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A simulation study on the comparison of Diagnosis and Recommendation Integrated System (DRIS), Modified-DRIS (M-DRIS), and Compositional Nutrient Diagnosis (CND) for pineapple nutrient diagnosis

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Abstract. Foliar diagnostic helps assess plant nutritional status and drives appropriate fertilizer recommendations to enhance quality and productivity of plants. Several foliar diagnostic methods are used but the literature is not sufficiently documented regarding the comparison of these methods using a varied range of comparison criteria. This study compared DRIS (Diagnosis and Recommendation Integrated System), M-DRIS (Modified-DRIS), and CND (Compositional Nutrient Diagnosis) in diagnosing pineapple leaf nutrient levels with varying sample sizes. Empirical data from a subtractive experiment was used to simulate and constitute a new database considering that nutrient contents were normally distributed. For each sample size, data were generated per treatment and replicated 3,000 times. DRIS, M-DRIS, and CND indices were computed from the simulated data for each nutrient. The methods were subsequently evaluated based on four criteria: (i) the Diagnosis Concordance Frequency, which assesses the consistency of diagnoses across different methods for determining nutritional indices; (ii) the sensitivity, or True Positive Rate, which gauges a model's ability to accurately identify a specific nutritional status when it is present; (iii) the precision, or Positive Predictive Value, which indicates the proportion of correctly identified diagnoses for a particular nutritional status relative to the total number of diagnoses made for that status; and (iv) the accuracy, which measures the closeness of the model's results to the true value. As results, we found that N, P, and K nutrient indices differed significantly between DRIS, M-DRIS, and CND models and with sample size. The nutritional diagnosis methods were also discordant, except DRIS versus M-DRIS (mean agreement = 66%). Compared to DRIS, and M-DRIS models, CND appeared to be the most sensitive and accurate model (average accuracy of 27.86%) for nutrient deficiency and excess diagnosis. The models' accuracy varies with the sample size, but it becomes almost unchangeable from a sample size of 330. For all sample sizes, the CND model was more accurate and efficient for N, P, and K nutrient status diagnosis, compared to DRIS and M-DRIS models.

Key words: accuracy, foliar analysis, true positive rate, precision, *Ananas comosus*.

Used abbreviations:

A: Concentration of nutrient A in the high-yielding subpopulation
AIC: Akaike Information Criterion
B: Concentration of nutrient B in the high-yielding subpopulation
CND: Compositional Nutrient Diagnosis
CV: Coefficient of Variation
DCF: Diagnosis Concordance Frequency
DRIS: Diagnosis and Recommendation Integrated System
f: DRIS function
FNA: False Negative Adequate
FND: False Negative Deficiency
FNE: False Negative Excess
FPA: False Positive Adequate
FPD: False Positive Deficiency
FPE: False Positive Excess
PFR: Potential Fertilization Response
G: Geometric mean
IA: Model Index of nutrient A
K: Potassium
LN: CND index for nutrient N
M-DRIS: Modified Diagnosis and Recommendation Integrated System
N: Azote
n: primary limiting by excess
NBIm: Nutrient Balance Index Mean
Nut: Nutrient
nz: negative or zero with lower probability
P: Phosphore
p: primary limiting by deficiency
PERMANOVA: Permutational multivariate analysis of variance
PFR: Potential Fertilization Response
PPV: Positive Predictive Value
PPAV: Positive Predictive Adequate Value
PPDV: Positive Predictive Deficiency Value
PPEV: Positive Predictive Excess Value
pz: positive or zero with lower probability
R: Residual value
RMSE: Root Mean Square Error
SD: Standard deviation
t ha^{-1}: Tonne per hectar
TPA: True Positive Adequate
TPAR: True Positive Adequate Rate
TPD: True Positive Deficiency
TPDR: True Positive Deficiency Rate
TPE: True Positive Excess
TPER: True Positive Excess Rate
TPR: True Positive Rate
VN: CND row-centred log ratio for nutrient N

INTRODUCTION

The diagnosis of the nutritional status of plants is a prerequisite for any rational fertilization. Nutrient balance determines crop yield and quality (Pineda-Álvarez et al., 2021). Foliar diagnosis can be a useful tool for correcting plant nutrient deficiencies and imbalances (Baldock & Schulte, 1996), optimizing crop production (Walworth & Sumner, 1988), and evaluating fertilizer requirements. A thorough diagnostic is essential to create appropriate fertilizer recommendations and enhance quality and productivity without negatively impacting the environment (Pacheco-Sangerman et al., 2022). However, foliar analysis can only help assess plant nutritional status if adequate methodologies for diagnosing from analytical data are available (Walworth & Sumner, 1988). Critical Levels and Sufficiency Ranges methods are commonly used to diagnose nutritional status of plants (Walworth & Sumner, 1988). Sufficiency Ranges methods have been used to investigate the nutrient status of different tomato cultivars grown under industrial greenhouse production (Osvalde et al., 2021) and to access the nutrient status of the American cranberry in Latvia (Karlsons & Osvalde, 2017). These methods involve comparing the nutrient concentration in the sample with an accepted normal value for a specific growth stage (Kania Kuhl & Callejas Rodríguez, 2011), are somewhat erroneous in that 'critical nutrient concentrations' are not independent diagnostics, but can vary in magnitude as the background concentrations of other nutrients increase or decrease in crop tissue (Bailey et al., 1997). Since nutrient uptake and distribution are affected by interactions within the plant, multi-nutrient approaches have been derived. Three common approaches used to identify nutritional imbalances are the DRIS (Beaufils, 1973), the M-DRIS (Hallmark et al., 1987), and the CND (Parent & Dafir, 1992).

DRIS is based on dual ratio functions (f(N/P), f(P/K), etc.) (DRIS, Beaufils, 1973). M-DRIS also considers nutrient contents, not just their dual relationships (Hallmark et al., 1987). CND is based on row-centred log ratios where each nutrient is adjusted to the geometric mean of all nutrients and a filling value (Parent & Dafir, 1992). These methods of nutritional diagnosis present discordant reports.

The effectiveness of the CND method compared to other methods is not often proven in the literature. Politi et al. (2013) discovered that both the CND and DRIS approaches performed comparably while analyzing the nutritional status of mango in Lower-middle San Francisco. When determining the nutritional status of sugarcane in Brazil, the CND diagnosis differed from the DRIS techniques for manganese and nitrogen (Calheiros et al., 2018). DRIS and CND methods were found similar for the evaluation of leaf nutrients in soybean in Brazil (Souza et al., 2023). The CND method was proven to be more sensitive for early detection of Zn stress in Muscat grapes compared to DRIS (Kumar et al., 2003). DRIS and/or CND have been used to diagnose the nutrient status of a range of crops including pineapple, maize, tomatoes, cotton, orange etc. (Parent et al., 1993; Magallanes-Quintanar et al., 2006; Camacho et al., 2012; Serra et al., 2016; López-Montoya et al., 2018; Morais et al., 2019; Khuong et al., 2024). The comparison of the three diagnosis methods (DRIS, M-DRIS and CND), primarily relies on the criterion of diagnosis concordance frequency (Silva et al., 2004). Since the development of the CND method, no study has compared all the existing methods (DRIS, M-DRIS and CND) based on a set of solid criteria such as the diagnosis

concordance frequency (DCF) (Silva et al., 2004), the sensitivity or rate of true positives, the precision or Positive predictive value (Trevethan, 2017) and accuracy (Morais et al., 2019; Powers, 2020; Chicco & Jurman, 2020; Tharwat, 2020).

