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Quantifying the uncertainty in critical N concentration for potato using Bayesian methods.

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**Abstract:** Multiple critical N dilution curves [CNDCs] have been previously developed for potato; however, attempts to directly compare differences in CNDCs across genotype [G] and environment [E] interactions have been confounded by non-uniform statistical methods and lack of proper quantification of uncertainty in critical N concentration and CNDC parameters. This study implements a hierarchical Bayesian framework to develop CNDCs for previously published and newly reported experimental data to systematically evaluate the difference between critical N concentration across G x E interactions. Differences in critical N concentration are primarily the result of differences in environmental factors (i.e., location) while genotype (i.e., variety) can cause differences within a given location. Additionally, the uncertainty range in critical N concentration should be used in subsequent, dependent calculations (e.g., N nutrition index) to propagate and account for uncertainty. The findings of this study provide additional evidence that critical N concentration is dependent upon G x E interactions.

**Keywords:** critical N dilution curve, nitrogen nutrition index, potato, Bayesian statistics

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| **Citation:** Lastname, F.; Lastname, F.; Lastname, F. Title. *Plants* **2021**, *10*, x. https://doi.org/10.3390/xxxxx  Received: date  Accepted: date  Published: date  **Publisher’s Note:** MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.    **Copyright:** © 2021 by the authors. Submitted for possible open access publication under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/). |

1. Introduction

Identifying optimal crop N status to maximize growth and yield production is an elusive goal. Traditionally, either the yield-goal approach or rate-response curves have been used to identify optimal N fertilizer application rate (Morris, et al., 2018). The N nutrition index [NNI] is an alternative approach to the current paradigm and comprises a well-developed framework to determine optimal crop N status (Lemaire, et al., 2019). Typically, NNI is used to determine crop N status using whole plant analysis and to direct adaptive N management within a growing season (Houlès, et al., 2007, Morier, et al., 2015). Unlike the yield-goal or rate-response approach, NNI is generalizable across environmental (e.g., year-to-year or geographic) variability (Sadras and Lemaire, 2014).

The NNI approach is defined based on the allometric relationship of declining N concentration with increasing biomass, referred to as the critical N dilution curve [CNDC], which defines the level of N concentration below which relative growth rate is reduced (Gastal et al., 2015). A robust theoretical framework has been developed to explain decline in N concentration as biomass increases, but the application of this theory is restricted to the vegetative period (Sadras and Lemaire, 2015; Greenwood et al., 1990; Justes et al., 1994). Dilution of N in vegetative tissue occurs in relationship to an increasing proportion structural biomass, with low N concentration, relative to metabolic (i.e. photosynthetic) biomass, with high N concentration (Lemaire and Gastal, 1997; Gastal et al., 2015).

Multiple previous studies have extended and empirically validated the CNDC relationships beyond its original theoretical justification to describe declining N concentration in relationship to whole plant biomass over the entire crop growth cycle (Plénet and Lemaire, 2000; Duchenne et al., 1997; Greenwood et al., 1986; Herrmann and Taube, 2004). Dilution of N beyond the vegetative period occurs as low N biomass (i.e. starch) accumulates in storage tissues such as grain or tubers, and the rate of decline is determined by the relative N concentration in storage biomass compared to vegetative biomass (Plénet and Lemaire, 2000; Duchenne et al., 1997). Duchenne et al. (1997) observed that as an increasing proportion of biomass accumulates in tubers (i.e. as harvest index increases), the rate of N decline with increasing biomass is also increased. Certain crops, such as potato, exclusively use a CNDC based on whole plant biomass due to the complex relationship between vine growth and tuber production (Duchenne et al., 1997; Bélanger et al., 2001; Ben Abdallah et al., 2016). Despite the empirical validity of this approach, the lack of a theoretical explanation makes interpretation of variation in CNDC observed between cultivars and geographies challenging.

However, recent work by Giletto et al. (2020) identified the theoretical relationships underpinning the observed empirical relationships in N dilution for potato. The CNDC on the basis of whole plant biomass reflects dilution in both the tuber and vine biomass, individually, and the increasing proportion of biomass allocated to low concentrations of N in biomass (i.e., tubers) as whole plant biomass increases. Giletto et al. (2020) also identified that varieties and locations with a greater proportion of biomass allocated to tubers have a greater value for parameter *b* of the CNDC. Parameter *b* of the CNDC represents the relative rate of decline in critical N concentration as biomass increases.

Based on this framework developed by Giletto et al. (2020), it is reasonable to conclude that variation in CNDC across environments [E] (e.g., climate, geography, etc.) and genotypes [G] (e.g., variety) would be expected due to known variation in total biomass and harvest index (i.e., relative partitioning of biomass to tubers) across these GxE gradients. Understanding the effects of GxE interactions on crop N requirements and status is critical to improving agronomic outcomes and nitrogen use efficiency within cropping systems (Lemaire and Ciampitti, 2020).

Previous development of CNDCs for potato has been conducted using a non-uniform set of statistical methods and with limited quantification of uncertainty in either the range of plausible critical N concentration values or the fitted parameter values themselves. This makes it difficult to ascertain whether observed differences in CNDCs are resulting from underlying GxE effects or confounded by the limitations of the statistical approach.

The conventional approach to fit a CNDC, consists of a two-step process: first, the critical N points are selected using statistical criterial; second, a negative exponential curve is fit to the subset of critical points using non-linear regression. There are two commonly used statistical approaches to identify critical points: (1) linear-plateau curve fit and (2) ANOVA and protected multiple comparison.

Using a linear-plateau curve to derive critical points was originally suggested by Justes et al. (1994). This approach is rigorous and requires sufficient empirical data such that a linear-plateau curve can be identified (i.e., at least two N limiting and at least two non-N limiting data points) for each observation date. Therefore, this approach can be difficult or impossible to implement due to potential limitations of the experimental data used such as insufficient levels of N treatments (i.e., less than 5 treatment levels) or interactions with environmental conditions (i.e., all observations are either N limiting or non-N limiting).

In contrast, many studies use methods similar to Ben Abdallah et al. (2017) where critical points are determined using a simplified statistical method. In this approach, ANOVA is first used to identify experimental dates where variation in biomass is statistically significant. Subsequently, a protected multiple comparisons analysis is used to identify which experimental treatments had the highest level of biomass – the treatment level with the significantly greatest level of biomass is then defined as the critical point. While this statistical method is more flexible to implement, it cannot resolve deficiencies in the underlying empirical data (i.e., insufficient level of N treatments, interactions with environmental conditions) that the linear-plateau method was designed to discriminate against. Therefore, the critical points selected using the simplified method may be biased when implemented using biased empirical data (e.g., without sufficient quantity of both N limiting and non-N limiting observations).

