Uncertainty in crop phenology simulations is driven primarily by parameter variability

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Abstract

Crop phenology has a major influence on crop yield and is a major aspect of crop response to global warming. Process-based models of phenology are often used to predict the effect of weather on the development rate of crops through their growth phases, but such models are associated with large uncertainties, as demonstrated by the large variability between simulation results of different models. The purpose of this study is to estimate the relative importance of model structure uncertainty (due to uncertainty in the model equations) and model parameter uncertainty. Previous studies have assumed that the choice of model parameters to be fitted to data is fixed, and have evaluated the effect of uncertainty in those parameters. This underestimates parameter variance, as it ignores uncertainty in many aspects of the calibration approach, in particular the choice of parameters to estimate, as well as uncertainty in the parameters not fitted by calibration. Here, we propose and apply two approaches for estimating parameter variance that take into account uncertainty in all aspects of calibration, and, for one approach, uncertainty in parameters not fitted by calibration. Both approaches are based on previously reported large multi-model studies. The first approach uses components of variance analysis, which is possible because these studies included different modeling groups using the same model structure. The second approach is based on a study where multiple modeling groups each applied two different calibration procedures. The variance calculated from the two calibration approaches gives an estimate of parameter variance. Both methods give an overall result of 69% of total variance coming from parameter variance, for those simulated variables for which there are observed data. We conclude that in order to reduce uncertainty in crop phenology predictions, improving and sharing calibration procedures is as or more important than improving model structure.

Keywords: Crop modeling, Model calibration, Parameter uncertainty, Phenology, Structure uncertainty, Wheat

1. Introduction

Crop phenology has a major effect on crop yield and is a major aspect of crop response to global warming (Cleland et al., 2007; Liu et al., 2022; Parmesan, 2006). Process-based models of phenology, usually embedded in crop or agroecosystem models, are often used to predict the effect of weather on phenology (Bindi et al., 2015; Muleke et al., 2022). It has become common to study crop performance in general and crop phenology, in particular, using multi-model ensembles, where multiple models are provided with identical inputs and the range of simulated outputs is examined. These studies have shown that the variability in simulated values is substantial (Asseng et al., 2013; Durand et al., 2018; Sándor et al., 2020; Wallach et al., 2021a, 2021b). In several studies where multiple crop models were combined with multiple global circulation models (GCMs), it was been found that the uncertainty contribution from crop models is as large or larger than that from the GCMs (Asseng et al., 2013; Müller et al., 2021; Wang et al., 2020). A reduction in uncertainty from crop models is necessary in order to increase confidence in the results of these models, especially for the simulation of climate change impact assessment and options for adaptation (Maiorano et al., 2017; Rötter et al., 2011).

For given inputs (i.e. weather, crop management, soil characteristics and initial conditions), the uncertainty in crop model simulations has two origins, the uncertainty in crop model structure, which encompasses both the processes included in the model and the specific forms of the equations used to model those processes, and the uncertainty in the parameter values. Only relatively few studies have targeted the relative importance of both structure and parameter uncertainty, and those studies mostly indicate that the contribution of parameter uncertainty is rather small compared to the contribution from structure uncertainty (Tao et al., 2018; Wallach et al., 2017; Xiong et al., 2020; Zhang et al., 2017). Here, we argue that those studies do not take into account the full extent of parameter uncertainty, and we explain why it is difficult to do so. Therefore, we present here a new analysis, based on multi-model

ensemble simulation studies of crop phenology, that show that parameter uncertainty is the major contributor to overall simulation uncertainty.

Model structure uncertainty refers to the range of plausible model structures, where a "plausible" structure is one that would be deemed acceptable by researchers knowledgeable in the field of crop modeling. Often an explicit or implicit requirement for participating in multi-model studies is that the model structure has been published in the scientific literature, and has thus undergone peer review. This can be considered to satisfy the plausibility condition. We also assume that in a multi-model ensemble study, the represented model structures are a random sample from the population of plausible structures, even though this assumption may be hard to fully justify. The problem is that crop multi-model ensembles, like those in other fields, are generally "ensembles of opportunity" (Knutti, 2010; Wallach et al., 2016). That is, whichever modeling groups wish to participate are accepted. In fact, this openness is a principle of the Agricultural Modeling Intercomparison and Improvement Project (AgMIP, Rosenzweig et al., 2013). As a result, the ensemble may well have the same model structure represented more than once, or there may be complex relationships among models, where some models are derived from others or share similarities in structure (Fronzek et al., 2018; Holzworth et al., 2014; van Ittersum et al., 2003) so that the structures are not independent. There have been attempts to account for model interrelatedness in climate modeling (Sanderson et al., 2015) , but this has not been done for crop models so far.

