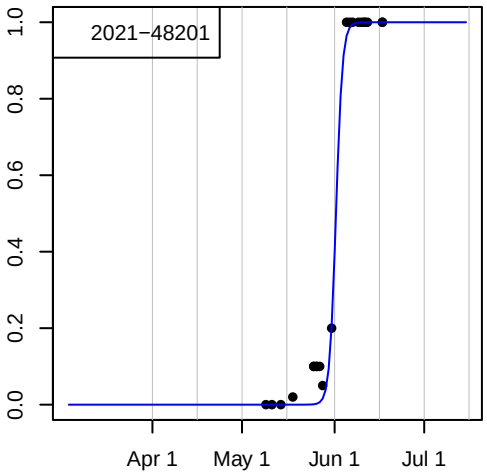
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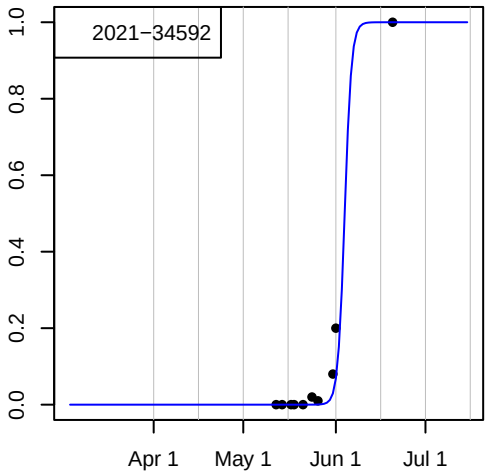
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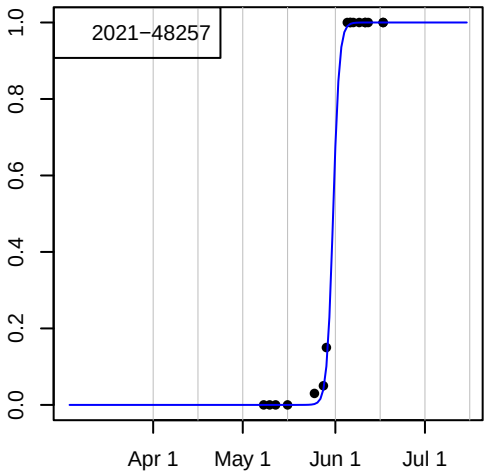
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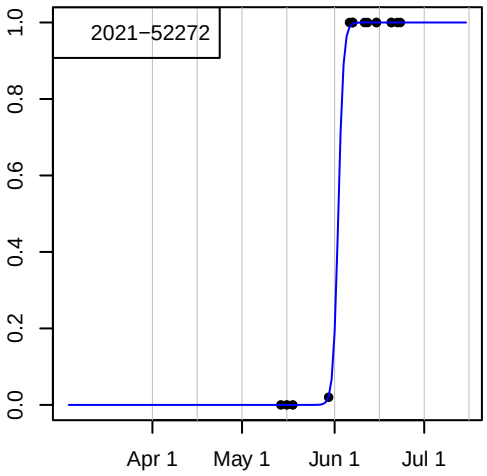
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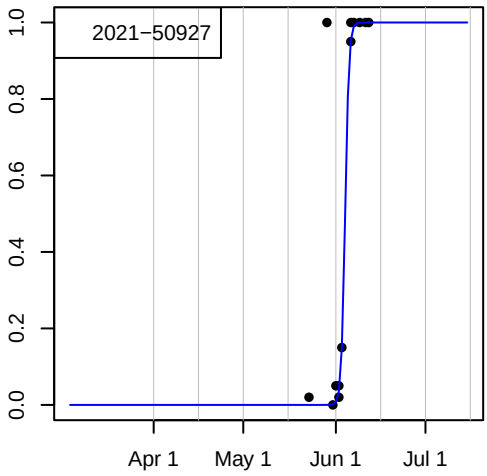
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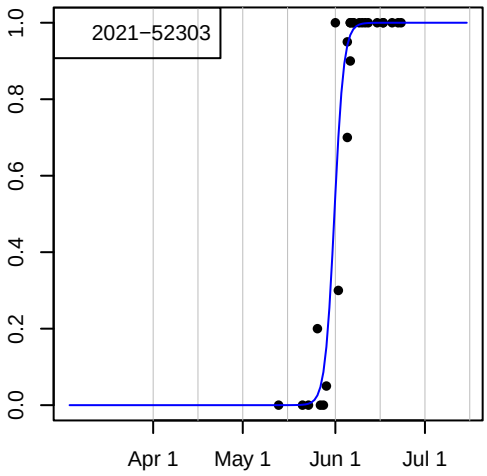