New statistical methods developed first by Makowski et al. (2020) provide a framework which allows for standardization in statistical approach, quantification of uncertainty, and a means to evaluation differences in CNDCs for various G x E interactions. In short, this novel framework implements a hierarchical Bayesian model which simultaneously identifies critical N points using the linear-plateau method (e.g., Justes et al., 1994) while fitting the negative exponential curve which defines critical N concentration. The advantage of this method is that it fits the CNDC from the whole set of experimental data and removes the arbitrary intermediate step of separately identifying critical N points. While this approach is newly developed, it has already been used by Ciampiti et al. (2021) and Yao et al. (2021) to evaluate differences in CNDCs across G x E interactions for maize and wheat cropping systems, respectively. Through a single-step process, the Bayesian hierarchical method both eliminates the need to separately identify critical points and implements the theoretically preferred method (e.g., linear plateau curve) to select critical points.

Building upon the previous work, the objectives of this paper are to 1) develop CNDCs using the hierarchical Bayesian framework for potato varieties in Minnesota (from both previously published and unpublished experimental data) and for potato varieties in Argentina, Canada, and Belgium (from previously published experimental data), 2) compare CNDCs across G x E interactions based on the uncertainty in critical N concentration and curve parameters identified with the hierarchical Bayesian framework, 3) identify the optimal methods to determine uncertainty in critical N concentration for use in propagation to secondary computations (e.g., NNI), and 4) compare CNDCs developed with the hierarchical Bayesian framework methods to previously published CNDCs for the same data with different statistical methods.

2. Materials and Methods

2.1. Experimental Data

This study combines experimental data from both newly reported and previously published sources (Giletto et al., 2020; Ben Abdallah et al., 2016). The data used for analysis in this study is summarized in Table 1 and the relevant methods related to the experimental trials is reported below. All individual experimental observations used in this study are presented in Appendix Table 1.

**Table 1.** Summary of experimental data used in this study

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Study** | **Location** | **Variety** | **Site-Years** | **Dates** | **Samples** |
| Present Study | Minnesota | Clearwater | 2 | 10 | 30 |
| Dakota Russet | 2 | 14 | 70 |
| Easton | 2 | 14 | 70 |
| Russet Burbank | 9 | 52 | 329 |
| Umatilla Russet | 2 | 10 | 30 |
| Giletto et al. (2020) | Argentina | Bannock Russet | 3 | 13 | 52 |
| Gem Russet | 4 | 18 | 72 |
| Innovator | 4 | 18 | 72 |
| Markies Russet | 2 | 9 | 36 |
| Umatilla Russet | 3 | 14 | 56 |
| Canada | Russet Burbank | 4 | 30 | 120 |
| Shepody | 4 | 30 | 120 |
| Ben Abdallah (2016) | Belgium | Bintje | 17 | 49 | 238 |
| Charlotte | 7 | 24 | 114 |

2.1.1. Newly Reported Data – Minnesota

Six individual plot-scale field experiments were conducted over a total of eight years (1991–1992, 2014–2016, 2018-2020) on irrigated plots at the Sand Plain Research Farm [SPRF] in Becker, MN (45º 23’ N, 93º 53’ W). Mean temperature at this station is 7.1 ºC and mean annual precipitation is 809 mm (Arguez et al., 2010). The soil at this station was characterized as a Hubbard loamy sand (Sandy, mixed, frigid Entic Hapludolls) and excessively well drained with low available water holding capacity (Hansen and Giencke, 1988; USDA NRCS, 2013). Apart from experimental nitrogen and variety treatments, all management and cultural practices were managed by the staff at the SPRF in accordance with common practices for the region (Egel, 2017), nutrients were applied based on soil samples and University recommendations (Franzen et al., 2018; Rosen, 2018), and supplemental irrigation was applied based on the University recommended checkbook method (Steele et al., 2010; Wright, 2002). Additional details on experimental procedures for these studies have been previously reported (Table 2).

**Table 2.** Summary of newly reported experimental small-plot trials in Minnesota, USA

|  |  |  |
| --- | --- | --- |
| **Experiment** | **Year** | **Reference** |
| MN-1 | 1991-1992 | Errebhi et al. (1998); Rosen et al. (1992); Rosen et al. (1993) |
| MN-2 | 2014-2015 | Sun et al. (2019); Sun (2017) |
| MN-3 | 2016 | Crants et al. (2017) |
| MN-4 | 2018-2019 | Gupta and Rosen (2019); Gupta and Rosen (2020) |
| MN-5 | 2019 | Bohman et al. (2020) |
| MN-6 | 2020 | Crants et al. (2021) |

A randomized complete block design with three or four replicates was used in each field experiment. All studies evaluated at least 3 nitrogen rates (0 – 400 kg N ha-1) for Russet Burbank potato [Solanum tuberosum (L.)], with some studies evaluating additional potato varieties (Table 2). Those studies that evaluated multiple varieties had either a factorial design, or split-plot design with variety treatment as the whole-plot and nitrogen treatment as the split-plot. Plots in these studies were between 5.4 – 6.4 m wide (6 or 7 x 0.9 m rows) and 6.1 – 9.1 m long. Planting density ranged between 36,000 – 48,000 plants ha-1, depending on year and variety. Experiments were planted each year in late-April to early-May and were mechanically harvested in mid-September with vines terminated one to two weeks prior to harvest. A summary of nitrogen management practices and varieties evaluated for each of these studies is summarized below (Table 3).

**Table 3.** Summary of N treatments and varieties evaluated in the newly reported experimental small-plot trials in Minnesota, USA

|  |  |  |  |
| --- | --- | --- | --- |
| **Experiment** | **N treatments**1 | **N rates** | **Varieties** |
| MN-1 | 10 | 0, 135, 180, 225, 270 | Russet Burbank |
| MN-2 | 5 | 135, 200, 270, 335, 400 | Russet Burbank, Dakota Russet, Easton |
| MN-3 | 4 | 45, 180, 245, 335 | Russet Burbank |
| MN-4 | 3 | 135, 270, 400 | Russet Burbank, Clearwater, Umatilla Russet |
| MN-5 | 8 | 45, 155, 245, 290, 335 | Russet Burbank |
| MN-6 | 8 | 55, 155, 245, 270, 290, 335 | Russet Burbank |

1 Including N source, timing, and placement combinations occurring at an equivalent N rate

Samples of vine biomass were harvested immediately prior to mechanical termination for determination of fresh weight vine yield. Harvested tubers were mechanically sorted into weight classes and graded (USDA, 1997), and fresh weight tuber yield was determined as the sum of all weight classes and tuber grades. Harvested biomass was oven dried at 60ºC to determine dry matter content of vines and tubers. Dry weight tuber and vine biomass was calculated as the product of fresh weight and dry matter content for each tissue respectively. Total N concentration of vines and tubers was determined from subsamples of plant tissues with either combustion analysis (Elementar Vario EL III, Elementar Americas Inc., Mt. Laurel, NJ) using standard methods (Horneck and Miller, 1998), or with the salicylic Kjeldahl method. Total N content of vines and tubers was calculated as the product of N concentration and dry weight biomass for each tissue respectively. Total plant N content [NPlant] (kg N ha-1) was calculated from the sum of tuber and vine N content. Total plant dry weight biomass [W] (Mg dry wt. ha-1) was calculated from the sum of vine and tuber dry weight biomass. Plant N concentration [%NPlant] (g N 100 g-1) was calculated as the ratio of NPlant to W.