Parameter uncertainty for a given model structure and data set refers to the range of plausible parameter vectors for that structure and data. Here "plausible" means that research teams working with that structure would consider those parameters, or the way in which the parameters are obtained, i.e. model calibration, reasonable. In almost all multi-model ensemble studies, models are calibrated using some data set (which is the same for all models). Thus, the uncertainty in parameterization is due to

variability in the calibration method and in the choice of default parameter values (the values of those parameters that are not affected by calibration).

To study the consequences of uncertainty in model structure and/or in model parameters, one needs a sample drawn from the range of plausible structures and/or from the range of plausible parameters for one or more structures. As discussed, the models represented in multi-model ensemble studies are generally accepted as a sample from plausible structures. How to sample from plausible parameter vectors on the other hand is not clear.

Wallach et al. (2022) identified several steps in crop model calibration, including the choice of default parameter values, the choice of observed data to use in the objective function for frequentist calibration, the choice of parameters to be estimated from the data and finally the choice of algorithm and software for doing the calibration. They showed that different modeling groups made different choices, and that even different modeling groups using the same model structure made different choices. We suggest that sampling from plausible parameter vectors thus involves sampling from the plausible choices for the default parameter values and from the plausible choices at each step of the calibration procedure.

There has been a range of previous studies that have sampled model parameters Zhang et al. (2017) used five rice phenology models and generated 50 randomly perturbed sets of parameter values for each to obtain a sample of parameter values. Wallach et al. (2017) estimated parameters for two rice phenology models using weighted least squares, then generated samples of parameters using the estimated variance-covariance matrix of the estimated parameters. Tao et al. (2018) using seven barley models identified a reasonable range for each parameter and generated a super ensemble, where each model was associated with multiple parameter values drawn from the range of that parameter. Xiong et al. (2020) compared three different crop models and four parametrization strategies that differed in the

amount of data available for calibration. Other studies have specifically considered the way in which the model parameters are estimated. Kawakita et al. (2019), in a study of time to heading in wheat, assessed three models and three different optimization algorithms for calibration, leading to three different parameter vectors for each model. Jha et al. (2022) compared three calibration approaches for CERES Maize, namely grid search, GLUE, and a genetic algorithm. Gao et al. (2020) compared the predictions and uncertainty estimates for the CERES Rice model using a weighted least squares calibration method, the GLUE method, and a Bayesian approach. Harrison et al. (2019) compared search techniques for calibrating the APSIM model. In these studies, the choice of parameters to be treated as uncertain, as well as the choices for most of the calibration steps listed above, are taken as given. Also, no uncertainty in the default parameter values is taken into account. Thus those studies ignore several causes of uncertainty in parameters that exist in multi-model ensemble studies (Albanito et al., 2022; Wallach et al., 2021c) and could be important, and thus, those studies are likely to underestimate the importance of parameter uncertainty.

A straightforward approach to estimating parameter and model structure uncertainty would be to specifically create a multi-model ensemble in which each model structure is used by more than one modeling group, each of which independently estimates the model parameters. In practice, this is difficult to achieve. Confalonieri et al. (2016) organized a study with five crop models and 20 users, leading to different model parameterizations. However, in that case, the groups responsible for calibration were students and not model experts, so the parameter vectors might not be considered "plausible" by model experts.

The goal of this study was to obtain estimates of parameter uncertainty, and of the relative importance of parameter and structure uncertainty, which are more realistic than previous estimates. The specific application is the estimation of wheat phenology in multiple environments. Two different approaches are employed. The first is based on two multi-model ensemble studies which were not

specifically designed to study parameter uncertainty, but where it turned out that some of the model structures were used by more than one modeling team. Those teams independently chose default parameter values and the calibration procedure. The differences between modeling groups using the same structure give information about parameter uncertainty. The second approach is based on a study where multiple modeling teams each used two different calibration procedures. The differences between the two procedures are used to estimate parameter uncertainty.

2. Materials and Methods

2.1 Data

This study revisits three simulation experiments on wheat phenology that have been previously reported (Wallach et al., 2021a, 2021b, 2022). In the previous studies, the emphasis was on prediction accuracy, whereas in the present study the simulation results are reanalyzed with the objective of estimating the contribution of parameter uncertainty to the overall uncertainty of the phenology prediction.

The simulations concern three data sets (**Table 1**). Two of the data sets are from winter wheat variety trials in France. These data sets have identical structures (same sites and sowing dates) but concern two different varieties, “Apache” and “Bermude”. Both varieties are of intermediate precocity, but Bermude has a longer cycle. The observed data from each environment consist of daes of stem elongation (BBCH30 on the BBCH scale, Meier, 1997) and middle of heading (BBCH55). The third data set is from a multi-site sowing date experiment on spring wheat variety “Janz” in Australia. The original data were observations of growth stage at weekly intervals. The data provided to modeling groups were the dates of each BBCH stage, from the first to the last observed stage, derived from interpolation of the original data. All data sets were split into two subsets, one for calibration and the other for evaluation.