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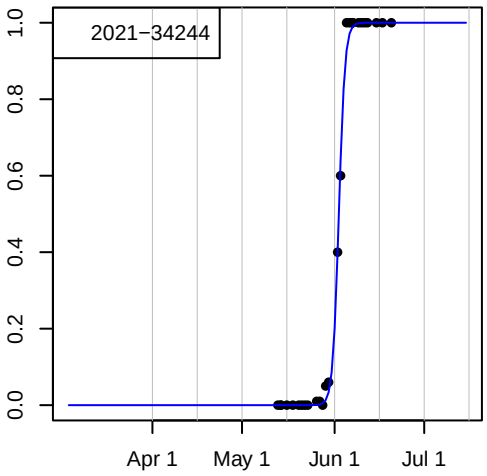
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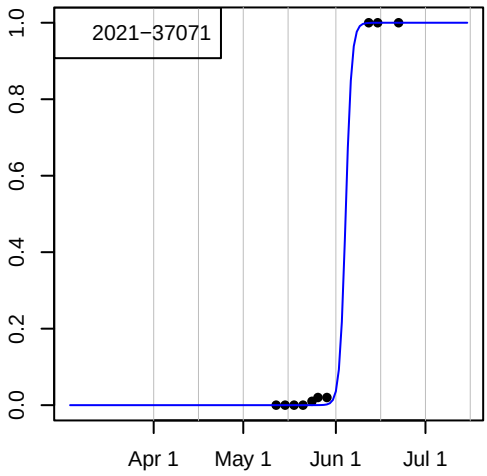
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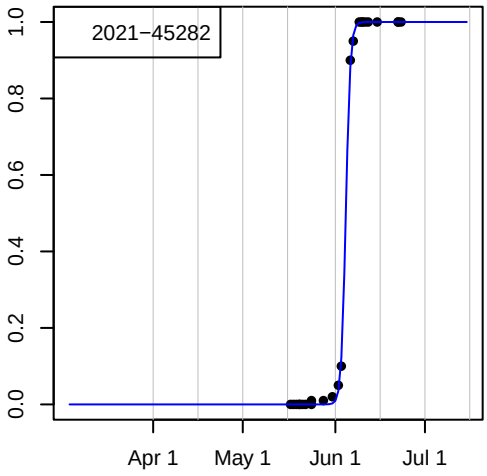
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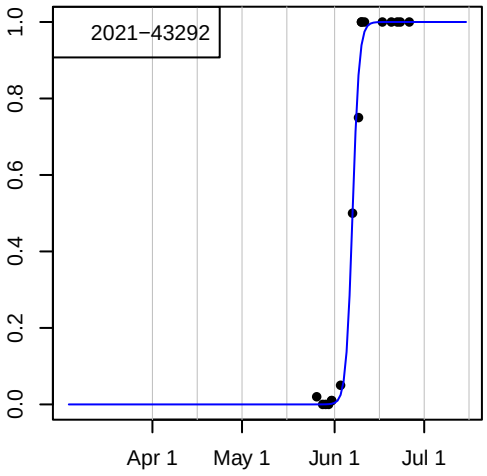
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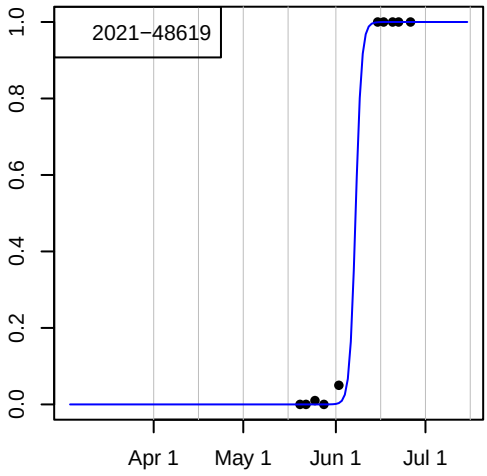