Indeed, sensitivity or True Positive Rate (TPR) represents the proportion in which a nutritional status is identified for a nutrient when this situation is true. Sensitivity refers to a model's ability to correctly detect nutritional status when true. It refers to the efficiency of the method to correctly diagnose the cases of a true nutritional status. Precision or Positive Predictive Value (PPV) represents the proportion of correctly detected nutritional statuses relative to the total number of diagnosed cases. It reflects the performance of the prediction. The accuracy is the proximity of the model execution output to the true value. It is the ratio between the correctly detected diagnoses to the total number of diagnoses results. Furthermore, the size of the database used for the development of diagnostic methods can have an impact on the precision of the result. The scientific literature reports a wide variation in the size of the database for setting DRIS standards, from as few as 24 observations (Leite, 1993) to approximately 2,800 (Sumner, 1977) or more. In this study, we hypothesize that as CND is a multivariate method involving all nutrients, it performs better over DRIS and M-DRIS in nutrient diagnosis as a function of database size considering all solid comparison criteria (CDF, Sensitivity, PPV, and Accuracy). In this study, we are interested in the comparison of the three diagnostic methods using the major plant nutrients which are nitrogen, phosphorus and potassium. Indeed, nitrogen is the most prevalent nutrient that plants need and is a key factor in determining plant growth (Prinsi & Espen, 2015). According to Nguyen et al. (2015), this nutrient is a crucial part of cellular macromolecules like proteins, nucleic acids, chlorophyll, and plant growth regulators. Phosphorus is one of the vital macronutrients needed for the synthesis of nucleic acid, the stability and building of membranes, the metabolism of energy, and many other vital physiological and biological activities during plant growth and development (Hasan et al., 2016). Critical processes including enzyme activation, osmotic adjustment, turgor generation, cell division, membrane electric potential modulation, and pH homeostasis are all facilitated by potassium (Ragel et al., 2019). Nitrogen (N), phosphorus (P), and potassium (K) are critical macronutrients required for pineapple growth and development throughout its production cycle. Potassium is extracted in the highest amounts by the plant, and enhancing fruit weight and quality (Carr, 2012; Silva et al., 2018). Adequate potassium supply is strongly associated with improved fruit sweetness, size, and resistance to diseases (Teixeira et al., 2020). Phosphorus, often the third most required nutrient, supports root development and early plant establishment, which are important for maximizing yield potential (Roy et al., 2018). Together, these nutrients are critical for optimizing pineapple productivity and ensuring high-quality fruit production. Apart from macronutrients, certain micronutrients such as boron are essential for the full development of pineapple. Indeed, pineapple needs boron for optimal growth. Boron deficiency causes orange and yellow leaf discoloration, minimal growth, and curling. It also leads to chlorosis with red margins, multiple crowned fruits, and necrotic tissue, sometimes resulting in small spherical fruits (Py et al., 1984; Souza & Reinhardt, 2007). Therefore, this study aimed to compare DRIS, M-DRIS , and CND in diagnosing pineapple leaf nutrient levels with varying sample sizes. In this study, we used data from

the pineapple subtractive trial of Angeles et al. (1990) to generate artificial data to compare the diagnostic methods. This database was used as it includes subtractive treatments that can provide all the possible outcomes of a nutritional diagnosis: nutrient deficiencies, balances or excesses.

MATERIALS AND METHODS

Data used

We used empirical data from a subtractive experiment in N, P, and K nutrients for pineapple. These data came from the study of Angeles et al. (1990), who used a size of 1185 leaf nutrients and yield database to create DRIS norms for pineapple. They are published data sets from trials including 14 treatment combinations in which yield responses to nutrients N, P, and K were determined. In this study, five (05) treatments including 0N-0P-0K, 2N-0P-0K, 0N-1P-1K, 1N-2P-0K, and 2N-2P-2K, were chosen and used based on the subtractive nutrients. They are treatments where certain nutrients are omitted, treatments with a single dose for specific nutrients, and treatments with double doses for some nutrients. These treatments were selected to ensure adequate representation of deficiency, adequacy, and excess nutrient conditions that we aim to evaluate in our research. These 5 treatments were specifically chosen to cover a full range of responses to N, P, and K nutrients, as documented in the empirical database of the subtractive trial used. These empirical data included: treatment, mean fruit yield (response variable), and pineapple (variety smooth cayenne) foliar mineral nutrients (explanatory variables) Nitrogen (N), Phosphorus (P), and Potassium (K) contents mean and standard deviation. This dataset allowed us to evaluate the ability of DRIS, M-DRIS, and CND models to accurately detect nutrient deficiencies, balances, or excesses under these different nutrient limiting conditions.

Simulation design

The simulation was realized in four main steps: identification of probable linear or non-linear regression, generation of data, model index computation, and model comparison criteria computation.

Step 1: Identification of probable linear or non-linear regression

The variable under investigation is the pineapple fruit yield (t ha^{-1}), a continuous quantitative variable. The relationship between the dependent variable (yield) and the independent variables (N, P, and K nutrients that are continuous quantitative variables) was examined using ten models, including linear and three common non-linear models (inverse, quadratic, and logarithm). Akaike Information Criterion (AIC, Narisetty (2020)), adjusted coefficient of determination (adjusted R^2), and Root Mean Squared Error (RMSE, Nayanaka et al. (2010)) were used to test and compare these models. The AIC is given by:

$$AIC = -2 * log(likelihood\ value\ from\ the\ model) + 2 * k \quad (1)$$

where k represents the model's number of parameters.

The Root Mean Squared Error was computed as follow:

$$RMSE = \sqrt{\frac{1}{n}\left(\sum_{i=1}^{n}[Z(x_i) - Z^*(x_i)]^2\right)} \quad (2)$$

where n is the sample size, is $Z^*(x_i)$ the predicted value and $Z(x_i)$ is the observed value (Javari, 2017).

Step 2: Generation of data

The response variable (Yield) was generated using Eq. (23). The nutrient concentrations related to pineapple fruit yield have been set to follow the normal distribution with parameters presented in Table 1 (Angeles et al., 1990). Nutrient data were simulated and yield was calculated accordingly for each treatment and varied sample size to ensure an extensive dataset that meets our study conditions including having treatments where certain nutrients are omitted, treatments with a single dose for specific nutrients, and treatments with double doses for some nutrients. Data size was varied to account for the effect of this factor on the performance of the models. Ten different sample sizes (30, 70, 80, 100, 210, 270, 330, 490, 630, and 860) were randomly selected from a generated sequence of sizes ranging from 10 to 1,000 by 10 using the seq() and sample() functions in R software. For each sample size and per treatment, the simulation was replicated 3,000 times (Hoad et al., 2007). The data was generated using the R software version 4.1.3 (R Core Team, 2021).

Table 1. Parameters used for data generation

Treatment			Mean concentration (%)			Standard deviation (%)			Fruit yield
N	P	K	N	P	K	N	P	K	(t ha^{-1})
0	0	0	0.97	0.47	0.64	0.4	0.52	1.32	42.7
2	0	2	2.14	0.36	3.95	0.21	0.16	0.26	131
0	1	1	0.67	0.54	3.29	0.27	0.46	0.38	55.5
1	2	0	0.8	0.56	3.38	1.2	0.37	0.7	62.5
2	2	2	1.8	0.32	2.64	0.34	0.23	0.41	134

The first three columns refer to the fertilization treatments used in the original database; 0: a specific nutrient is omitted; 1: a single dose for a specific nutrient; 2: double doses for a specific nutrient. Source: Angeles et al. (1990)

Step 3: Model index computation

The nutritional status was evaluated using the DRIS and M-DRIS (Beaufils, 1973) methodologies, taking into account all forms of nutrient ratios (direct and inverse). Additionally, the CND approach, as described by Parent & Dafir (1992), was used for the diagnosis. The yield population was separated into two subpopulations of yields using the average yield added to half of the standard deviation (mean + 0.5*Standard deviation) as a subdivision criterion. The high-yielding subpopulation corresponds to the yield greater than the mean plus half of the standard deviation and the low-yielding subpopulation was the yield less or equal to the mean plus half of the standard deviation (Silva et al., 2004). The high-yielding subpopulation was defined as a population of reference. DRIS and M-DRIS indices were calculated using two steps. First, for each ratio of nutrients, observations were related to norms using standardization and index

equations (Hallmark et al., 1987; Bailey et al., 1997; Agbangba et al., 2010; Calheiros et al., 2018) as shown in the examples below (Eqs (3), (4) and (5)):

$$f\left(\frac{A}{B}\right) = 100\left[\frac{\frac{A}{B}}{\frac{a}{b}} - 1\right] / CV \; if \; \left(\frac{A}{B}\right) > \left(\frac{a}{b}\right) + SD \tag{3}$$

$$f\left(\frac{A}{B}\right) = 100\left[1 - \frac{\frac{a}{b}}{\frac{A}{B}}\right] / CV \; if \; \left(\frac{A}{B}\right) < \left(\frac{a}{b}\right) - SD \tag{4}$$

$$f\left(\frac{A}{B}\right) = 0 \; if \; \left(\frac{a}{b}\right) - SD \leq \left(\frac{A}{B}\right) \leq \left(\frac{a}{b}\right) + SD \tag{5}$$

where A/B is the dual relation between the 'A' and 'B' nutrient concentrations (%) of the diagnosed population; a/b, CV and SD are respectively the mean, the coefficient of variation and the standard deviation of A/B in the high-yielding subpopulation.