The calibration and evaluation data sets had neither site nor year in common. Thus evaluation was a true test of how well models could predict for out-of-sample conditions.

Table 1

Data set	Number of calibration environments	Number of evaluation environments	Observed development stages*	Simulated development stages used for analysis*
France Variety Apache	14	8	BBCH30, BBCH55	BBCH10, BBCH30, BBCH55
France Variety Bermude	14	8	BBCH30, BBCH55	BBCH10, BBCH30, BBCH55
Australia Variety Janz	24	18	BBCH stage at weekly intervals	BBCH10, BBCH30, BBCH65, BBCH90

*The development stages, using the BBCH scale (Meier, 1997) are emergence (BBCH10), start of stem elongation (BBCH30), middle of heading (BBCH55), full flowering (BBCH65), and maturity (BBCH90).

Table 1. The three data sets used in the multi-model ensemble studies analyzed here.

2.2 Participating modeling groups and model structures

The call for participants in the first study was published using the mailing lists of several models and of AgMIP. All modeling groups that volunteered (a modeling group is one or more individuals that work together to run a model) were accepted. All groups used model structures that have been published. A total of 30 modeling groups using 23 different structures (SI) participated in one or more of the simulation experiments. In all cases, the phenology models were embedded in general crop models,

so model structure here refers to the overall crop model. Most but not all of the groups participated in all the studies.

No specific attempt was made to encourage or discourage participation by different groups that used the same structure. In the event, there were two or three (depending on the simulation study) model structures were used by more than one group. In particular, in the first two studies three structures were used by 2-4 different modeling groups (Table 2).

In all studies, it was decided to identify the different modeling groups were identified by a code (M1, M2 etc.) without further identification of the group or giving the name of the model structure used. The same codes are used here. In addition, we assign here codes to the different model structures (S1, S2, etc.). The same model structure can be associated with more than one modeling group.

Table 2

Simulation study	Data set (country, cultivar)	Calibration procedure	Number of modeling groups	Repeated structures*
1	France, Apache	Usual	27	S2 (4), S4 (3), S18 (2)
1	France, Bermude	Usual	27	S2 (4), S4 (3), S18 (2)
2	Australia, Janz	Usual	28	S2 (3), S4 (3), S18 (2)
3	France, Apache	Protocol	19	S2 (3), S4 (2)
3	France, Bermude	Protocol	19	S2 (3), S4 (2)
3	Australia, Janz	Protocol	19	S2 (3), S4 (2)

*The model structures used by more than one modeling group, and in parentheses, the number of groups that used that structure.

Table 2. The three different simulation studies analyzed here.

2.3 Simulation studies

In the first simulation study (Wallach et al., 2021a), based on the French data sets, each participating modeling group implemented their usual calibration method to calibrate their model using the calibration data subsets and then simulated days from sowing to phenological stages BBCH10, BBCH30, and BBCH55 for both varieties and for both the calibration and evaluation environments (Table 2). In the second study (Wallach et al., 2021b), each participating modeling group again used their usual calibration method and then simulated days from sowing to phenological stages BBCH10, BBCH30, BBCH65, and BBCH90 for the Australian environments. Neither the French nor the Australian data sets had observations of BBCH10, which was included in the variables to simulate in order to have an example of a simulated stage without calibration data.

The detailed descriptions of the calibration procedures used by each team in the first two studies were used to identify the range of decisions for each calibration step. Based on an analysis of the different choices, and following discussions with the participating teams, a new detailed calibration procedure (hereafter the calibration "protocol") was proposed and applied to all three data sets by all participating teams. Any group that participated in the third study but that had not participated in the first two studies first did the calibration using their usual method, before applying the protocol.

The proposed calibration protocol is described in detail in Wallach et al. (2022). The protocol covers all steps in phenology model calibration and includes templates for documenting the different steps. A major innovation, compared to the usual calibration procedures, is in the choice of parameters to estimate. In the protocol, this is done in two stages. First, parameters that play an almost additive role, i.e.affect all environments to a similar extent are identified. At most, there can be as many almost additive parameters as the number of different variables used for calibration (for example, two almost additive parameters if BBCH30 and BBCH55 are used for calibration). In most cases, the almost additive parameters are degree days to development stages at or near the observed stages. Those parameters

are estimated based on the calibration data. This should remove bias in the simulations, or nearly do so. Then a series of candidate parameters, thought likely to explain part of the remaining unexplained variability between environments, is identified, and those parameters are tested one by one. If the estimation of a candidate parameter, together with all previously chosen parameters, sufficiently improves the fit to the data, as measured by the Bayesian Information Criterion (BIC), it is included in the final list of estimated parameters. If not, it is kept at its default value. A comparison between usual and protocol calibration for the participants in the third study showed major differences between the two. For example, the number of estimated parameters differed between the two procedures for the great majority of participants (Wallach et al., 2021c).