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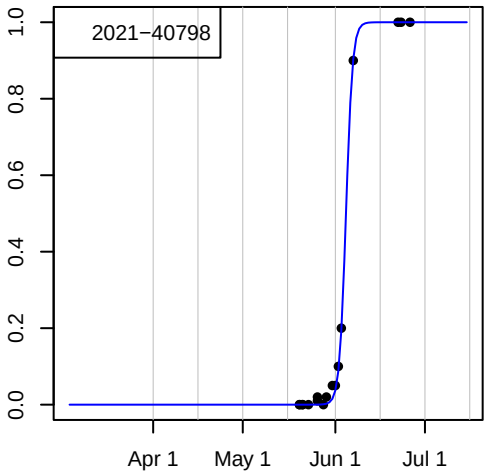
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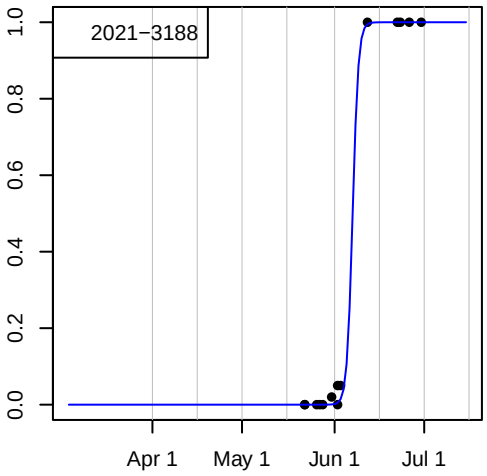
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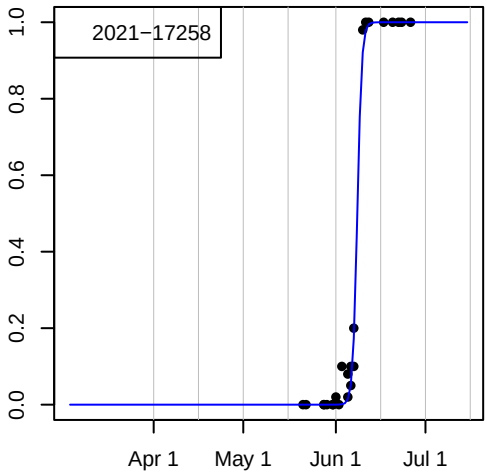
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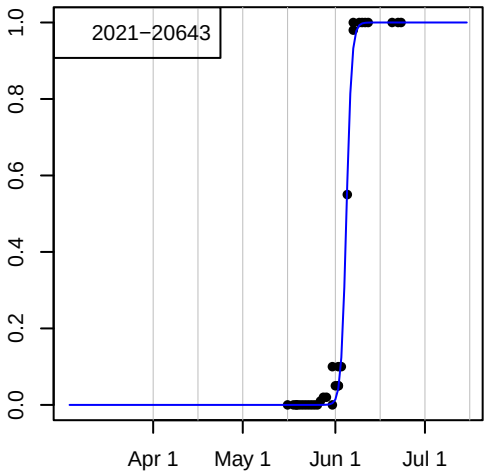
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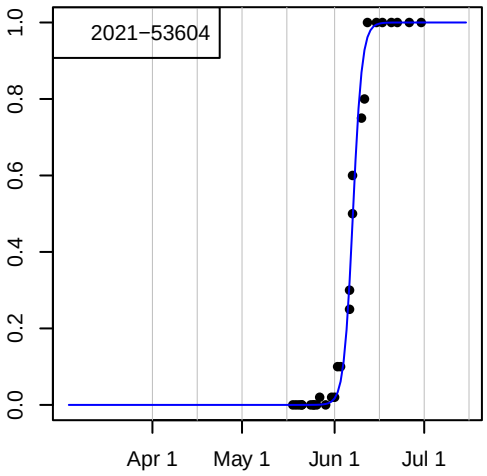