Next, values from the standardization equations were used to calculate indices as shown in the examples below (Eq. 6):

$$I_A = \frac{\sum_{i=1}^{n} f\left(\frac{A}{B_i}\right) - \sum_{i=1}^{n} f\left(\frac{B_i}{A}\right)}{z} \tag{6}$$

where I_A = DRIS index of 'A'; $\sum_{i=1}^{n} f\left(\frac{A}{B_i}\right)$ = Sum of functions presenting concentration of nutrient 'A' is in the numerator; $\sum_{i=1}^{n} f\left(\frac{B_i}{A}\right)$ = Sum of functions presenting concentration of nutrient 'A' is in the denominator and z = Number of DRIS functions (f).

The M-DRIS (Hallmark et al., 1987), not only considers the interdependence between nutrients but also incorporates the nutrient concentrations in its computing. The M-DRIS is calculated using the following equations:

$$f(A) = 10\left(\frac{A - a}{SD}\right) \; if \; A > a + SD \tag{7}$$

$$f(A) = 10\left(\frac{A-a}{SD}\right)\left(\frac{a}{A}\right) \; if \; A < a - SD \tag{8}$$

$$f(A) = 0 \; if \; a - SD \leq A \leq a + SD \tag{9}$$

where $f(A)$ = Nutrient concentration function of ; A = Sample nutrient concentration; a = High-yielding subpopulation nutrient concentration; SD = Standard deviation of the high-yielding subpopulation nutrient concentration.

The M-DRIS index is produced for each nutrient based on the outcome of each M-DRIS function, indicating that nutrient concentration as well as nutrient ratios are considered:

$$I_A = \frac{\sum_{i=1}^{n} f\left(\frac{A}{B_i}\right) - \sum_{i=1}^{n} f\left(\frac{B_i}{A}\right) + f(A)}{z + 1} \tag{10}$$

where I_A = Nutrient 'A' M-DRIS index; $\sum_{i=1}^{n} f\left(\frac{A}{B_i}\right)$ = Addition of functions in which concentration of nutrient 'A' appears in the numerator; $\sum_{i=1}^{n} f\left(\frac{B_i}{A}\right)$ = Addition of

functions in which concentration of nutrient 'A' appears in the denominator; $f(A)$ = Nutrient concentration 'A' function and z = Number of M-DRIS functions (f).

After computing the nutrient DRIS and M-DRIS indices, the mean nutritional balance index (NBI_m) (Wadt et al., 1998) was calculated. This process involves summing the absolute values of the nutrient index for each nutrient and then dividing by the number of nutrients (d), as shown in the following equation:

$$NBI_m = \frac{1}{d}\sum_{i=1}^{d}|Indice\ A_i| \quad (11)$$

In the CND model, the full composition array for d nutrient compositions in plant tissues can be described by the following simplex S^d with $d + 1$ nutrient concentrations (d nutrients plus a filling value R) (Parent & Dafir, 1992):

$S^d = [(N, P, K, R) : N > 0, P > O, K > 0, R > 0; N + P + K + R = 100]$,

where 100 is the concentration of dry matter (%); N, P, K are the concentrations of nutrients (%); d is the number of evaluated nutrients ; and R is the filling value (residual value) between 100 and sum of the nutrients concentrations, computed as:

$$R = 100 - (N + P + K) \quad (12)$$

A geometric mean (G) computed as (Eq. 13):

$$G = (N \times P \times K \times R)^{\frac{1}{d+1}}, \quad (13)$$

was used to derive row-centred log ratios as follows (Eq. 14):

$$V_N = ln\left(\frac{N}{G}\right), \ldots, V_R = ln\left(\frac{R}{G}\right) \quad (14)$$

and $VN + VP + VK + VR = 0$, where VN is the CND row-centred log ratio expression for nutrient N.

The row-centred log-ratios were used to calculate the CND indices, represented by $I_N, \ldots, I_R$, as per Eq. (15):

$$I_N = \frac{V_N - V_N^*}{SD_N}, \ldots, I_R = \frac{V_R - V_R^*}{SD_R} \quad (15)$$

where $V_R^*, \ldots, V_R^*$ are the means and $SD_N, \ldots, SD_R$ the standard deviations of the row-centred log-ratios in the high-yielding subpopulation (> than mean + 0.5 standard deviation) of each sample.

As for the NBIm (Wadt et al., 1998) calculated for the DRIS and M-DRIS models, this index is also computed for the CND. For each sample size and treatment combination, DRIS, M-DRIS and CND index values for N, P and K nutrients were calculated using Eqs (6), (10) and (15), respectively. Each model index was applied separately for each treatment and sample size.

Step 4: Models comparison criteria

Four (04) criteria were used to compare the models. These criteria were: the Diagnosis Concordance Frequency (Silva et al., 2004), the sensitivity or True Positive Rate, the precision or Positive Predictive Value (Trevethan, 2017) and the accuracy (Morais et al., 2019; Powers, 2020; Chicco & Jurman, 2020; Tharwat, 2020). The 3,000 replications databases per treatment and sample size were used to compare the index models. The five treatments in the database involve scenarios where specific nutrients are either omitted, applied in a single dose, or applied in a double dose. The omission of

a nutrient indicates its deficiency, a single dose represents an adequate concentration, and a double dose signifies an excess of the nutrient. Specifically, 0 means a nutrient is omitted, 1 corresponds to a single dose, and 2 indicates a double dose. The models were evaluated based on their ability to detect these three situations. For instance, if a treatment has a value of 0 for a nutrient and the model correctly identifies it as deficient, then the model has accurately detected the situation.

DCF evaluates the consistency of diagnoses between different methods of determining nutritional indices. This is crucial for ensuring the reliability of the models. It is calculated based on the Potential Fertilization Response (PFR) (Silva et al., 2004). It focuses on two situations: separating nutrients and identifying the principal limiting deficient nutrient (p) and excessive nutrient (n). The following criteria were used to evaluate the degree of agreement between the diagnoses made using the various techniques for determining the nutritional indices: (i) For a nutrient, if the diagnosis (deficiency, adequate and excess, or p and n) was the same between two distinct methods, it was considered concordant; (ii) If two methods produce different diagnoses for the same nutrient, the diagnosis is considered non-concordant. The concordance rate is then calculated for all evaluated methods, providing an indicator of the consistency of different diagnoses. A high DCF indicates strong agreement between models in identifying nutrient status.

TPR: measures a model's ability to correctly identify a particular nutritional status when that status is indeed present. It refers to the efficiency of the method at correctly diagnosing the cases of a true nutritional status. This criterion includes three subcategories including the True Positive Deficiency Rate (TPDR), True Positive Adequate Rate (TPAR), and True Positive Excess Rate (TPER) that were computed for the nutritional deficiency, adequate, and excess, respectively. A high TPR for a specific nutritional status indicates that the model is able to identify this status. Indeed, TPDR is the proportion of deficiency diagnosed by a model when the nutrient is deficient, and is calculated by:

$$TPDR = \frac{TPD}{TPD + FND} = \frac{TPD}{TPD + FNA|D + FNE|D} \quad (16)$$

where TPD = True Positive Deficiency = [Deficient nutrient correctly identified as deficient]; FND = False Negative Deficiency = [Deficient nutrient incorrectly identified as excessive or adequate]; FNA|D = [Deficient nutrient incorrectly identified as adequate] and FNE|D = [Deficient nutrient incorrectly identified as excessive].

TPAR is the proportion of adequate diagnosed by a model when the nutrient is adequate, and is calculated by:

$$TPAR = \frac{TPA}{TPA + FNA} = \frac{TPA}{TPA + FND|A + FNE|A} \quad (17)$$

where TPA = True Positive Adequate = [Adequate nutrient correctly identified as adequate]; FNA = False Negative Adequate = [Adequate nutrient incorrectly identified as deficient or excessive]; FND|A = [Adequate nutrient incorrectly identified as deficient] and FNE|A = [Adequate nutrient incorrectly identified as excessive].

TPER is the proportion of excess diagnosed by a model when the nutrient is excessive, and is calculated by:

$$TPER = \frac{TPE}{TPE+FNE} = \frac{TPE}{TPE+FND|E+FNA|E}$$
$$TPER = \frac{TPE}{TPE + FNE} = \frac{TPE}{TPE + FND|E + FNA|E} \quad (18)$$

where TPE = True Positive Excess = [Excessive nutrient correctly identified as excessive]; FNE = False Negative Excess = [Excessive nutrient incorrectly identified as deficient or adequate]; FND|E = [Excessive nutrient incorrectly identified as deficient] and FNA|E = [Excessive nutrient incorrectly identified as adequate].