Whole-plant samples were also regularly collected during the period of late-May to early-September (Table 4). Two to three plants were harvested from each plot on four to six dates each year with vines, roots, and tubers each measured separately. Dry weight biomass, N concentration, and N content for vines and tubers were determined for these in-season plant tissue samples using the methods described above. Calculations for W, NPlant, and %NPlant were also equivalent to the methods previously described.

**Table 4.** List of in-season whole plant sampling dates and harvest sampling date in the newly reported experimental small-plot trials in Minnesota, USA

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Experiment** | **Year** | **In-Season** | | | | | | **Harvest** |
| **1** | **2** | **3** | **4** | **5** | **6** |
| MN-1 | 1991 | 12 June | 24 June | 2 July | 16 July | 30 July | 13 Aug | 10 Sept. |
| MN-1 | 1992 | 10 June | 25 June | 17 July | 5 Aug. | 26 Aug. |  | 15 Sept. |
| MN-2 | 2014 | 30 June | 15 July | 24 July | 11 Aug. | 26 Aug. | 8 Sept. | 15 Sept. |
| MN-2 | 2015 | 23 June | 7 July | 21 July | 4 Aug. | 17 Aug. | 1 Sept. | 16 Sept. |
| MN-3 | 2016 | 28 June | 13 July | 26 July | 3 Aug. | 10 Aug. |  | 13 Sept. |
| MN-4 | 2018 | 26 June | 10 July | 18 July | 1 Aug. |  |  | 13 Sept. |
| MN-4 | 2019 | 26 June | 11 July | 24 July | 7 Aug |  |  | 16 Sept. |
| MN-5 | 2019 | 25 June | 9 July | 23 July | 6 Aug | 21 Aug |  | 16 Sept. |
| MN-6 | 2020 | 24 June | 7 July | 22 July | 4 Aug |  |  | 16 Sept. |

2.1.2. Previously Published Data – Belgium, Argentina, and Canada

Experimental data reported in two previous studies, Giletto et al. (2020) and Ben Abdallah et al. (2016), was included in the analysis conducted for the present study. The data from Giletto et al. (2020) comprises two separate experimental data sets from Argentina (Giletto and Echeverría, 2015) and Canada (Bélanger et al., 2001, Bélanger et al., 2000).

In the Canadian study, two varieties (Russet Burbank and Shepody) and four N fertilization rates (0, 50, 100, and 250 kg ha-1) were evaluated under non-water limiting conditions with each variety having 4 site-years of experimental data and 10 sampling dates per site year (Table 1). In the Argentina study, five varieties (Bannock Russet, Gem Russet, Innovator, Markies Russet, and Umatilla Russet) and four N fertilization rate (0, 80, 150, 250 kg N ha-1) were each evaluated under non-water limiting conditions for between 2 to 4 site-years with between 4 to 5 sampling dates per site year (Table 1). All data from the Giletto et al. (2020) study used in the present analysis was included in this previous publication.

The data from Ben Abdallah et al. (2016) represents multiple experimental data set from Belgium. In the Belgium studies, three to six N rates (ranging from 0 to 250 kg N ha-1) were evaluated for two varieties (Bintje and Charlotte) for 17 and 7 site-years, respectively, and with 1 to 8 sampling dates per site year (Table 1). Only a portion of the data from the Ben Abdallah et al. (2016) study used in the present analysis was included in this previous publication – while the dry weight biomass data were previously reported, the nitrogen concentration data from the Ben Abdallah et al. (2016) experiment is reported for the first time in this manuscript.

2.2. Statistical Methods

Based on the general approach outlined by Makowski et al. (2020), this study implemented a Bayesian hierarchical framework to infer CNDC parameters for each location and variety within location, assess the uncertainty in model parameters and critical N concentration, and compare fitted CNDCs across the effects of location and variety.

In summary, this statistical approach uses the entire set of experimental data (Figure 1a) and does not require any preliminary or intermediary statistical analysis. At the level of each experimental sampling date, a linear-plateau curve is fit for biomass as a function of nitrogen concentration (Figure 1b) and the join point of the linear-plateau curve is used to define the critical N concentration. Simultaneously, a negative exponential curve (i.e., CNDC) is fit across all experimental sampling dates for a given level of the hierarchical model (i.e., location, variety within location) where the critical N point of each linear-plateau curves lies exactly upon the negative exponential curve (Figure 1b). In this manner, the linear-plateau curve fitted for any given date is influenced by the data from all other experimental sampling dates through the fitting of the negative exponential curve. In comparison, the conventional statistical approach fits a negative exponential curve to the subset of critical points (Figure 1c) which are identified via an intermediate statistical analysis (i.e., ANOVA and protected multiple comparisons).

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**Figure 1.** Hypothetical example of statistical methods used showing **(a)** raw experimental data, **(b)** linear-plateau curves (solid colored lines) fitted for each experimental sampling date (points with each date distinguished by color) and the critical N dilution curve (solid black line) fitted using the hierarchical Bayesian method based on Makowski et al. (2020), and **(c)** critical points (opaque) and non-critical points (transparent) selected using conventional statistical analysis (i.e., ANOVA and protected multiple comparison) with critical N dilution curve (dotted line) fitted using conventional methods (i.e., non-linear regression using only the critical points).

The Bayesian hierarchical framework outlined by Makowski et al. (2020) was extended to explicitly include Environmental (e.g., location) and Genotype (e.g., variety) interactions within the fitted model. This was implemented through the nesting of experimental data according to location and variety within location (Figure 2). The linear-plateau curve fitted for each experimental sampling date can be pooled at various nested levels of location or variety within location.