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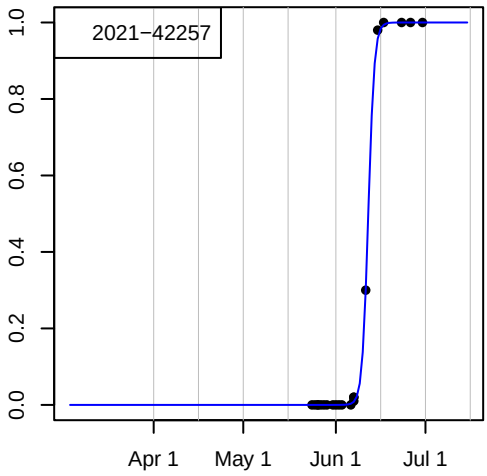
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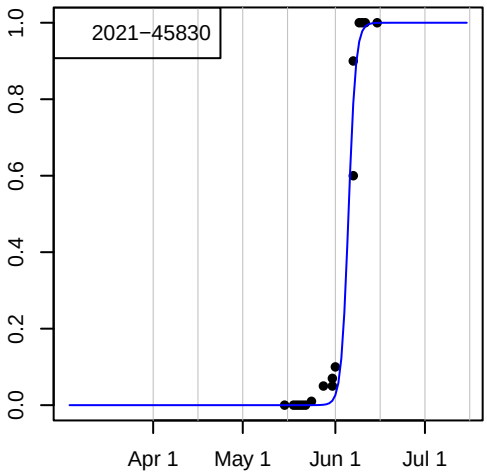
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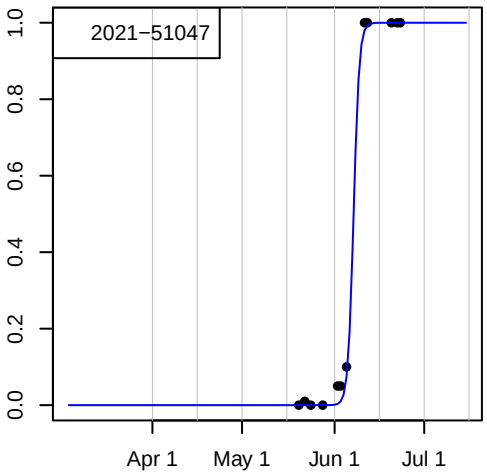
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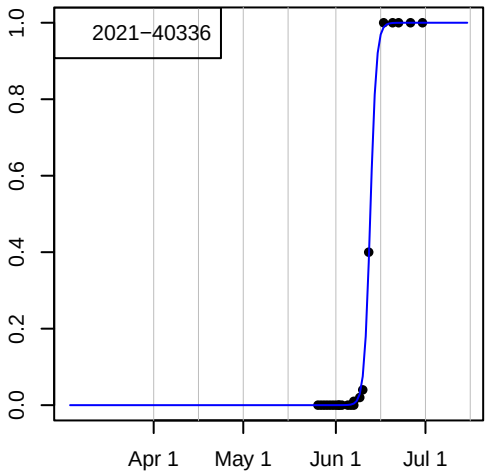
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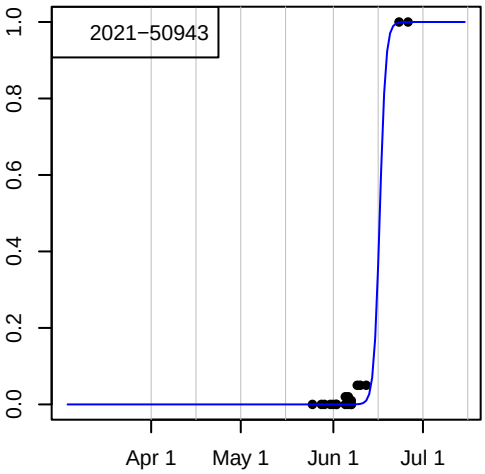
