

**Supplementary Materials to the Manuscript:
Combining temperate fruit tree cultivars to fit spring
phenology models**

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9 **Abstract**

10 Phenological datasets for temperate fruit trees are often short , fragmented and
 11 geographically restricted, which hampers the development of cultivar-specific
 12 spring phenology models. To address this, we propose a novel calibration approach
 13 (“combined-fitting”), which pools observations from several cultivars of the same
 14 species, distinguishing between shared and cultivar-specific parameters. This method
 15 requires fewer observations per cultivar and allows jointly analyzing cultivars of
 16 the same species. We evaluate combined-fitting using the PhenoFlex framework,
 17 comparing it to a baseline model and to models that are fitted only with data for
 18 single cultivars (“cultivar-fit”). Our analysis is based on flowering data from nine
 19 almond, six apricot and six sweet cherry cultivars across Mediterranean (Spain,
 20 Morocco, Tunisia) and German climates. The combined-fit model failed to achieve
 21 higher prediction accuracy compared to the cultivar-fit and the baseline approach,
 22 as evidenced by similar root mean square errors across the data splits and calibra-
 23 tion dataset sizes. When comparing the estimated parameters of the chill and heat
 24 accumulation submodels, we observed a large variation among cultivars of the same
 25 species in the cultivar-fit models. In contrast and by design, the combined-fit yielded
 26 only one parameter set for cultivars of the same species. Our findings demonstrate
 27 that integrating data from multiple cultivars can yield spring phenology models
 28 with high accuracy. Even though the combined-fit approach did not outperform the
 29 cultivar-fit approach, combined-fitting offers a practical solution for spring phenology
 30 modeling with limited datasets and facilitates comparison across cultivars of the
 31 same species.

32 **1 Introduction**

33 This document contains supplementary materials for the journal article: *Combining*
 34 *temperate fruit tree cultivar to fit spring phenology models*. It includes additional ta-
 35 bles and files that were not part of the main article, as well as the code to replicate
 36 the analyses.

37 The phenology analyzed here are part of a long-term phenology dataset (Luedeling
 38 et al., 2024a) compiled within the *Adapting Mediterranean Orchards (AdaMedOr)*
 39 project. Of the more than 270 cultivars in the dataset, a subset of 110 cultivars has
 40 been analyzed by Caspersen et al. (2025) using the PhenoFlex framework (Luedeling
 41 et al., 2021), available via the R package *chillR* (Luedeling et al., 2024b). In addi-
 42 tion to model calibration, the analysis includes climate change impact projections on
 43 future bloom dates.

44 More than 50% of the cultivars in the dataset were not analyzed because the bloom
 45 observations were considered too short for calibration with PhenoFlex. We propose
 46 an alternative calibration method, **combine- fitting**, which reduces the number
 47 parameters estimated per cultivar and may allow the joint analysis of cultivars of
 48 the same fruit tree species. We evaluate combined-fit approach for three temperate
 49 fruit and nut species (almond, apricot, sweet cherry) and compare the results with
 50 those from a baseline model and from a common calibration approach in which each
 51 cultivar is calibrated seperately. We perform the analysis for the full dataset and for
 52 an artificially shortened dataset.

53 Parts of the function that we present in this document are available via the R pack-
 54 ages *evalpheno* (Caspersen, 2025a) and *LarsChill* (Caspersen, 2025b). Both packages
 55 are currently available via GitHub.

56 **2 Supplementary Table**

Table 1: Overview on the full bloom dataset for almond, apricot and sweet cherry cultivars

Species	Location	Country	Cultivar	Year Start	Year End	n
Almond	Meknes	Morocco	Ferragnes	1977	2014	38
Almond	Meknes	Morocco	Marcona	1977	2014	38
Almond	Meknes	Morocco	Tuono	1974	2014	41
Almond	Santomera	Spain	Achaak	1997	2019	13
Almond	Santomera	Spain	Desmayo	1997	2022	21
Almond	Santomera	Spain	Marta	2005	2021	14
Almond	Sfax	Tunisia	Fasciuneddu	1981	2015	22
Almond	Sfax	Tunisia	Mazzetto	1981	2015	22
Almond	Sfax	Tunisia	Nonpareil	1981	2016	23
Apricot	Cieza	Spain	Bulida	2003	2022	21
Apricot	Cieza	Spain	Dorada	2003	2022	20
Apricot	Zaragoza	Spain	Goldrich	1999	2021	21
Apricot	Zaragoza	Spain	Harcot	1999	2022	22
Apricot	Zaragoza	Spain	Henderson	1999	2021	21
Apricot	Zaragoza	Spain	Sunglo	1999	2022	22
Sweet	Klein-Altendorf	Germany	Burlat	1978	2015	29
Cherry						
Sweet	Klein-Altendorf	Germany	Regina	1988	2020	32
Cherry						
Sweet	Klein-Altendorf	Germany	Schneiders	1984	2019	32
Cherry						
Sweet	Zaragoza	Spain	Rainier	1991	2022	24
Cherry						
Sweet	Zaragoza	Spain	Sam	1991	2022	24
Cherry						
Sweet	Zaragoza	Spain	Van	1991	2022	24
Cherry						