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**Figure 2**. Flowchart showing nested structure used in the present analysis to fit critical N dilution curves using the Bayesian hierarchical method based on Makowski et al. (2020). Linear-plateau curves and critical points are identified at the level of each experimental sampling date and pooled at various levels of location and variety within location to determine the critical N dilution curve (CNDC) for that level. The structure of the model fits all individual levels for location and variety within location, as well as the global level of all experimental data, simultaneously which allows for direct comparison across levels.

Using *R* (R Core Team, 2021), the *brms* package (Bürkner 2017; Bürkner, 2018) was used to implement the statistical method outlined by Makowski et al. (2020). The *brms* package, an interface to *Stan* (Carpenter et al., 2017), was chosen due to the ability to include group-level (i.e., random effects) which allows for the fit of a single model for all of the experimental data and improves model performance through the inclusion of partial pooling (i.e., data from all other levels of an effect influence the inference for a particular level) (McElreath, 2020). The *brms* package includes a user-friendly modeling language, robust documentation, and a diverse set of tools to analyze and assess models.

A non-linear *brms* model was defined by combining the two separate expressions used by Makowski et al. (2020) to parameterize the Bayesian hierarchical model as implemented with *rjags* (Plummer, 2019) and *JAGS* statistical software (Plummer, 2013).

The first expression from Makowski et al. (2020) represents the linear-plateau component:

|  |  |
| --- | --- |
| *W* = *min*(*Wmaxi* + *Si* \* (*%NPlant* – *%Nc*), *Wmaxi*) | (1) |

where *%Nc* is the critical N concentration, *Si* and *Wmaxi* are the slope of the linear-plateau curve and the maximum value of biomass (i.e., plateau) for a given date [*i*], respectively, *min* represents the minima function (i.e., the plateau component), and *W* and *%NPlant* have the same meaning as previously defined in this present study. This linear-plateau curve is defined with nitrogen concentration as the independent variable and biomass as the dependent variable and is written in point-slope form where the reference point used is the critical point.

The second expression from Makowski et al. (2020) represents the CNDC component:

|  |  |
| --- | --- |
| *%Nc* = *a* (*Wmaxi*) –*b* | (2) |

where *a* and *b* are the parameters that define the negative exponential curve and *%Nc* and *Wmax,i*have the same meanings as defined above.

Using algebraic substitution (for *%Nc*), these two expressions were combined to produce following non-linear *brms* model formula:

|  |  |
| --- | --- |
| *W* ~ *min*(*Wmaxi* + *Si* \* (*%NPlant* – (*a* \* (*Wmaxi*) –*b*)), *Wmaxi*) | (3) |

Two group-level (i.e., random) effects were specified for this *brms* model to parameterize the nested structure (Figure 2). First, the parameters *S* and *Wmax* included group-level effects to fit a linear-plateau curve to each experimental sampling date:

|  |  |
| --- | --- |
| *Wmax* + *S* ~ 1 + (1|*index*) | (4) |

where *index* represents the unique level of each experimental sampling date nested within the variety x location. Second, the parameters *a* and *b* included group-level effects to fit the CNDC:

|  |  |
| --- | --- |
| *a* + *b* ~ 1 + (1|*location*) + (1|*location:variety*) | (5) |

where *location* and *location:variety* represents the unique level for location and variety within location, respectively.

The *brms* model was fitted using 4 chains and 10000 iterations with 3000 warmups per chain. The priors for this model were chosen based on expert knowledge (i.e., previously reported values), empirical observations (i.e., summary values from the data set), and the joint prior predictive distribution (i.e., if a set of relatively uninformative priors led to biologically or physically impossible predictions, the prior ranges were narrowed) (Schad et al., 2021). This is particularly important for hyperparameters dealing with the standard deviation between groups in a hierarchical model. A summary of the prior values used in this model is given below (Table 5).

**Table 5.** Priors used in fitting the *brms* model.

|  |  |  |  |
| --- | --- | --- | --- |
| **Parameter** | **Distribution** | **Bounds** | |
| **Lower** | **Upper** |
| *a* | Normal (5.3, 0.1) | 0 | ∞ |
| *σ(alocation)* | Normal (0.10, 0.02) | –∞ | ∞ |
| *σ(alocation:variety)* | Normal (0.05, 0.01) | –∞ | ∞ |
| *b* | Normal (0.40, 0.01) | 0 | 1 |
| *σ(blocation)* | Normal (0.05, 0.02) | –∞ | ∞ |
| *σ(blocation:variety)* | Normal (0.02, 0.01) | –∞ | ∞ |
| *Wmax* | Normal (8.0, 0.1) | 1 | ∞ |
| *σ(Wmaxindex)* | Normal (7.0, 1.0) | –∞ | ∞ |
| *S* | Normal (6.0, 0.1) | 0 | ∞ |
| *σ(Sindex)* | Normal (1.0, 0.1) | –∞ | ∞ |
| *σ* | Student\_T (3.0, 1.0, 0.1) | –∞ | ∞ |

The entire workflow used to generate this analysis is reproducible and available via as a GitHub repository (<https://github.com/bohm0072/cndc_bayesian_eval>). The *renv* package (Ushey, 2021) was used to document the computing environment utilized while conducting this analysis to ensure code portability and reproducibility.

2.3. Evaluating Uncertainity

2.3.1. Critical N Dilution Curve Parameter Uncertainty

After the statisticalmodel was successfully fit to the data (n=28,000 draws), values for parameters *a* and *b* of the CNDC were reported at the 0.05, 0.50 (i.e., median) and 0.95 quantiles for the levels of location and variety within location to determine the 90% credible region. The correlation between values for parameters *a* and *b* was determined for each level of variety within location using the fitted parameter values for individual draws.

2.3.2. Critical N Concentration Uncertainty

The critical N concentration for a set of discrete values of W between 1 Mg ha-1 and the maximum observed value of W in the experimental data set was calculated for each individual draw based on the fitted values of parameters *a* and *b* for that draw. From the distribution of critical N concentration values, the 0.05, 0.50 (i.e., median) and 0.95 quantile values were identified for each level of variety within location to determine the 90% credible region.

To approximate the upper and lower boundaries of the 90% credible region for critical N concentration (i.e., the 0.05 and 0.95 quantile values, respectively), a negative exponential curve of the same form as the CNDC (i.e., *y* = *a* \* (*x*)–*b*) was fit using *nls* (R Core Team, 2021) to the set of data previously identified as defining the boundaries of the 90% credible interval (i.e., 0.05 and 0.95 quantile values).

Additionally, an estimate of the 90% credible region was calculated by using the boundary values of the 90% credible interval of parameters *a* and *b*. The estimate for the upper boundary of the credible interval was determined from the 0.95 quantile value for parameter *a* and 0.05 quantile value for parameter *b*; the estimate for the lower boundary of the credible interval was determined from the 0.05 quantile value for parameter *a* and 0.95 quantile value for parameter *b*.