PPV: represents the proportion of correctly detected diagnoses of a particular nutritional status to the total number of diagnosed cases of that status. This criterion reflects the model's prediction performance. A high PPV for a specific nutrient status indicates diagnosis for that status are reliable. There are three subcategories: Positive Predictive Deficiency Value (PPDV), Positive Predictive Adequate Value (PPAV), and Positive Predictive Excess Value (PPEV). Indeed, PPDV is the proportion of deficiency that was correctly identified to the total number of deficient cases diagnosed. It is given by:

$$PPDV = \frac{TPD}{TPD + FPD} \quad (19)$$

where TPD = [Deficient nutrient correctly identified as deficient] and FPD = False Positive Deficiency = [Adequate or excessive nutrient incorrectly identified as deficient].

PPAV is the proportion of adequacy that was correctly identified to the total number of adequate cases diagnosed, and is given by:

$$PPAV = \frac{TPA}{TPA + FPA} \quad (20)$$

where TPA = [Adequate nutrient correctly identified as adequate] and FPA = False Positive Adequate = [Deficient or excessive nutrient incorrectly identified as adequate].

PPEV is the proportion of excess that was correctly diagnosed to the total number of excessive cases diagnosed, and is given by:

$$PPEV = \frac{TPE}{TPE + FPE} \quad (21)$$

where TPE = [Excessive nutrient correctly identified as excessive] and FPE = False Positive Excess = [Deficient or adequate nutrient incorrectly identified as excessive].

Accuracy: measures how close the model's results are to the true value. It is the ratio of correctly detected diagnoses to the total number of diagnosis results. Accuracy provides an overall view of the model performance. A high accuracy indicates the model performs well overall in identifying nutrient deficiencies, adequate levels, and excesses.

$$Accuracy = \frac{TPD + TPA + TPE}{TPD + TPA + TPE + FND + FNA + FNE} \quad (22)$$

where TPD = True Positive Deficiency, TPA = True Positive Adequacy, TPE = True Positive Excess, FND = False Negative Deficiency, FNA = False Negative Adequacy, and FNE = False Negative Excess.

In summary, these performance criteria provide a comprehensive picture of how well models can diagnose plant nutrient status. DCF assesses agreement between models, while TPR and PPV evaluate a model's ability to correctly identify true nutrient deficiencies, adequate levels, and excesses.

Data analysis

The fruit yield population was separated into high and low subpopulation data arrays based on the confidence interval method proposed by Silva et al. (2004). Descriptive statistics were calculated for pineapple fruit yield, leaf nutrient concentrations, nutrient ratios, and row-centred log ratio expression data (Eq. 15) using R software version 4.1.3 (R Core Team, 2021). Descriptive statistics included, means, standard deviations, CVs, skewness, and kurtosis values, where a skewness value of zero indicates perfect symmetry, and values greater than 1 indicate marked asymmetry. We computed DRIS (Eq. 6), M-DRIS (Eq. 10), and CND (Eq. 15) index values per treatment based on the index function and the row-centred log-ratios for the high-yielding subpopulation. The more negative is the index value for a nutrient, the more limiting is that nutrient. The mean nutrient balance index (NBIm) was also computed for each model. The mean indices of the three models for each nutrient and the NBIm were plotted against the sample size using plot() function from the base stats package in R software. They were plotted to see the trends for the distribution of N, P, and K indices and NBIm for the different models.

A permutational multivariate analysis of variance (PERMANOVA) test ($p < 0.05$) was performed on the nutrient indices using Euclidean method (Anderson, 2001) under the null hypothesis that there is no difference between these indices for DRIS, M-DRIS, and CND models with 0.05 significance level. Model and treatment were considered as factors. We calculated also the percentages of agreement between the models, the sensitivity (Eqs (16), (17) and (18)), precision (Eqs (19), (20) and (21)) and accuracy (Eq. 22) for each model and by sample size that were used to compare model performance. Performance criteria values including sensitivity, precision, and accuracy of each model were then averaged and plotted against the sample size using function plot from the base stats package in R software. All the computations and plots were done using R software version 4.1.3.

Interpretation of DRIS, M-DRIS, and CND indices

The nutrient index and the NBIm were used to interpret the diagnosis made by DRIS, M-DRIS, and CND (Wadt, 2005). Using this method, each nutrient's DRIS, M-DRIS, and CND index modules are compared with the NBIm. According to Wadt et al. (1998), the technique determines if the imbalance ascribed to a particular nutrient is larger or smaller than the imbalance given to the average of all nutrients. The method has the advantage of detecting even excess nutrients. According to this author, for a nutrient *Nut*, the following conclusions could be drawn:

$$Deficiency = INut < 0 \; and \; |INut| > NBIm$$

$$Adequate = |INut| \leq NBIm$$

$$Excess = INut > 0 \; and \; |INut| > NBIm$$

The DRIS, M-DRIS, and CND indices (Table 2) were interpreted using the theory of potential fertilization response (PFR) (Wadt et al., 1998). The nutrients of the high-productivity subpopulation were classified according to the potential fertilization response as follows: zero (z), positive (p), negative (n), positive or zero (pz), and negative or zero (nz).

Table 2. Criteria for interpreting DRIS, M-DRIS, and CND indices based on PFR

Nutritional state	Criteria	Potential response fertilization
Deficient and limiting	INut < 0 |INut| > NBIm INut is lower index value	Positive, with higher probability (p)
Probably deficient	INut < 0 |INut| > NBIm	Positive or zero, with lower probability (pz)
Adequate	|INut| ≤ NBIm	zero (z)
Probably excessive	INut > 0 |INut| > NBIm	Negative or zero, with lower probability (nz)
Excessive	INut > 0 |INut| > NBIm INut is higher index value	Negative, with higher probability (n)

PFR= Potential Fertilization Response, NBIm = nutrient balance index mean and INut = DRIS, M-DRIS or CND index nutrient. Source: Calheiros et al. (2018).

The flow chart (Fig. 1) below presents the different steps of this study.

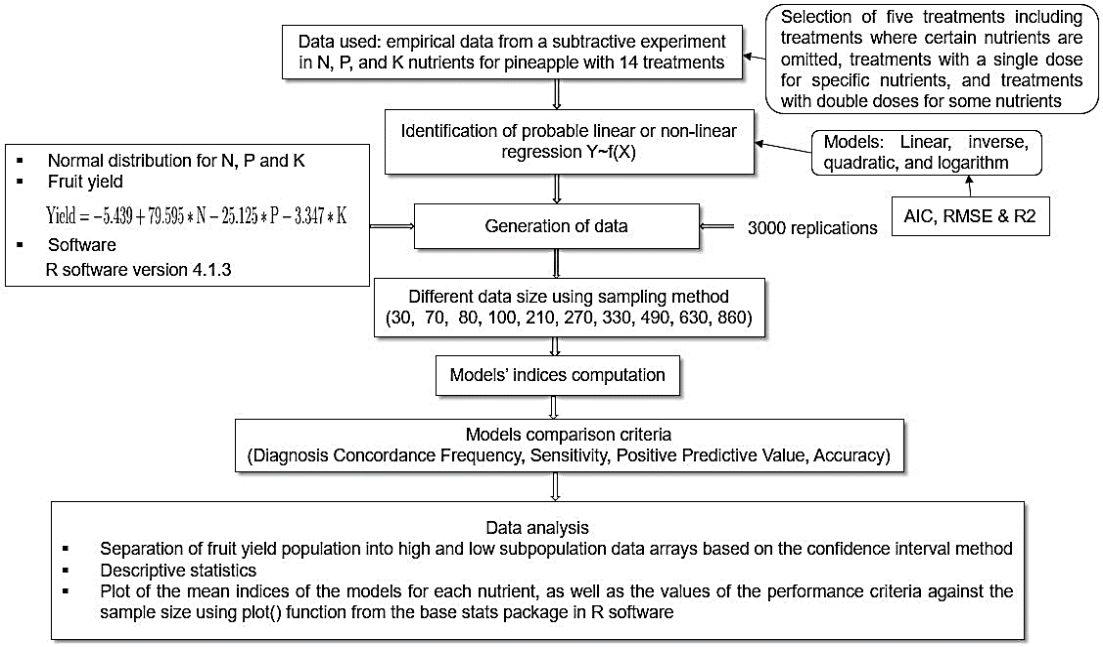

Figure 1. Research scheme.

RESULTS AND DISCUSSION

Relationship between yield and nutrients

Among the 10 regression models performed to identify the relationship between yield and nutrients, the multiple linear regression model has the lowest AIC (210.39) and RMSE (15.73) values, as well as the highest R^2 (78.01; Table 3). Therefore, it is considered the best model, and its equation is as follows:

$$Yield = -5.44 + 79.6 * N - 25.13 * P - 3.35 * K \quad (23)$$

This equation was then used to generate the yields corresponding to the nutrient levels, in keeping the linear functional link between the data.