2.4 Estimation of structure and parameter variance

Variance components approach

For a given environment, with given inputs, the variability in the simulated values comes from the variability in structures and parameters. We assume that for each simulation experiment, the model structures are a random sample from a plausible structure. It is further assumed that the parameter vector used by each modeling group in simulation studies 1 and 2 is an independent random draw from plausible parameter vectors for the corresponding model structure, consisting of a random draw from plausible default parameter values and a random draw from plausible calibration approaches. Presumably all the modeling teams were well-versed in using their model, which fulfills the plausibility requirement for the parameters.

The statistical model for a simulated value is then

$$y_{sp} = \mu + \alpha_s + \beta_{sp} \tag{1}$$

where y_{sp} is the simulated value for model structure *s* and parameter vector *p*, μ is the overall mean ,α_s is the effect of model structure and β_{sp} is the effect of parameter vector nested within the model structure. There is no residual term because these are simulated values with no measurement error. We treat α_s and β_{sp} as random effects, since we are interested in the variability in the population not in the specific model structures or parameter vectors in the sample. The variances are noted $\mathrm{var}(\alpha_s) = \sigma^2_{structure}$ for all *s* and $\mathrm{var}(\beta_{sp}) = \sigma^2_{parameters}$ for all *sp*. The random terms are assumed independent so that the total variance for one environment and one simulated variable is the sum of model structure variance and of parameter variance (Scheffé, 1959):

$$\sigma^2_{total} = \sigma^2_{structure} + \sigma^2_{parameters} \tag{2}$$

To estimate parameter and model structure variance simultaneously , we use the lmer function of the lme4 package (Bates et al., 2015) in R (R Core Team, 2017), which is designed to analyze linear mixed effect models (SI). This components of variance approach to estimating parameter variance is not used for simulation study 3, since there were too few model structures used by more than one modeling group. An illustration of the data used in this approach is given in Figure 1. As that figure shows, three of the model structures (S2, S4, and S18) were used by more than one modeling group. It is the variability between the different groups using the same model structure that allows us to estimate parameter variance. The results for all groups contribute to the estimation of structure variance. Note, that the simplified approach to estimating parameter uncertainty using these same data in Wallach et al. (2021a, 2021b) did not fully take into account the contribution of parameter uncertainty.

Figure 1

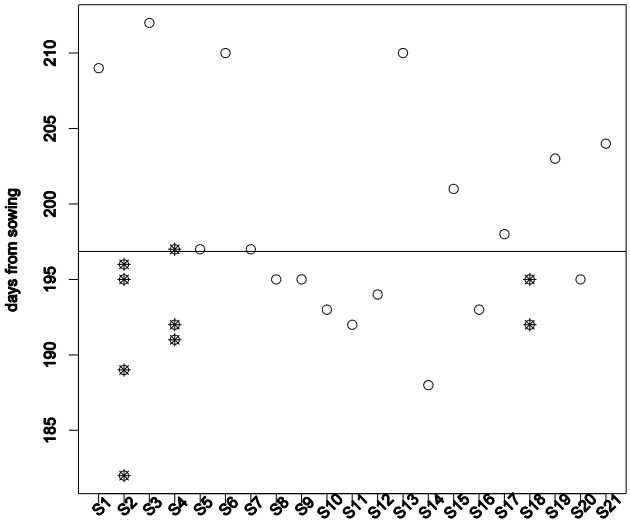

Figure 2. Example of data used for variance components approach to estimating parameter and structure uncertainty. Simulation of days from sowing to mid-heading (stage BBCH55) for variety Apache in one environment from simulation study 1. All modeling groups used the same inputs. The x-axis shows the model structure. In most cases, each structure was used by a single modeling team, but structures S2, S4, and S18 were used respectively by 4, 3, and 2 teams (data shown as stars). It is the variability between simulations from different groups using those model structures that is the basis for estimating parameter uncertainty. The horizontal line is the average of all simulated values.

Comparison of usual and protocol calibration

The second estimation of parameter uncertainty is based on all three simulation studies (see Table 2). In studies 1 and 2 Every group used their usual calibration approach and in this study used the newly proposed protocol calibration approach to obtain parameters for each data set. The estimate of

parameter uncertainty here is based on the difference between these two calibration methods. The two simulation results for every modeling group for one environment are shown in Figure 2.