These approximation and estimation methods were then compared to the true credible region for each level of variety within location.

2.3.3. Comparing Critical N Dilution Curves across Genotype x Environment Effects

Similar to the above methods, the critical N concentration for each draw was calculated across a set of discrete values of W over the range of 1 Mg ha-1 and the maximum observed value of W in the experimental data set. At the level of variety within location, the difference between the critical N concentration for a given comparison and reference CNDC was calculated at each value of W. From this computed set of difference in critical N concentration, the 0.05, 0.50 (i.e., median) and 0.95 quantile values were identified for each level of variety within location to determine the 90% credible region. For a given range of W values, the comparison curve considered to be not significantly different from the reference curve if the 0.05 and 0.95 quantile value were respectively less than and greater than zero (i.e., the 90% credible interval contains zero). In the case where the 0.05 quantile value was greater than zero, the comparison curve was said to have a significantly greater critical N concentration than the reference curve. In the case where the 0.95 quantile value was less than zero, the comparison curve was said to have a significantly lesser critical N concentration than the reference curve.

To evaluate the differences between curves fit in the present study, the CNDC for a given level of variety within location was compared to all other levels of variety within location using this method. This approach allows for the direct evaluation of differences in critical N concentration across G x E effects.

2.3.4. Comparing Critical N Dilution Curves across Statistical Methods

An analogous method was also used to compare the CNDCs fitted in the present study to the CNDCs published in previous studies (i.e., Ben Abdallah et al., 2016; Giletto et al., 2020). Specifically, the previously published curve was evaluated to see if it fell within the 90% credible interval for the corresponding curve fitted in the present study. Using the previously identified credible interval for critical N concentration, it is possible to identify the range for which two CNDCs are significantly different. If the previously identified critical N concentration value falls outside of the credible interval for critical N concentration identified in this study, then the two curves are determined to be significantly different over the range for which the previous value falls outside of the credible interval. This approach allowed for direct evaluation of differences in critical N concentration for CNDCs developed from the same set of data across various statistical methods.

**3. Results**

3.1. Fitted Parameter Values and Uncertainity

3.1.1. Overall Model Fit

Critical N dilution curves were fit for each level of variety within location. The experimental data, median linear-plateau curve for each experimental sampling date, and median value of critical N concentration are presented below (Figure 3). The individual linear-plateau curves fitted to each experimental sampling date for each variety within location is presented in Appendix Figure 1.

3.1.2. Critical N Dilution Curve Parameter Fit and Uncertainty

The distribution of fitted values for CNDC parameters *a* and *b* are presented below (Figure 4) showing the median value and 90% credible interval (i.e., 0.05 and 0.95 quantile values).

For parameter *a*, there was no significant difference for the effect of either location or variety within location at 90% credible interval threshold (Figure 4a). Although Argentina has a numerically greater value of parameter *a* (4.95) than the other three locations (4.74-4.77), these differences are not significant. Additionally, the variation in parameter *a* at the variety within location level is negligible.

For parameter *b*, there were significant differences at both the levels of location and variety nested within location at 90% credible interval threshold (Figure 4b). For location, Argentina had the lowest value for parameter *b* (0.175), while Canada had a greater value for parameter *b* (0.448)than Argentina but lower than either Belgium (0.561) or Minnesota (0.582). The difference between parameter *b* for Belgium and Minnesota was not significant.

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**Figure 3.** Median fitted critical N dilution curve for each location x variety interaction shown as solid black line. Biomass and nitrogen concentration data used for fitting the statistical model are displayed as points with the median fitted linear-plateau curve for each sampling date shown as grey line. The number of samples [n] and the number of sampling dates [i] used to fit the linear-plateau curves are displayed for each location x variety interaction.

For variety within location, parameter *b* significantly varied for varieties in Argentina and Canada while there were no significant differences in parameter *b* within either Belgium or Minnesota. For Argentina, Innovator had the greatest value for parameter *b* (0.212), followed by Gem Russet, Umatilla Russet, Markies Russet, and Bannock Russet (0.178, 0.165, 0.155, and 0.140, respectively). The difference between Innovator and Umatilla Russet, Markies Russet, and Bannock Russet was significant, while all other differences between varieties was not significant. For Canada, Russet Burbank had a significantly greater value for parameter *b* (0.489) than Shepody (0.412).

3.1.3. Correlations between Critical N Dilution Curve Parameters

There was a positive correlation found between parameter *a* and *b* for all levels of variety within location (Figure 5) and the Pearson correlation coefficient ranged from 0.40 to 0.80. The positive correlation of parameter *a* and *b* indicates that quantifying uncertainty and differences in these parameter values independently is not sufficient to describe the combined uncertainty in critical N concentration described by the correlated parameters. Stated alternatively, non-significant differences in parameters *a* and *b* does not ensure that differences in critical N concentrations are non-meaningful or not significant.

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**Figure 4.** Posterior distribution of variety x location interaction effect and of location effect for (**a**) parameter *a*; and (**b**) parameter *b*. Points represent median value and thin line represents 0.05 and 0.95 quantile range. Values displayed adjacent to distributions are for the median value with the values for the 0.05 and 0.95 quantile range displayed within the parentheses.

3.2. Critical N Concentration Uncertainity

The credible region for critical N concentration varies across levels of variety within location and across levels of biomass within a given level of variety within location (Figure 6). The symmetry of the credible region distribution varies across levels of variety within location with some levels, such as Argentina x Gem Russet, having a skewed distribution, while other levels, such as Canada x Shepody, having a symmetrical distribution. There are also differences in the range of the credible region where some levels of variety within location, such as Argentina x Umatilla Russet, have greater uncertainty in critical N concentration than other levels, such as Minnesota x Russet Burbank. The uncertainty in critical N concentration also varies across the level of biomass for a given CNDC. For example, as level of biomass increases, Argentina x Umatilla Russet has increasing credible region range, Minnesota x Russet Burbank has decreasing credible region range, and Argentina x Bannock Russet has nearly constant credible region range.

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**Figure 5.** Distribution of posterior values for parameters *a* and *b* for each location x variety interaction shown as a scatterplot with marginal density distribution given for each parameter. Pearson correlation coefficient [R] is displayed for the relationship between parameters *a* and *b* for each location x variety interaction. Data are shown at the level of individual draws (n=28,000)

Approximations of the upper and lower boundaries of the 90% critical region by fitting a negative exponential curve to the 0.05 and 0.95 quantile data were successfully made (Table 6) and this method appears to be reasonable based on graphical evaluation (Figure 6). While critical regions with boundaries that are non-monotonic (e.g., Argentina x Innovator) have portions of the curve fit approximation that are poorer performing, the critical regions with monotonic boundaries (e.g., Minnesota x Dakota Russet) seem to be satisfactory across the entire range of the curve. Therefore, in the absence of the critical region defined directly from the fitted model, this approximation method is an appropriate first-order representation of the credible region.