Table 3. Linear and non linear equation to yield on the explanatory variables

Model	Equation	AIC	R^2 (%)	RMSE
Multiple linear regression	Yield = e +a*N + b*P + c*K	210.39	78.01	15.73
Logarithm transformation	Yield = e +a*log(N) + b*log(P) + c*log(K)	214.12	74.3	17.01
Inverse	Yield = e +a*(1/N) + b*(1/P) + c*(1/K)	244.09	52.85	35.98
Quadratic of N	Yield = e +a*N^2 + b*P + c*K	227.16	61.07	18.86
Quadratic of P	Yield = e +a*N + b*P^2 + c*K	241.2	60.28	28.98
Quadratic of K	Yield = e +a*N + b*P + c*K^2	225.04	63.53	20.35
Quadratic of N and P	Yield = e +a*N^2 + b*P^2 + c*K	219.45	64.12	18.25
Quadratic of N and K	Yield = e +a*N^2 + b*P + c*K^2	222.23	63.55	20.22
Quadratic of P and K	Yield = e +a*N + b*P^2 + c*K^2	235.1	60.05	28.43
Quadratic of N, P and K	Yield = e +a*N^2 + b*P^2 + c*K^2	228.64	61.75	19.62

AIC = Akaike Information Criterion; R^2: Coefficient of determination; RMSE = Root Mean Square Error; e = the intercept or constant term; a = the regression coefficient for N; b = the regression coefficient for P; c = the regression coefficient for K.

Binary nutrients ratio and row-centred log ratio statistics

Binary nutrient ratio combinations and row-centred log ratios of all three nutrients were calculated for the different sample sizes, and summary statistics were evaluated for each of the resulting nutrient ratio expressions (Table 4). We noticed that the values of the dual relations and the multi-nutrient variables with the means differed for the high-productivity subpopulation. The DRIS and M-DRIS norms, i.e. means and CVs of the nutrient ratios, for high-yielding subpopulations were presented in Table 4.

Indeed, a total of six (06) nutrient ratios were established and used to determine the DRIS and M-DRIS standards. These ratios were N/P, N/K, P/K, P/N, K/N, K/P. Considering the different sample sizes, except 30, the ratio P/N had the lowest average ratio and K/P had the highest for the control treatment (Table 4). For the treatments 2N-0P-2K, 1N-2P-0K, and 2N-2P-2K, the ratios of P/K had the lowest standard deviation, while the ratios of K/P had the highest standard deviation. On the other hand, for treatment 0N-1P-1K, the nutrient ratios of N/K had the lowest standard deviation, whereas the ratios of K/P had the highest standard deviation. These values were computed using CVs and $\overline{X}$, and were presented in Table 3. The means, standard deviation (SD), and CV (%) of ratios for high-yielding subpopulations were computed for the DRIS and M-DRIS norms. These norms were used to calculate nutrient indices of DRIS and M-DRIS and the Mean Nutrient Balance Indices.

The CND norms, i.e. means and CVs, of row-centred log ratios of N, P, and K, for the high yielding- subpopulation were presented in Table 4. N and P nutrients had the lowest and highest standard deviations, respectively, with regard to the CND criteria for all sample sizes and the control treatment. For K nutrient, the standard deviation was 0.83% (computed using $\overline{X}$ and CV; Table 4).

Table 4. Mean ($\bar{X}$) and coefficient of variation (CV) of the N, P, and K dual relations, and the CND variables in pineapple, subpopulation of high productivity. T1 = 0N-0P-0K, T2 = 2N-0P-2K, T3 = 0N-1P-1K, T4 = 1N-2P-0K, T5 = 2N-2P-2K 3

Treatment	Variable	N = 30		N = 70		N = 80		N = 100		N = 210		N = 270		N = 330		N = 490		N = 630		N = 860	
T1		$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)	$\bar{X}$ (%)	CV (%)
	N/P	15.37	3,126.18	11.35	1,758.45	11.95	3,490.88	13.87	5,212.54	12.22	388.06	10.70	2,238.14	11.62	3,497.12	11.69	4,020.45	18.53	1,7751.22	14.14	1,0689.08
	N/K	4.98	1,690.33	5.74	2,261.84	5.90	3,426.84	6.99	3,298.59	5.47	145.05	8.27	9,418.30	5.32	2,242.48	6.82	4,830.60	7.09	6,515.75	6.06	4,084.55
	P/K	3.31	2,244.86	3.04	1,542.54	4.27	5,397.85	3.50	2,386.91	3.12	60.37	3.95	4,620.40	3.23	2,808.28	3.72	4,070.1	4.58	9,754.43	3.64	5,425.93
	P/N	1.45	2,965.01	1.05	758.34	1.16	1,634.93	1.04	845.66	1.25	34.03	1.28	3,754.39	1.18	1,608.89	1.54	10,641.27	1.42	5,249.52	1.26	2,650.42
	K/N	2.36	1,037.95	2.36	1,203.78	2.31	1,571.24	2.20	1,080.42	2.5	55.54	2.68	3,694.32	2.44	1,898.23	2.51	3,603.57	2.71	5,422.62	2.57	2,566.6
	K/P	18.45	3,534.8	14.35	2,859.62	14.21	2,938.93	13.04	2,258.48	14.24	550.48	13.64	3,164.33	13.77	3,555.40	13.82	4,577.69	26.84	23,281.8	16.45	12,463.73
	G	3.07	23.15	3.07	23.08	3.06	23.24	3.07	23.21	3.06	23.11	3.07	23.24	3.06	23.24	3.07	23.26	3.06	23.22	3.06	23.28
	Log (N/G)	-1.24	52.23	-1.24	-52.23	-1.24	-52.47	-1.23	-52.45	-1.23	-52.85	-1.24	-52.57	-1.23	-52.75	-1.23	-52.33	-1.24	-52.61	-1.24	-52.71
	Log (P/G)	-2.01	-55.20	-2.01	-55.20	-2.004	-54.63	-2.02	-54.82	-2.01	-54.69	-2.02	-55.002	-2.02	-54.71	-2.02	-54.94	-2.02	-55.16	-2.02	-54.93
	Log (K/G)	-1.32	-62.39	-1.32	-62.39	-1.33	-62.19	-1.33	-62.67	-1.33	-62.13	-1.33	-62.62	-1.33	-62.36	-1.33	-62.64	-1.33	-62.55	-1.33	-62.55
T2	N/P	15.03	1,724.80	15.36	2,259.69	20.11	6,309.45	12.55	1,033.16	26.13	15,606.77	14.35	2,330.56	150.6	35,245.83	15.71	3,514.99	14.41	2,598.88	17.53	8,389.27
	N/K	0.54	11.87	0.54	11.85	0.54	11.83	0.54	11.83	0.54	11.92	0.54	11.89	0.54	11.87	0.54	11.89	0.54	11.86	0.54	11.91
	P/K	0.09	43.99	0.09	44.13	0.09	43.96	0.09	43.93	0.09	44.08	0.09	44.10	0.09	44.08	0.09	43.99	0.09	44.05	0.09	43.97
	P/N	0.17	44.49	0.17	44.95	0.17	44.79	0.17	44.75	0.17	44.86	0.17	44.84	0.17	44.78	0.17	44.80	0.17	44.81	0.7	44.71
	K/N	1.86	12.06	1.86	12.02	1.86	12.03	1.86	12.04	1.86	12.13	1.86	12.08	1.86	12.08	1.86	12.09	1.86	12.07	1.86	12.11
	K/P	27.84	1,662.23	28.02	2,115.26	36.39	6,067.38	22.90	968.54	47.6	15,312.52	26.44	2,377.52	310.83	35,474.45	28.94	3,340.91	26.92	2,748.18	32.27	7,900.48
	G	4.41	1.57	4.41	1.58	4.21	1.59	4.41	1.58	4.41	1.59	4.40	1.59	4.41	1.59	4.40	1.59	4.41	1.59	4.41	1.58
	Log (N/G)	-0.73	-13.76	-0.73	0.1	-0.73	-13.78	-0.72	-13.77	-0.73	-13.86	-0.72	-13.82	-0.73	-13.78	-0.73	-13.82	-0.73	-0.73	-0.73	-13.84
	Log (P/G)	-2.65	-24.91	-2.64	-24.91	-2.64	-24.66	-2.64	-24.6	-2.65	-24.72	-2.64	-24.73	-2.65	-24.81	-2.64	-24.73	-2.64	-2.64	-2.64	-24.59
	Log (K/G)	-0.11	-44.62	-0.11	-44.63	-0.11	-44.87	-0.11	-44.51	-0.11	-44.7	-0.11	-44.92	-0.12	-44.73	-0.11	-44.74	-0.11	-0.11	-0.11	-44.68