Each group's usual calibration approach can be considered to be a random draw from plausible calibration approaches for their model structure. The protocol calibration approach, which was developed in collaboration with all participating modeling teams, is also by construction a plausible calibration approach. It is essentially independent of the usual approach since the contribution of any single group to the protocol was limited. Furthermore, the protocol did not mimic closely any single usual calibration approach. Therefore, for each modeling group we treat the usual and the protocol calibration as two random draws from the population of plausible calibration approaches for the model structure used by that group. For each environment, we calculate the variance of the two calibration approaches, noted var_i for modeling group *i* (eq. 3), and then average over modeling groups to obtain an estimated parameter variance for that environment (eq. 4).

$$\mathrm{var}_i = \left(y^{usual} - \bar{y}\right)^2 + \left(y^{protocol} - \bar{y}\right)^2 \tag{3}$$

$$\hat{\sigma}^2_{parameters} = 1/n \sum_{i=1}^{R} \mathrm{var}_i \tag{4}$$

where $\bar{y} = (y^{usual} + y^{protocol})/2$.

We do not have a rigorous method of estimating structure variance from these data. The difficulty is that the assumptions underlying the random effects model described above are not satisfied; the parameter vectors obtained by protocol calibration are not independent between modeling groups, since all use the same protocol. We therefore use, for each environment, the estimate of structure variance from the variance components approach above.

Figure 2

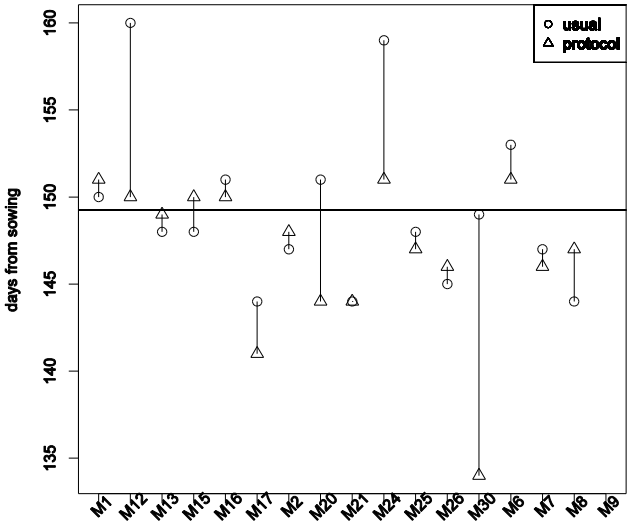

Figure 2. Example of data used for usual compared to protocol approach to estimating parameter uncertainty Simulated days from sowing to stem elongation (stage BBCH30) for variety Bermude in one environment from simulation study 3, which compared usual and protocol calibration for each modeling group. Each code (M1, etc.) refers to a specific modeling group (x-axis). For each modeling group, there are two simulated values, one using parameters based on usual calibration and the other using parameters based on protocol calibration. The differences between the two values are used to estimate parameter variance. The horizontal line shows the mean of simulations using usual calibration.

3. Results

First, all calculations were done for the calibration and evaluation data subsets separately, however we found that there were no systematic differences between the two (Fig. S1 and Fig. S2). All results here are therefore based on the combined calibration and evaluation data.

Figure 3 shows parameter variance as a fraction of total variance for each environment of the two French data sets, using variance components or usual compared to protocol calibration. Figure 4 shows the same information for the Australian data set. Table 3 and Table 4 show parameter variance, and parameter variance as a fraction of total variance, averaged over all environments for the French and Australian data sets, respectively.

Table 4 shows results averaged over all environments of both the French and Australian data sets. Separate values are given for BBCH10 (for which there was no observed data) and for all other stages.

Two aspects of the results in Table 3 and Table 4 are worth emphasizing. First, the estimated contribution of parameter variance to total variance is always much less for BBCH10 than for the other simulated development stages. This is the case for both approaches, but the difference is particularly important for the approach based on comparison of usual and protocol calibration.

Secondly, for development stages other than BBCH10, the estimated contribution of parameter uncertainty is large. It ranges from 24 to 93%, and is larger than 50% for 11 out of the 14 combinations of data set, development stage and approach for estimating the contribution of parameter variance.