However, the estimate based directly on uncertainty in CNDC parameters *a* and *b* (Table 6) contains the entire credible region and for all variety within location levels (Figure 6). Therefore, this estimate approach is more conservative than the curve fit approximation approach and should be used if a more restrictive definition of critical N concentration uncertainty is required and the credible region defined from the original model fit is unavailable.

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**Figure 6.** Comparison of the difference in critical N concentration values [%N Difference] between the median critical N concentration, represented by the solid black line at constant value of zero and various methods to represent uncertainty in critical N concentration. The grey shaded region represents the 90% credible region (lower bound, 5% quantile; upper bound, 95% quantile) for the critical nitrogen concentration values fitted by the Bayesian hierarchical model. The dotted lines represent an estimation of the upper and lower bound of the 90% credible region using non-linear regression to fit a negative exponential curve of the same equation form as the critical nitrogen dilution curve. The dashed lines represents a conservative approximation of the upper and lower bounds of 90% credible region based on the posterior distribution of parameters *a* and *b* where the estimated lower bound is defined using the 95% quantile value of parameter *a* with the 5% quantile value of parameter *b* and the estimated upper bound is defined using the 5% quantile value of parameter *a* with the 95% quantile value of parameter *b*.

**Table 6.** Paired critical nitrogen dilution curve parameter values for each variety x location interaction defining a conservative approximation for the lower (Conserv. Low) and upper (Conserv. High), the estimate values for the credible region lower (Cred. Est. Low) and upper (Cred Est. Up), and the median value from the posterior distribution for critical nitrogen concentration from the fitted Bayesian hierarchical model.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Location** | **Variety** |  | Conserv. Low | Cred. Est. Low | **Median** | Cred. Est. Up. | Conserv. Up. |
|  |  |  |  | CNDClo | **CNDC** | CNDCup |  |
| Argentina | Bannock Russet | *a* | 4.72 | 4.82 | 4.96 | 5.10 | 5.20 |
| *b* | 0.163 | 0.146 | 0.140 | 0.135 | 0.118 |
| Gem Russet | *a* | 4.72 | 4.80 | 4.96 | 5.07 | 5.20 |
| *b* | 0.207 | 0.190 | 0.178 | 0.152 | 0.139 |
| Innovator | *a* | 4.70 | 4.83 | 4.94 | 5.06 | 5.19 |
| *b* | 0.253 | 0.241 | 0.212 | 0.193 | 0.177 |
| Markies Russet | *a* | 4.72 | 4.82 | 4.96 | 5.08 | 5.20 |
| *b* | 0.183 | 0.167 | 0.155 | 0.135 | 0.121 |
| Umatilla Russet | *a* | 4.71 | 4.85 | 4.95 | 5.06 | 5.19 |
| *b* | 0.206 | 0.195 | 0.165 | 0.143 | 0.131 |
| Belgium | Bintje | *a* | 4.42 | 4.52 | 4.72 | 4.90 | 4.98 |
| *b* | 0.640 | 0.606 | 0.579 | 0.567 | 0.531 |
| Charlotte | *a* | 4.44 | 4.56 | 4.74 | 4.89 | 5.00 |
| *b* | 0.637 | 0.607 | 0.559 | 0.531 | 0.499 |
| Canada | Russet Burbank | *a* | 4.46 | 4.53 | 4.74 | 4.93 | 5.01 |
| *b* | 0.531 | 0.498 | 0.489 | 0.480 | 0.447 |
| Shepody | *a* | 4.48 | 4.55 | 4.77 | 4.95 | 5.03 |
| *b* | 0.448 | 0.416 | 0.412 | 0.406 | 0.376 |
| Minnesota | Clearwater | *a* | 4.47 | 4.56 | 4.75 | 4.93 | 5.01 |
| *b* | 0.648 | 0.622 | 0.585 | 0.558 | 0.531 |
| Dakota Russet | *a* | 4.46 | 4.54 | 4.75 | 4.94 | 5.01 |
| *b* | 0.647 | 0.619 | 0.599 | 0.588 | 0.559 |
| Easton | *a* | 4.46 | 4.54 | 4.75 | 4.91 | 5.01 |
| *b* | 0.636 | 0.608 | 0.592 | 0.567 | 0.543 |
| Russet Burbank | *a* | 4.46 | 4.51 | 4.74 | 4.95 | 5.00 |
| *b* | 0.595 | 0.562 | 0.566 | 0.567 | 0.534 |
| Umatilla Russet | *a* | 4.47 | 4.56 | 4.75 | 4.92 | 5.01 |
| *b* | 0.655 | 0.631 | 0.588 | 0.546 | 0.523 |

3.3. Evaluating Differences between Critical N Concentration

3.3.1. Differences Related to Genotype x Environment Effects

While an evaluation of the differences between all levels of variety within location was conducted (Appendix Figure 2), a subset of the results comparing Minnesota x Russet Burbank to all other levels is presented in detail here (Figure 7).

For Minnesota x Russet Burbank, there were no significant differences in critical N concentration for any level of W evaluated with any of the other varieties in Minnesota (i.e., Clearwater, Dakota Russet, Easton, and Umatilla Russet) or with the Belgium varieties (i.e., Bintje, and Charlotte). The critical N concentration for both of the Canadian varieties (i.e., Russet Burbank, and Shepody) were significantly greater than that for Minnesota x Russet Burbank when biomass values were greater than 2 Mg ha-1. The critical N concentration for Canada x Russet Burbank and Canada x Shepody were up to 0.3 and 0.6 g N 100g-1 greater than that for Minnesota x Russet Burbank, respectively. The critical N concentration for the Argentina varieties (i.e., Bannock Russet, Gem Russet, Innovator, Markies Russet, and Umatilla Russet) were significantly greater than for Minnesota x Russet Burbank, except for at a biomass value of 1.0 Mg ha-1, with a difference in value depending on variety of up to 2.4 g N 100 g-1.

There are two notable findings to callout here. First, there were no significant differences between Minnesota x Russet Burbank and any other varieties evaluated in Minnesota (i.e., no significant differences between Genotype when Environment was controlled for). This finding did not hold across all Locations, however; while there was no significant difference between the Varieties evaluated in Belgium, there were significant differences between the Varieties evaluated in Canada and some of the Varieties evaluated in Argentina (Appendix Figure 2).