Table 4 (continued)

T3	N/P	6.19	1,650.93	5.38	1,452.75	5.46	1,660.36	7.55	4,206.58	11.4	12,837.01	7.18	3,725.06	7.79	6,289.36	6.67	4,211.49	12.83	18,240.64	17.79	32,345.07
	N/K	0.2	41.91	0.21	41.8	0.21	41.72	0.21	41.76	0.2	41.72	0.21	41.74	0.21	41.82	0.21	41.96	0.21	41.77	0.21	41.93
	P/K	0.18	66.92	0.18	66.48	0.18	66.72	0.18	66.91	0.18	66.78	0.18	66.48	0.18	66.88	0.18	66.66	0.18	66.64	0.18	66.62
	P/N	1.47	587.16	2.59	5,853.87	4.26	12,386.18	1.73	2,742.32	1.66	2,071.21	1.93	2,716.81	1.66	2,142.14	1.7	2,416.8	1.99	5,442.97	3.42	33,140.85
	K/N	8.94	905.35	15.02	6,296.99	20.62	11,248.19	9.75	2,272.68	8.94	1,551.59	10.81	2,761.16	9.91	3,781.15	9.68	2,363.47	10.84	6,261.52	20.05	32,399.43
	K/P	31.13	1,725.96	26.64	1,396.35	28.13	1,555.03	34.04	3,137.97	44.41	7,851.88	33.87	3,194.79	36.58	5,137.91	33.44	3,780.51	57.78	14,136.23	68.42	25,110.33
	G	4.22	2.83	4.21	2.83	4.22	2.83	4.21	2.82	4.21	2.82	4.22	2.83	4.22	2.82	4.21	2.83	4.22	23.23	4.22	23.28
	Log (N/G)	-1.96	-29.7	-1.96	-29.7	-1.95	-29.45	-1.94	-29.07	-1.94	-29.04	-1.95	-29.36	-1.68	-29.22	-1.95	-29.38	-1.95	-29.32	-1.95	-29.19
	Log (P/G)	-2.29	-44.52	-2.29	-44.53	-2.29	-44.39	-2.30	-44.5	-2.3	-44.61	-2.29	-44.55	-2.3	-44.82	-2.29	-44.51	-2.3	-44.68	-2.29	-44.62
	Log (K/G)	-0.25	-35.07	-0.25	-35.07	-0.25	-35.17	-0.25	-35.02	-0.25	-34.93	-0.25	-35.03	-0.25	-34.94	-0.25	-34.97	-0.25	-34.97	-0.25	-34.95
T4	N/P	18.3	6,675.43	12.81	3,452.28	6.53	672.48	14.5	3,432.38	9.37	2,480.93	31.8	21,885.95	9.46	2,304.91	11.35	5,284.76	41.48	41,737.89	11.24	5,462.52
	N/K	0.35	79.06	0.36	79.8	0.36	80.47	0.36	79.77	0.36	79.2	0.36	79.31	0.36	79.71	0.36	79.76	0.36	80.91	0.36	79.94
	P/K	0.18	64.2	0.18	64.5	0.18	65.21	0.18	64.2	0.18	64.4	0.18	64.68	0.18	64.67	0.18	64.71	0.18	65.93	0.18	64.63
	P/N	2.61	977.89	3.50	2,290.19	5.10	5,156.76	3.15	1,779.13	624.72	32,159.3	4.68	11,755.1	3.47	2,447.74	3.95	7,641.35	4.001	6,117.44	3.5	3,386.52
	K/N	15.22	930.3	21.07	2,000.73	27.13	3,702.31	18.35	1,656.8	1,631.002	31,945.30	27.35	11,299.61	19.67	2,068.73	22.83	7,715.36	26.002	6,489.78	20.96	3,166.57
	K/P	47.15	5,113.71	1.53	3,552.3	20.42	995.8	43.29	4,806.56	27.26	2,144.36	74.38	18,235.6	33.08	4,065.54	36.51	7,780.84	60.65	26,061.09	33.58	6,103.32
	G	4.23	5.18	4.23	5.27	4.24	5.25	4.23	5.22	4.23	5.21	4.23	5.23	4.23	5.24	4.23	5.26	4.23	5.23	4.23	5.22
	Log (N/G)	-1.69	-65.23	-1.69	-65.23	-1.69	-65.22	-1.69	-65.16	-1.69	-65.15	-1.68	-65.17	-1.68	-65.25	-0.26	-65.19	-1.69	-65.21	-1.69	-65.18
	Log (P/G)	-2.25	-41.09	-2.25	-41.09	-2.25	-40.70	-2.25	-41.17	-2.25	-40.98	-2.26	-41.20	-2.25	-41.09	-2.25	-41.09	-2.26	-41.05	-2.25	-41.07
	Log (K/G)	-0.24	-67.71	-0.25	-67.71	-0.24	-68.57	-0.25	-67.38	-0.24	-67.60	-0.25	-67.81	-0.25	-67.92	-1.68	-68.11	-0.25	-67.71	-0.25	-67.78
T5	N/P	24.87	1,193.63	34.85	5,748.19	29.65	4,117.35	28.72	1,896.02	29.61	2,780.58	38.87	7,120.04	27.31	2,263.61	32.94	5691.68	32.71	7,922.83	38.17	10,933.74
	N/K	0.69	25.47	0.69	25.72	0.69	25.61	0.69	25.5	0.69	25.68	0.7	25.52	0.7	25.44	0.7	25.45	0.7	25.53	0.7	25.55
	P/K	0.13	63.5	0.13	63.98	0.13	63.99	0.13	63.47	0.13	63.55	0.13	63.66	0.13	63.40	0.13	63.49	0.13	63.61	0.13	63.61
	P/N	0.19	65.43	0.19	65.82	0.19	66.12	0.19	65.13	0.19	65.37	0.20	65.63	0.19	65.39	0.19	65.36	0.2	65.43	0.2	65.56
	K/N	1.53	26.92	1.52	27.06	1.52	28.66	1.52	26.78	1.52	26.92	1.53	26.94	1.52	26.81	1.52	26.74	1.52	26.92	1.53	26.91
	K/P	37.54	1,189.09	46.46	4,817.31	43.27	4,468.23	42.51	1,966.38	43.47	2,711.17	56.38	6,296.80	39.51	2,083.57	49.25	6,417.43	49.64	9,042.45	55.13	10,223.39
	G	3.99	3.88	3.99	3.9	4	3.89	4	3.87	3.99	3.88	3.99	3.86	3.99	3.85	4.23	3.86	3.99	3.87	3.99	2.87
	Log (N/G)	-0.82	-25.01	-0.82	-25.01	-0.81	-24.92	-0.81	-24.72	-0.81	-24.93	-0.81	-24.89	-0.81	-24.79	-0.81	-24.77	-0.81	-24.86	-0.81	-24.82
	Log (P/G)	-2.77	-34.84	-2.77	-34.84	-2.77	-34.95	-2.76	-34.85	-2.77	-35.05	-2.76	-34.93	-2.76	-34.81	-2.76	-34.71	-2.76	-34.75	-2.76	-34.77
	Log (K/G)	-0.42	-28.71	-0.42	-28.71	-0.42	-28.71	-0.42	-28.58	-0.42	-28.54	-0.42	-28.44	-0.42	-28.36	-0.42	-28.48	-0.43	-28.53	-0.42	-28.50

For the treatments 2N-0P-2K, 0N-1P-1K, and 2N-2P-2K, potassium (K) had the lowest standard deviation, while phosphorus (P) had the highest standard deviation. Potassium (K) and nitrogen (N) exhibited the lowest and highest standard deviations for the treatment 1N-2P-0K, respectively. The standard deviation of phosphorus (P) ranged between 0.91% and 0.93% (computed using $\overline{X}$ and CVs). Negative values in the CND criteria mean that the nutrient's foliar content is lower than the geometric mean of the nutritional composition in the multi-nutrient variable.