Figure 3

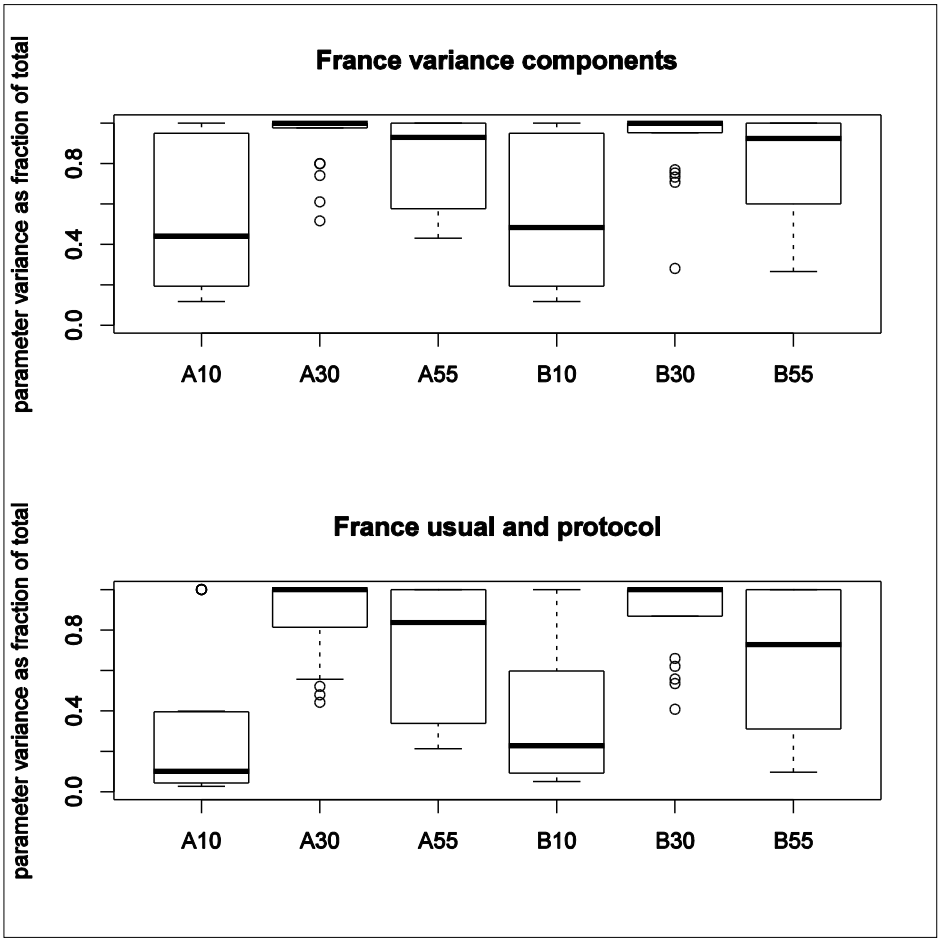

Figure 3. Fraction of total variance due to parameter variance, for the French data sets, based on two different approaches: based on variance components (top) or based on the comparison of usual and protocol calibration (bottom). A10, A30, and A55 (B10, B30, B55) refer respectively to simulations of days from sowing to emergence, to start of stem elongation and to middle of heading for the variety Apache (Bermude). Boxes indicate the lower and upper quartiles. The solid line within the box is the median. Whiskers indicate the most extreme data point which is no more than 1.5 times the interquartile range from the box, and the outlier dots are those observations that are beyond that range.

Figure 4

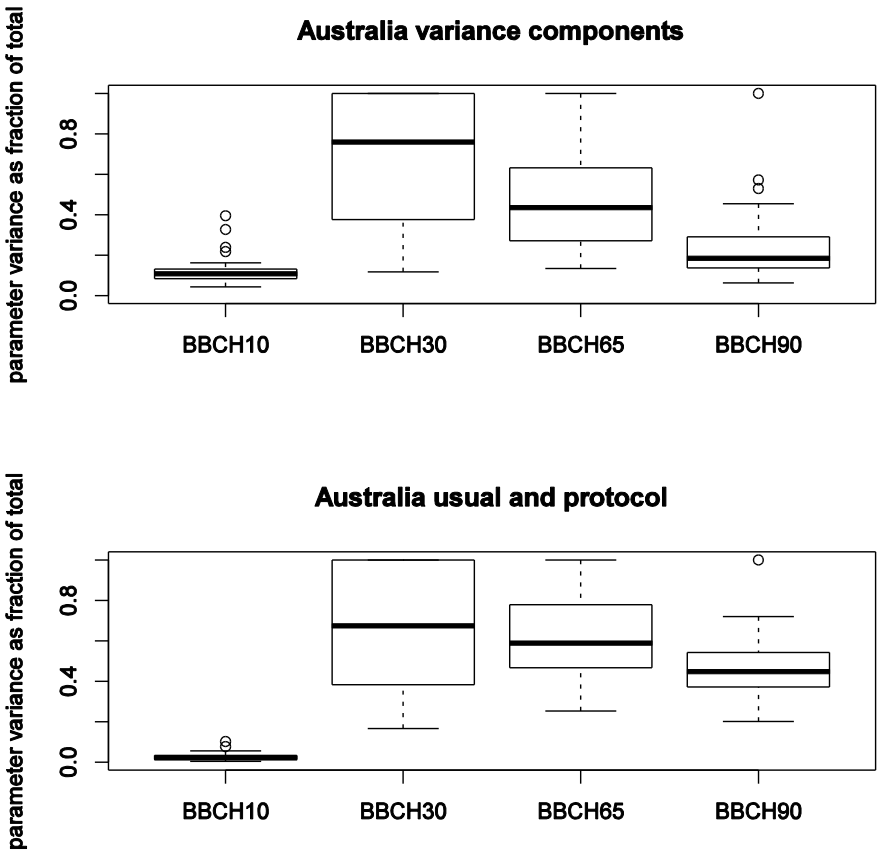

Figure 4. Fraction of total variance due to parameter variance, for the Australia data set, based on two different approaches: based on variance components (top) or based on comparison of usual and protocol calibration (bottom). Simulations are of days from sowing to emergence, start pf stem elongation, full flowering and maturity. Boxes indicate the lower and upper quartiles. The solid line within the box is the median. Whiskers indicate the most extreme data point which is no more than 1.5 times the interquartile range from the box, and the outlier dots are those observations that are beyond that range.