Second, the Minnesota x Russet Burbank and Canada x Russet Burbank curves were significantly different (i.e., a significant difference between Environment when Genotype was controlled for). The only other comparison controlling for Genotype across Environment, Minnesota x Umatilla Russet and Argentina x Umatilla Russet, conducted in this study was also significantly different (Appendix Figure 2).

Taken together, these findings provide evidence that the effect of Environment (i.e., Location), even when controlling for Genotype (i.e., Variety), can result in significantly different critical N concentration; additionally, this provides evidence that differences in Genotype within a given Environment do not necessarily result in significant different critical N concentration. Therefore, these findings suggest that Environment is relatively more important than Genotype in determining critical N concentration.

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**Figure 7.** Comparison of the difference in critical N concentration values [%N Difference] between Russet Burbank x Minnesota and all other levels of Location x Variety evaluated in the present study. The grey shaded region represents the 90% credible region (lower bound, 5% quantile; upper bound, 95% quantile) and the colored points represent the median value for the difference in critical N concentration values between the reference and comparison critical N dilution curves computed from the difference of the individual draws from the posterior distribution of the fitted Bayesian hierarchical model. Red or blue points for a given Biomass value respectively indicate that the difference in critical N concentration between the reference and comparison curves at that point is significant (i.e., does not contains the value zero) or is not significant (i.e., contains the value zero). The solid black line represents a constant value of zero. The range of biomass values for which the difference in critical N concentration between the comparison and reference curve is not significantly is given in brackets.

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**Figure 8.** Comparison of the difference in critical N concentration values [%N Difference] from the critical N dilution curves reported in previous studies (i.e., Argentina – Giletto and Echeverría (2015); Belgium – Ben Abdallah et al. (2016; Canada – Bélanger et al. (2001)) and from the critical N dilution curve developed in the present study for each Location x Variety pair. The grey shaded region represents the 90% credible region (lower bound, 5% quantile; upper bound, 95% quantile) and the black solid line represents the median value for the posterior distribution of the Bayesian hierarchical model fitted in the present study. Red or blue points for a given Biomass value respectively indicate that the difference in critical N concentration between the previous critical N dilution curve and median value at that point is significant (i.e., falls outside the credible region) or is not significant (i.e., falls within the credible region). The range of biomass values for which the difference in critical N concentration between the critical N dilution curves from the present and previous studies in not significantly is given in brackets.

3.3.2. Differences Related to Statistical Methods

Comparing the curves fit in the present study with the Bayesian hierarchical method to the curves fit in the previous studies using conventional statistical methods, there were significant differences between statistical curve fit methods for all Variety within Location levels (Figure 8). None of the previous CNDCs fall entirely within credible interval for the respective CNDC developed in the present study.

The critical N concentration from the previously developed CNDCs for the Argentina varieties (Giletto and Echeverría, 2015) was significantly less than that from the present CNDCs across all varieties for biomass levels of greater 5 Mg ha-1 (Figure 8). The magnitude of this difference was relatively large with the critical N concentration from the previous method ranging up to 0.6 to 1.1 g N 100 g-1 less than median critical N concentration form the present method, depending on variety. Based on the CNDCs fitted in the present study for the Argentina varieties (Figure 3), more than 60% of the observed data fall below the CNDC (i.e., represent N limiting conditions) with over 40% of sampling dates having exclusively N limiting conditions observed (Appendix Figure 1).Therefore, it appears that the statistical methods used by Giletto and Echeverría (2015) selected biased critical points due to a overrepresentation of N limiting observations in the experimental dataset leading to a systematic underestimation of the critical N concentration.

The critical N concentration from the previously developed CNDCs for Belgium (Ben Abdulla et al., 2016) were significantly greater than that from the CNDCs developed in the present study (Figure 8). While the magnitude of this difference in critical N concentration was 0.7 g N 100 g-1, there was no level of biomass for which the critical N concentration from the previous and present methods weere not significantly different. Based on the CNDCs fitted in the present study for the Belgium varieties (Figure 3), more than 80% of the observed data fall above the CNDC (i.e., represent non-N limiting conditions) with almost 30% of sampling dates having exclusively non-N limiting conditions observed (Appendix Figure 1). Therefore, it appears that the statistical methods used by Ben Abdallah et al. (2017) selected biased critical points due to overrepresentation of non-N limiting observations in the experimental dataset leading to a systematic overestimation of the critical N concentration.

The critical N concentration from the previously developed CNDCs for Canada (Bélanger et al., 2001) was significantly greater for both Canada x Russet Burbank and Canada x Shepody than the present CNDCs for biomass levels of less than 3 Mg ha-1 and greater than 6 Mg ha-1, respectively (Figure 8). Relative to the other locations, however, the CNDCs for Canada were the most similar between statistical methods, with magnitude of difference in critical N concentration of 0.2 g N 100 g-1. Based on the CNDCs fitted in the present study for the Canada varieties (Figure 3), over 60% of observed data represented non-N limiting conditions but less than 10% of sampling dates had exclusively non-N limiting conditions observed (Appendix Figure 1). Therefore, it appears that the statistical method used by Bélanger et al. (2001) did not select biased critical points likely due to the minimal bias observed in this experimental dataset.

4. Discussion

4.1. Communicating Uncertainity in Critical N Concentration

The findings of this present study as well as those of other previous studies which have implemented Bayesian statistical methods to derive critical N dilution curves (Ciampiti et al., 2021; Yao et al., 2021) clearly indicate that there is meaningful uncertainty in critical N concentration values. Therefore, the use of critical N concentration in subsequent calculations should include this inherent uncertainty. However, the direct use of the credible region defined from posterior distribution of the fitted Baysian hierarchical model in subsequent calculations is impractical and a method to concisely and accurately communicate the credible region remains necessary.

Our finding that the credible region can be satisfactorily estimated using an equation of the same form as the CNDC (Figure 6) suggest that an additional set of two negative exponential curves representing the upper and lower boundary of the credible region should be reported in future studies; these additional curves representing uncertainty in critical N concentration can be referred to respectively as the lower boundary of the critical N dilution curve [CNDClo] and the upper boundary of the critical N dilution curve [CNDCup]. Together, these three curves are defined by a concise set of 6 parameters (i.e., CNDC – *a*, *b*; CNDCup – *aup*, *bup*; CNDClo – *alo*, *blo*) (Table 6) which can be easily communicated and used in subsequent computations.