Nutrient indices computed by DRIS, M-DRIS, and CND methods

The N, P, and K indices and as well as the NBIm were calculated for each treatment and each sample size using DRIS, M-DRIS, and CND models. When all nutrient indices for DRIS, M-DRIS, and CND were plotted in one graph, the models showed different trends for the distribution of N, P, and K indices as well as NBIm (Fig. 2). Nutrient indices were different between models and with sample size. Indeed, we noticed that N, P, and K averaged indices as well as NBIm for M-DRIS (red dashed lines) were positive, whereas DRIS average indices (black lines) were negative for P and positive for K and NBIm. N varied between negative (I_N = -36.78) and positive values (I_N = 158.28). CND averaged indices (blue lines) were between negative and positive values for all nutrients with the sample size (ranging from $-1.57*10^{-16}$ to $1.31*10^{-16}$ for N, $-9.68*10^{-17}$ to $5.83*10^{-17}$ for P, and $-1.23*10^{-16}$ to $8.66*10^{-17}$) and were very close to 0, which explained the approximately linear shape of its curves in the figure.

For all three models, the calculated indices became approximately stable from the sample size of 490 (Fig. 2). P was the most limiting nutrient by deficiency, compared to the other nutrients.

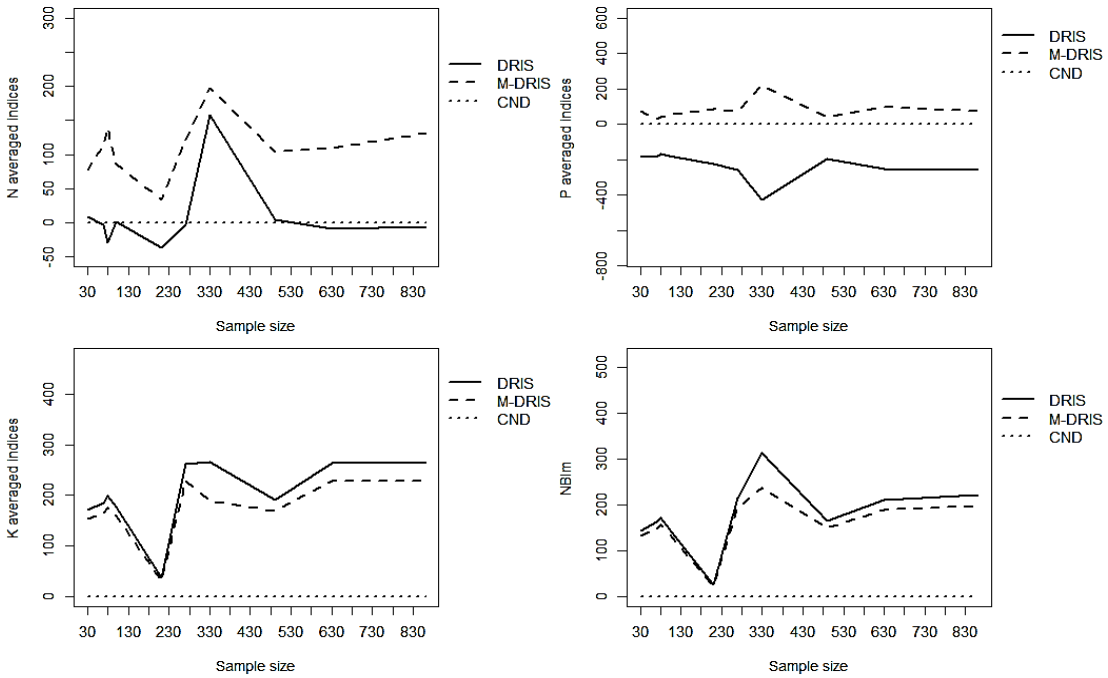

Figure 2. Averaged indices of N, P, K and mean nutrient balance index (NBIm) for DRIS, M-DRIS, and CND models relative to the different data size.

Table 5. Results of permutational multivariate analysis of variance on the nutrient indices considering the models and treatment as factors

Sample size	Source of variation	Df	Sum of squares	R^2	F	Pr(>F)
30	Model	2	276,236	0.40	5.01	0.001***
	Treatment	4	194,099	0.28	1.76	0.12
	Residual	8	220,393	0.32	-	-
	Total	14	690,729	1	-	-
70	Model	2	269,961	0.34	4.77	0.007**
	Treatment	4	288,337	0.37	2.55	0.025*
	Residual	8	226,224	0.29	-	-
	Total	14	784,522	1	-	-
80	Model	2	321,217	0.37	4.09	0.002**
	Treatment	4	233,648	0.27	1.49	0.168
	Residual	8	314,105	0.36	-	-
	Total	14	868,969	1	-	-
100	Model	2	269,792	0.36	4.45	0.004**
	Treatment	4	239,334	0.32	1.97	0.052
	Residual	8	242,563	0.32	-	-
	Total	14	751,689	1	-	-
210	Model	2	165,972,252	0.15	1.03	0.393
	Treatment	4	296,526,975	0.27	0.92	0.933
	Residual	8	646,655,531	0.58	-	-
	Total	14	1,109,154,758	1	-	-
270	Model	2	556,484	0.31	3.4	0.007**
	Treatment	4	602,948	0.33	1.84	0.076
	Residual	8	654,686	0.36	-	-
	Total	14	1,814,118	1	-	-
330	Model	2	4,802,704	0.23	1.51	0.065
	Treatment	4	3,394,142	0.16	0.53	0.913
	Residual	8	12,707,887	0.61	-	-
	Total	14	20,904,733	1	-	-
490	Model	2	303,415	0.35	4.38	0.004**
	Treatment	4	286,785	0.33	2.07	0.043*
	Residual	8	277,008	0.32	-	-
	Total	14	867,208	1	-	-
630	Model	2	579,664	0.38	4.47	0.006**
	Treatment	4	444,592	0.29	1.71	0.133
	Residual	8	519,244	0.34	-	-
	Total	14	1,543,499	1	-	-
860	Model	2	576,084	0.36	4.35	0.003**
	Treatment	4	486,791	0.31	1.84	0.048*
	Residual	8	530,319	0.33	-	-
	Total	14	1,593,194	1	-	-

Df: Degree of freedom; ***, **, and * indicate significance at 0.001, 0.01, 0.05, and 0.1 levels, respectively.

The permutational multivariate analysis of variance (PERMANOVA) results indicated that there was a significant difference between the DRIS, M-DRIS and CND indices for the sample sizes of 30 (p.value = 0.001), 70 (p.value = 0.007), 80 (p.value = 0.002), 100 (p.value = 0.004), 270 (p.value = 0.007), 490 (p.value = 0.004), 630 (p.value = 0.006), and 860 (p.value = 0.003). For the sample sizes of 210 and 330,

the nutrient indices calculated did not differ significantly between the DRIS, M-DRIS, and CND models. Considering the treatments, there was also a difference between the dispersions of the models' indices calculated for the sample size of 70 (p.value = 0.025) at a 5% significance level (Table 5).

Comparison of the Performance of DRIS, M-DRIS, and CND

Frequency of concordance in diagnosis using the DRIS, M-DRIS, and CND models

The comparison of multiple models employing specific norms based on the frequency of concordant diagnoses (DCF) (Silva et al., 2004) produced varying findings depending on the method of comparison and the concentration of nutrients in pineapple leaves. A set of all treatments combined was used to assess the effect of the index model and sample size. All sample sizes yielded mean values of 66% (DRIS versus M-DRIS), 43.33% (DRIS vs CND), and 28.7% (M-DRIS vs CND) (Table 6).When comparing N, P, and K nutrients, the concordance is lower with CND involved. Consequently, the DRIS and M-DRIS models showed more similarity in diagnosing nutritional status for pineapple compared to each of them versus the CND model. Overall, the models disagreed, and when it came to determining the status of N, P, and K minerals, the nutritional diagnostic obtained through the CND technique was not the same as that obtained through the DRIS and M-DRIS methods. Our results are consistent with those of Silva et al. (2004) when assessing the nutritional status of eucalyptus trees and with the work of Urano et al. (2006) when assessing the nutritional diagnosis of soybeans. They found that the DRIS and M-DRIS methods were concordant.