Table 3

		Apache			Bermude		
Method of estimating parameter variance as fraction of total	Development stage	BBCH10	BBCH30	BBCH55	BBCH10	BBCH30	BBCH55
Variance components	Average number of modeling groups	23	25	27	23	25	27
	Number of model structures	17	19	21	17	19	21
	Parameter variance	11.74	52.94	26.77	12.05	71.25	36.41
	Structure variance	5.05	4.29	9.65	4.99	10.86	12.73
	Parameter variance as fraction of total	0.55	0.93	0.81	0.56	0.92	0.8
Usual compared to protocol calibration	Average number of modeling groups	14	16	17	14	16	16.9
	Parameter variance	0.75	16.62	10.35	2.57	28.52	10.01
	Parameter variance as fraction of total	0.28	0.88	0.71	0.39	0.89	0.65

Table 3. Parameter and structure variance averaged over environments of the French data sets. The variance components estimate is based on ensemble studies where some model structures were used by multiple modeling groups. The usual compared to protocol estimate is based on comparing usual and protocol calibration results for each modeling group.

Table 4

Method for estimating parameter variance as fraction of total	Development stage	BBCH10	BBCH30	BBCH65	BBCH90
Variance components	Average number of modeling groups	22.95	23.93	27.64	26.05
	Average number of model structures	17.95	19.93	22.64	21.05
	Parameter variance	40.69	102.88	47.1	30.3
	Structure variance	276.33	45.74	48.4	90.71
	Parameter variance as fraction of total	0.12	0.66	0.49	0.24
Usual compared to protocol calibration	Average Number of modeling groups	13.9	16.9	18.9	17.3
	Parameter variance	8.41	62.54	67.12	80.76
	Parameter variance as fraction of total	0.026	0.65	0.61	0.46

Table 4. Parameter and structure variance averaged over environments of the Australian data set. The variance components estimate is based on ensemble studies where some model structures were used by multiple modeling groups. The usual compared to protocol estimate is based on comparing usual and protocol calibration results for each modeling group.

Table 5

Method for estimating parameter variance as fraction of total	BBCH10	All other stages
Variance components	0.41	0.69
Usual compared to protocol calibration	0.23	0.69

Table 5. Fraction of total variance due to parameter variance based on two estimation procedures: variance components and comparison of usual and protocol calibration. Averages are over all environments of both the French and Australian data sets, either for the development stage BBCH10 or for all other development stages.

4. Discussion

There are relatively few studies that have estimated separately the contributions of parameter uncertainty and model structure uncertainty to total simulation uncertainty in ensemble studies with crop models or crop phenology models. Those studies focused on parameter variability when the list of parameters to be estimated is fixed. This includes studies where the parameter distribution is based on expert opinion (Tao et al., 2018; Zhang et al., 2017) where parameters differ due to the use of different levels of gridded information (Xiong et al., 2020) or where the variance-covariance matrix of the parameter vector is estimated during least squares parameter estimation (Wallach et al., 2017). These studies have systematically found that structural uncertainty is substantially more important than parameter uncertainty.

390 Those studies sampled from the distribution of values for some fixed subset of model
391 parameters. However, this does not really take into account the full parameter uncertainty in crop or
392 phenology models, which arises from all aspects of the calibration approach, not just from uncertainty in
393 a fixed subset of parameters (Albanito et al., 2022; Wallach et al., 2021c). In addition, there is
394 uncertainty in the values of the fixed parameters. The two approaches we propose here take into
395 account more realistically the full uncertainty in model parameterization.

396 Our first approach is based on variability in simulated values between different modeling groups
397 using the same model structure. The underlying hypothesis is that the most realistic way to sample true
398 parameter uncertainty in crop or phenology models is to sample established crop modeling groups using
399 the same model structure. If they are provided with the same input data and the same observational
400 data for calibration, the parameter vectors they obtain is by construction a sample from plausible
401 parameter vectors for that structure and those data. It was found in the studies that were analyzed here,
402 that different groups took different decisions at all steps in the calibration procedure, including the
403 choice of which parameters to estimate, the form of the objective function, and the algorithm used for
404 searching for the best parameters (Wallach et al., 2021c). This confirms that uncertainty in calibrated
405 parameters arises from uncertainty in all aspects of the calibration procedure. Our approach
406 automatically takes all those differences in calibration procedure into account, as well as differences in
407 the choice of default parameter values. A limitation of the present study is that only three model
408 structures were used by more than one group, and at most four groups used the same model structure.