4.1. Computing based on Uncertainity in Critical N Concentration

The critical N concentration and associated CNDC parameters are commonly used to derive and calculate other related parameters. For example, the calculation of NNI depends on both the actual plant N concentration [%NPlant] and the critical N concentration [%Nc]:

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| --- | --- |
| NNI = %NPlant / %Nc = %NPlant / (a W–b) | (6) |

However, to properly account for the uncertainty in critical N concentration when computing NNI, the upper [%Nc,up] and lower [%Nc,lo] bounds of the credible region should also be used to determine the upper [NNIup] and lower [NNIlo] bounds of NNI, where %Nc,up and %Nc,lo are calculated using the CNDCup and CNDClo, respectively:

|  |  |
| --- | --- |
| NNIup = %NPlant / %Nc,up = %NPlant / (aup W–bup) | (7) |
| NNIlo = %NPlant / %Nc,lo = %NPlant / (alo W–blo) | (8) |

This has important practical implications for interpreting NNI values. For example, in a case where NNI is less than 1 but NNIup is greater than 1, then it follows that crop N status would not be considered deficient (i.e., NNI is not significantly different from 1); comparingly, in a case where both NNI and NNIlo are greater than 1, then it follows that crop N status would be considered surplus (i.e., NNI is significantly greater than 1). The conclusions of a small-plot trial evaluating various N fertilizer treatments and using NNI to interpret the effects of those treatments on yield and biomass (e.g., Bohman et al., 2021) may draw different conclusions in light of considering uncertainty in calculated NNI values.

Additionally, the parameters of the CNDC (i.e., *a*, *b*) are also used to parameterize other related curves such as the critical N uptake curve [CNUC] or the critical N utilization efficiency curve [CNUtEC] (Bohman et al., 2021). When computing the critical N uptake [Nc] or critical N utilization efficiency [NUtEc] values defined by these curves, respectively, the parameters from the CNDClo (i.e., *alo, blo*) and CNDCup (i.e., *aup, bup*) should be used to calculate the upper and lower bounds of these same values. In general, any calculation depending on either %Nc or any equation that uses the parameters of the CNDC, should also additionally use the CNDClo and CNDCup to account for uncertainty in critical N concentration.

4.2. Implication of G x E effects for Critical N Concentration on N Use Efficiency

Understanding and properly interpreting the impact of G x E effects on N use efficiency [NUE] is a critical goal necessary to improve N fertilizer use (Ciampitti and Lemaire, 2020). The previous findings of Bohman et al. (2021) demonstrated that interpreting N use efficiency [NUE] and its constituent component of N utilization efficiency [NUtE] is directly dependent on the parameters of the CNDC through the critical N utilization efficiency curve [CNUtEC]:

|  |  |
| --- | --- |
| NUtEc = 1000 (10 a W–b)–1 | (9) |

where parameters *a*, *b*, and *W* have the same meaning and units as previously defined in the present study.

Briefly, the CNUtEC defines the critical value of NUtE [NUtEc] for a given level of biomass where crop N status is sufficient (i.e., NNI equal to 1). When NUtE is greater than NUtEc, crop N status is deficient (i.e., NNI less than 1); conversely, when NUtE is less than NUtEc, crop N status is excessive (i.e., NNI greater than 1).

The finding in the present study that the CNDC can vary across G x E effects and the finding from Bohman et al. (2021) of the intrinsic relationship between NUE and the CNDC together lead to the conclusion that CNUtEC must also vary across the same G x E effects as the CNDC. Therefore, the effect of G x E on variation of the CNUtEC is one of the multiple set of factors that control ultimately control NUE. Understanding and accounting for this mechanism of this G x E effect that partially controls NUE is therefore critically important goal.

4.2. Implication of G x E effects of Critical N Concentration

While the present study presents direct evidence of significant differences between CNDCs across G x E effects, other previous studies help describe the potential mechanism for this source of this variation. The findings of Giletto et al. (2020) suggest that variation in CNDCs for potato across G x E effects is primarily due to differences in the relative rate of partitioning of biomass to tubers. For example, G x E effects that result in greater partitioning of biomass from vines (i.e., high N vegetative tissue) to tubers (i.e., low N storage tissues) will have resultingly greater N dilution (i.e., lower critical N concentration) at the same level of total plant biomass.

Following from the above discussion of the CNUtEC and the findings of Giletto et al. (2020), G x E effects that increase the relative proportion of biomass partitioned to tubers will decrease the critical N concentration which will subsequently increases the critical NUtE value. Therefore, efforts to systematically improve NUE in potato should focus on identifying G x E effects that result in a increased proportion of biomass partitioned to tubers.

Based on the larger magnitude of differences in critical N concentration between Locations compared to differences between Varieties within Location observed in this study (Figure 7, Appendix Figure 2), it is reasonable to conclude that increases in NUE for potato resulting from decreasing critical N concentration will be of a greater magnitude from Environmental rather than Genotype effects. However, in order to improve the understanding of this relationship between NUE and critical N concentration, future work should continue to evaluate the relative partitioning of potato biomass to tubers across G x E effects.

4.3. Understanding Differences between Statistical Methods

While the observation of difference in CNDCs derived using the Bayesian hierarchical model compared to the conventional statistical methods used in previous studies (Figure 7) is not necessarily remarkable, the magnitude of these differences as found in the present study is, however. Because of its strong theoretical underpinning, critical N concentration and NNI are typically considered to be “gold standard” measurements of crop N status, feed from the subjectivity of other methods and based on absolute rather than relative or arbitrary thresholds (CITATION). However, the findings of the present study strongly suggest that the “gold standard” ideal of the NNI framework must be qualified by the statistical methods used to derive the CNDC for a particular experimental dataset.

Unfortunately, the direct evaluation of different statistical methods to calculate the CNDC from the same experimental dataset cannot directly answer the question of which statistical method or resulting CNDC is “correct” (i.e., most accurate, least biased). However, we can reasonably conclude from both deduction and from the findings of the present study that a Bayesian hierarchical model utilizing the linear-plateau method and leveraging partial pooling across effect levels will result in an inference that is less subjected to potential bias in the experimental data set compared to the conventional statistical methods.

Therefore, it appears preferable for the future development of CNDCs to utilize the Bayesian hierarchical method to both quantify uncertainty and reduce bias in critical N concentration. Without addressing these limitations (i.e., bias and uncertainty), both directly resulting from the statistical methods used, the NNI framework cannot not fulfill its core objective of providing an absolute reference of crop N status.

Additionally, with the further development adequate tools for this scientific computing task, the implementation of the Bayseian hierarchical framework for deriving the CNDC can be made trivial and may enable the development of CNDCs from existing but unutilized experimental datasets. Therefore, the development of a dedicated software library to implement the Bayesian hierarchical method is a priority for future research efforts.

5. Conclusions

**Appendix Table 1.**

**Appendix Figure 1.**

**Appendix Figure 2.**