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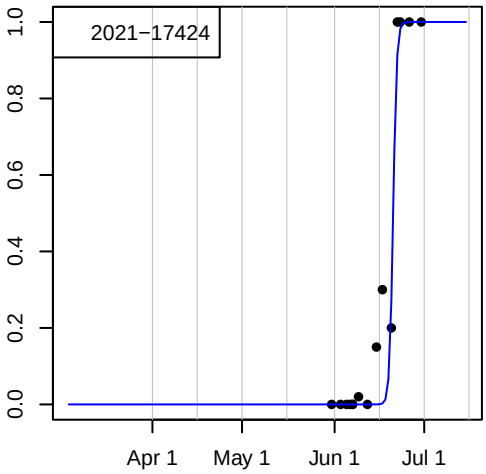
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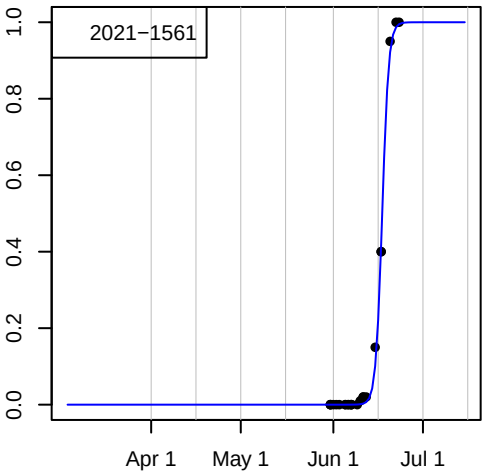
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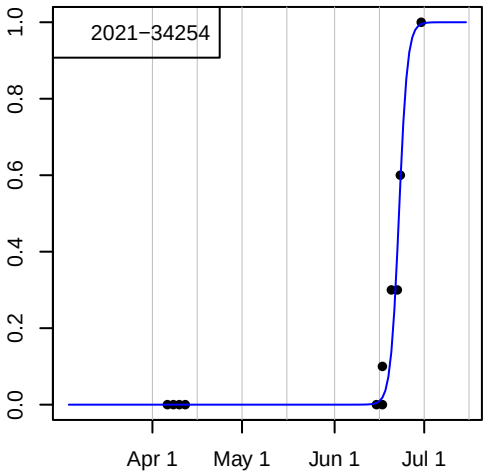
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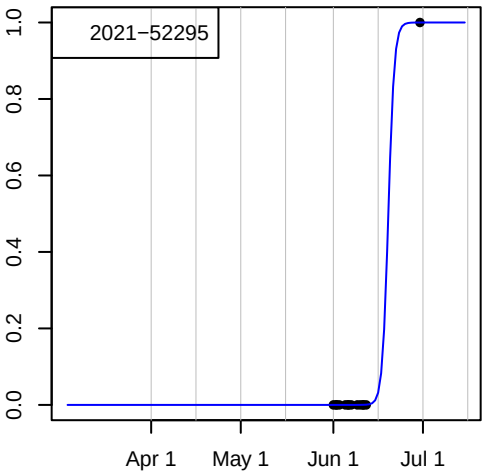
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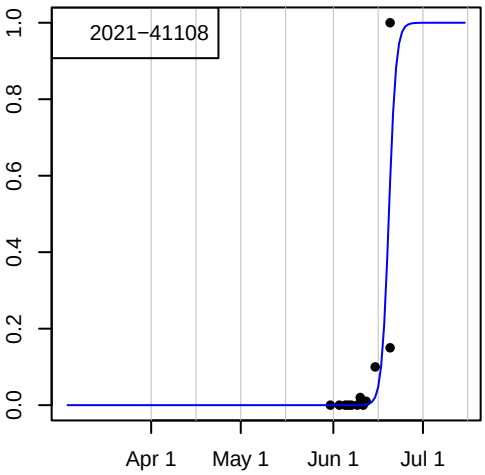
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