409 Our second estimate of parameter uncertainty is based on a comparison, for multiple modeling
410 groups, between two different calibration procedures, their usual procedure, and a new protocol
411 procedure. In general, there were major differences between the two calibration procedures for each
412 group (Wallach et al., 2022). Both are plausible in the sense that they were developed and used by
413 modeling teams well-versed in the use of their model structure. It seems reasonable then to assume that

414 for each modeling group, the two are a random sample of size two of plausible procedures for the
415 corresponding model structure. One limitation of this second estimate is that the same modeling group
416 implemented both calibration procedures. It seems likely that the default parameter values were mostly
417 unchanged between the two calibration approaches. Since the variability in the fixed parameter values is
418 not sampled, this approach underestimates the contribution of parameter uncertainty to the total
419 uncertainty.

420 In the estimates obtained here, parameter variance as a fraction of total variance is
421 systematically smaller for emergence (stage BBCH10) than for the other stages. The fraction is
422 particularly small for the estimates based on usual compared to protocol calibration. This is likely due to
423 the fact that there were no data for days to emergence, and so simulated days to emergence were
424 usually determined by the default parameter values. Probably, most modeling groups used the same
425 default values for usual and protocol calibration, leading to no difference in simulated days to
426 emergence between usual and protocol calibration. The contribution of parameter uncertainty to total
427 uncertainty for stages other than BBCH10, as estimated here, is similar for the two approaches to
428 estimation of parameter uncertainty. This suggests that when there are data related to a development
429 stage, differences between groups are mostly due to differences in calibration procedure rather than to
430 differences in default values.

431 The contribution of parameter uncertainty to total uncertainty, averaged over development
432 stages and data sets, is 69%. This implies that in a multi-model ensemble study simulating phenology,
433 over two thirds of the variability is due to parameter uncertainty and only 31%, or about one third is due
434 to structure uncertainty, i.e. to the variability among plausible model structures. The estimates obtained
435 here come from three different data sets, with 22 or 42 different environments. At least 19 modeling
436 groups participated in each study used here. There is substantial variability between environments and

437 simulated variables, but the range of situations analyzed gives some confidence in the overall conclusion,
438 that parameter uncertainty is the major contribution to overall model uncertainty

439 It is important to obtain information on the contribution of parameter uncertainty in other
440 conditions than those considered here. The most realistic estimate of parameter uncertainty is based on
441 independent modeling groups using the same model structure. One possibility would be to proactively
442 create multi-model ensembles where the same structure is represented by multiple modeling groups.
443 Another approach would be to take advantage of those multi-model ensemble studies where, by chance,
444 the same structure is represented by more than one modeling group. The variance components
445 calculation applied here could be applied quite generally to those studies. In some cases, the results of
446 past multi-model ensemble studies have been documented in data journals (e.g. Martre et al., 2018).
447 Those studies could be revisited in order to estimate parameter and structure uncertainty.

448 The major role of parameter uncertainty emphasizes the importance of documenting all
449 parameter values, both fixed and calibrated, for each model in each study, since these may have as much
450 or more effect on simulated values as the model equations. Without that information, the results of a
451 simulation study cannot be reproduced.

452 Much, though not all, of the parameter uncertainty, comes from the variability in calibration
453 approaches between modeling groups. The obvious path to the reduction of this source of uncertainty is
454 to have a single calibration approach for each model structure. Of course, this is only worthwhile if the
455 common calibration approach leads to a parameterized model that predicts well. There is no consensus
456 on the best calibration approach for crop models. However, there have been recent attempts to define a
457 calibration protocol that could be applied generally to phenology models, and that has been found both
458 to reduce uncertainty and to reduce mean squared error of prediction (Wallach et al., 2022).

The results here focus on simulating phenology, one component of crop models. Full crop models simulate many other processes and not just development, which may lead to larger structure uncertainty. However, full crop models have many more parameters than phenology models and parameter estimation of an entire crop model is more complex, which may increase parameter uncertainty. It is thus not clear how the results here scale up to more complex models. In any case, however, it is important to take into account the full extent of parameter uncertainty in analyzing structural versus parameter uncertainty for full crop models.

5. Conclusions

The large uncertainties associated with crop models in general and crop phenology models in particular clearly limit the utility and acceptance of these models for impact assessment and other practical applications. Previous studies that have aimed at quantifying the separate contributions of model structure and model parameter uncertainty have concluded that model parameter uncertainty is relatively less important, leading to the implicit conclusion that research should be focused on the processes and equations in crop models. We find here that when one takes into account the full uncertainty in calibration procedure and also uncertainty in the default parameter values, parameter uncertainty is the major cause of uncertainty in simulated values of crop phenology models The development and application of improved, shared calibration procedures as well as increased attention to the choice of default parameter values should thus be a major goal of the crop modeling community.

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