3 Supplementary Figure

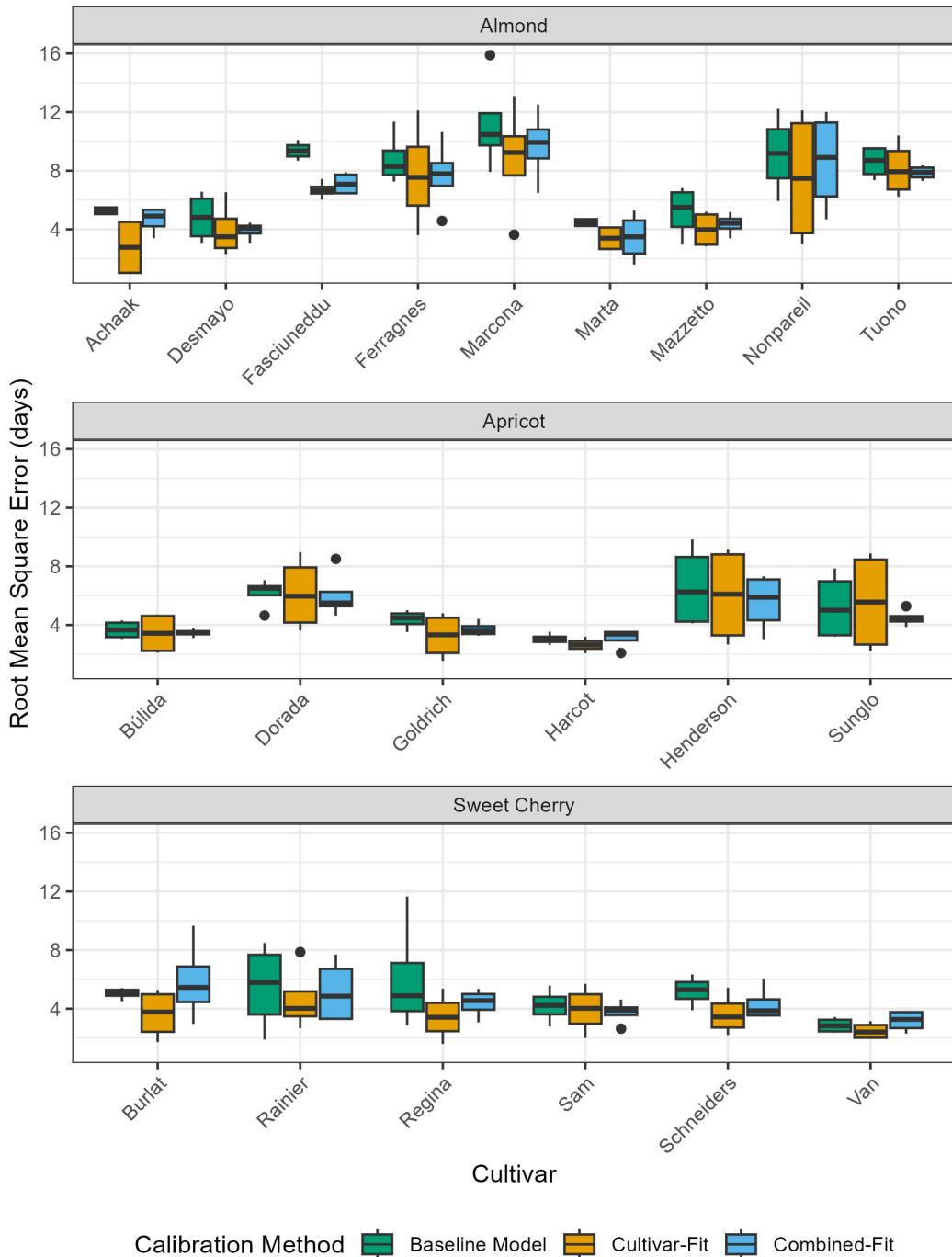


Figure 1: Root Mean Square Error (RMSE, days) of predicted bloom dates for each species (almond, apricot, sweet cherry) and cultivar (indicated at the x-axis). Boxplot summarizes RMSE for calibration and validation split and for ‘scarce’ and ‘full’ calibration sets. Calibration methods are indicated by color, green for ‘Baseline Model’, yellow for ‘Cultivar-Fit’ and blue for ‘Combined-Fit’.

59 **4 Supplementary Code**

60 **4.1 Data splitting**

61 This notebook shows the preparation of the phenology data. Performs calibration
62 and validation data splits. Check out the notebook for more details:

63 [Split data in calibration and validation](#)

64 **4.2 Model Calibration**

65 When calibrating the model, we specified the search space for each model parameter.
66 We substituted the model parameters E_0 , E_1 , A_0 and A_1 of the chill submodel
67 with intermediate parameters θ^* , θ_c , π_c and τ , following Egea et al. (2021) and
68 implemented for PhenoFlex by Caspersen et al. (2024). Additionally, we restricted
69 parameters, so that the E_{10} quotient of the process modeling chill formation and
70 degradation ranges between 1.5 and 3.5, a range said to be realistic in biological
71 systems (Egea et al., 2021; Luedeling et al., 2021). During model calibration, the
72 optimization algorithm ran for 5,000 iterations for baseline model; 30,000 evaluations
73 for single-fit; 50,000 evaluations for combined fit. We chose different total number
74 of evaluations for the calibration methods, to account for varying number of model
75 parameters estimated during each individual calibration step. The optimization
76 algorithm estimates model parameters by minimizing the residual sum of squares
77 (RSS) of predicted and observed bloom dates. In a pre-trial we confirmed that by
78 the end of the total number of model evaluations the RSS converged, indicating that
79 the algorithm fails to find parameters providing better model performance.

80 These three notebooks perform the model calibration. The notebook for almond cal-
81 ibration has also some more comments on the different procedures. The notebooks
82 for apricot and sweet cherry only contain the uncommented code.

- 83 • [Almond calibration](#)
- 84 • [Apricot calibration](#)
- 85 • [Sweet Cherry calibration](#)

86 **4.3 Model Evaluation**

87 This code shows how the calibrated models are evaluated. This script generates
88 figures and tables for the manuscript.

89 [Generate figures for the manuscript](#)

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