Table 6. Agreement percentages of concordant diagnoses of N, P, and K status in pineapple, subpopulation of high productivity, among the methods DRIS, M-DRIS, and CND for each sample size, applied to the leaves

Sample size	DRIS vs M-DRIS				DRIS vs CND				M-DRIS vs CND			
	N (%)	P (%)	K (%)	Mean (%)	N (%)	P (%)	K (%)	Mean (%)	N (%)	P (%)	K (%)	Mean (%)
30	80	20	80	60	40	20	40	33.33	60	40	40	34
70	100	80	80	86.66	40	40	80	53.33	40	40	60	27.67
80	40	20	0	20	100	40	0	46.67	40	0	40	14
100	80	60	40	60	40	20	40	33.33	60	40	80	34.67
210	80	40	80	66.67	40	0	20	20	40	60	20	33.67
270	100	20	80	66.67	60	80	60	66.67	60	40	40	34
330	100	60	80	80	40	40	20	33.33	40	60	20	33.67
490	80	40	80	66.67	40	40	60	46.67	40	40	40	27.33
630	100	60	80	80	80	20	80	60	80	0	60	27.67
860	80	60	80	73.33	60	20	40	40	60	0	20	20.33
Mean	84	46	68	66	54	32	44	43.33	52	32	42	28.7

The DCF of the potential fertilization response (PFR) for the principal limitation by deficiency (p) for DRIS vs. M-DRIS, DRIS vs. CND, and M-DRIS vs. CND were 45.32%, 50.43%, and 40.75%, respectively, for the second criterion (Table 7). Furthermore, for the same comparison, the main excess (n) constraint was 31.8%, 39.07%, and 45.82%, respectively. This comparison showed the highest degree of

similarity among the three approaches. As observed for the negative response (n), the concordance was smaller when DRIS was considered in the comparisons. M-DRIS and CND models were more consistent in identifying primary limiting by excess (n), whereas DRIS and CND were more comparable in diagnosing principal limiting by deficiency (p), when compared to the other duals.

Table 7. Agreement percentages of concordant diagnoses of the potential fertilization response in a subpopulation of high productivity, among the methods DRIS, M-DRIS, and CND using specific norms for each sample size, applied to the leaves

Sample size	Method	p (%)	n (%)
30	DRIS vs M-DRIS	26.67	33.33
	DRIS vs CND	40.67	23.33
	M-DRIS vs CND	30	55
70	DRIS vs M-DRIS	25.33	30.67
	DRIS vs CND	50	35.5
	M-DRIS vs CND	20	33.33
80	DRIS vs M-DRIS	60.33	40.67
	DRIS vs CND	26.7	60
	M-DRIS vs CND	50	10.67
100	DRIS vs M-DRIS	12.5	10
	DRIS vs CND	40	65.33
	M-DRIS vs CND	50.5	12.5
210	DRIS vs M-DRIS	70	50
	DRIS vs CND	60	24.67
	M-DRIS vs CND	45.67	75
270	DRIS vs M-DRIS	70.67	6.67
	DRIS vs CND	13.33	70
	M-DRIS vs CND	36	53.33
330	DRIS vs M-DRIS	20.33	60
	DRIS vs CND	80	27.33
	M-DRIS vs CND	20	60.67
490	DRIS vs M-DRIS	30.33	16.67
	DRIS vs CND	64.5	29.33
	M-DRIS vs CND	35.33	50.33
630	DRIS vs M-DRIS	73.33	40
	DRIS vs CND	43.67	30.5
	M-DRIS vs CND	60	67.33
860	DRIS vs M-DRIS	63.67	30
	DRIS vs CND	75.67	24.67
	M-DRIS vs CND	60	40
Mean	DRIS vs M-DRIS	45.32	31.8
	DRIS vs CND	50.43	39.07
	M-DRIS vs CND	40.75	45.82

p = primary limiting by deficiency, n = primary limiting by excess.

Sensitivity, positive predictive value and accuracy of DRIS, M-DRIS and CND models

DRIS, M-DRIS, and CND models were also compared based on their sensitivity or true positive rate (TPR, Fig. 3), positive predictive value (PPV, Fig. 4, A-C) and accuracy (Fig. 4, D). Compared with DRIS and M-DRIS, CND appeared to be more sensitive for early detection of N, P, and K deficiency and excess in pineapple leaves when the situations were true (Fig. 3, A and C). Parent & Dafir (1992) showed that CND is theoretically more robust than DRIS and M-DRIS. CND recognizes high-order interactions between nutrients, which was partially addressed by DRIS and M-DRIS (Parent & Dafir, 1992). CND has been found to be more efficient to determine the nutritional status of crops because of its sound mathematical and statistical bases (René et al., 2013; Valdez-Cepeda et al., 2013; Morais et al., 2019). In the case of pineapple, Cunha et al. (2020) found that CND was better at capturing nutrient imbalances affecting fruit development and ripening stages, suggesting that it is a more sensitive tool for managing the nutrition of fruit crops. However, for all sample sizes considered, Cunha et al. (2020) found that CND was better at capturing nutrient imbalances affecting fruit development and ripening stages, suggesting that it is a more sensitive tool for managing

the nutrition of fruit crops. However, for all sample sizes considered, the DRIS method was more sensitive to identifying N, P, and K balance in pineapple leaves when the situation was true (Fig. 3, B).

Then, the CND model was more appropriate to identify situations where nutrients were deficient or excessive. Using the CND method may be more suitable for leaves with lower or excessive nutrient contents, despite its lower sensitivity to identify non-nutritional problems. Therefore, if low productivity is due to nutritional issues, applying the CND method for nutritional diagnosis could lead to reliable recommendations for correcting imbalances and increasing crop productivity. CND was connected to DRIS and M-DRIS but, being based on compositional data analysis and principal component analysis had greater potential for improving plant leaf diagnosis (Parent & Dafir, 1992).

Furthermore, a comparison of the diagnostic precision (positive predictive value) of DRIS, M-DRIS, and CND models revealed that CND was the most precise in detecting correctly deficiency and excess to the total number of deficiency and excess cases, respectively for N, P and K nutrients, followed by the M-DRIS model (Fig. 4, A and C). Kumar et al. (2003) showed that CND appeared to be more sensitive and efficient for projecting nutrient imbalances in turmeric. CND was the sensitive diagnosis and could be instrumental in adjusting fertilization to crop needs after crop emergence (Kumar et al., 2003). However, the DRIS model was more precise in detecting correctly adequacy (sufficiency) to the total number of adequacy cases for N, P, and K nutrients in pineapple leaves (Fig. 4, B). Fig. 4, D showed the accuracy of DRIS, M-DRIS, and CND models in function of sample size.

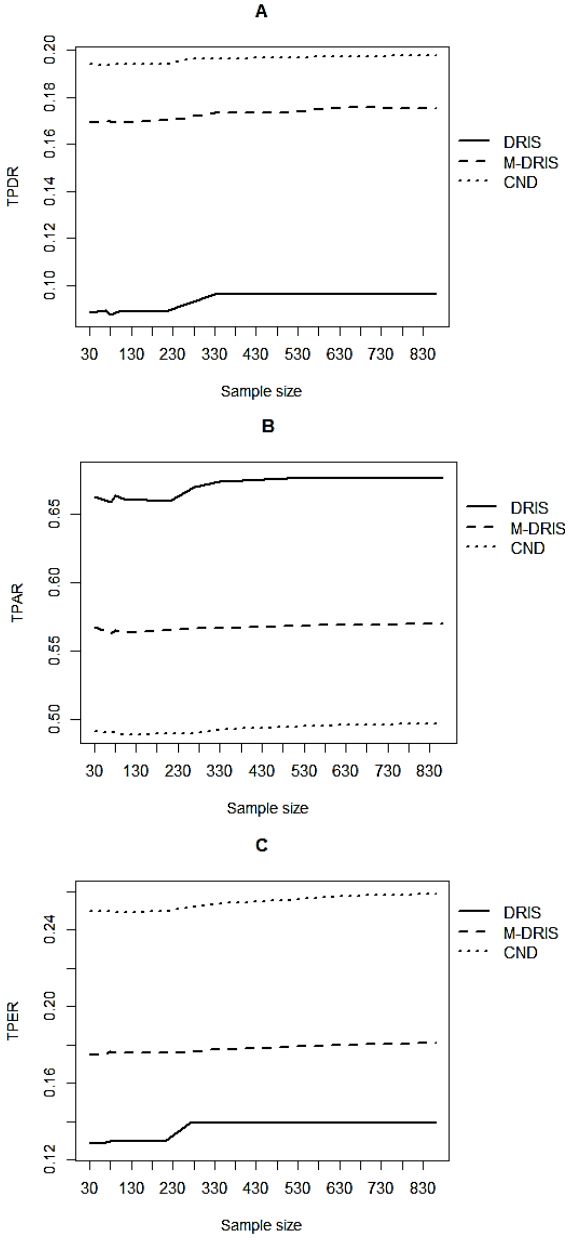

Figure 3. Sensitivity of DRIS, M-DRIS and CND models.

A = True Positive Deficiency Rate diagnosed by the models, B = True Positive Adequate Rate diagnosed by the models and C = True Positive Excess Rate diagnosed by the models.

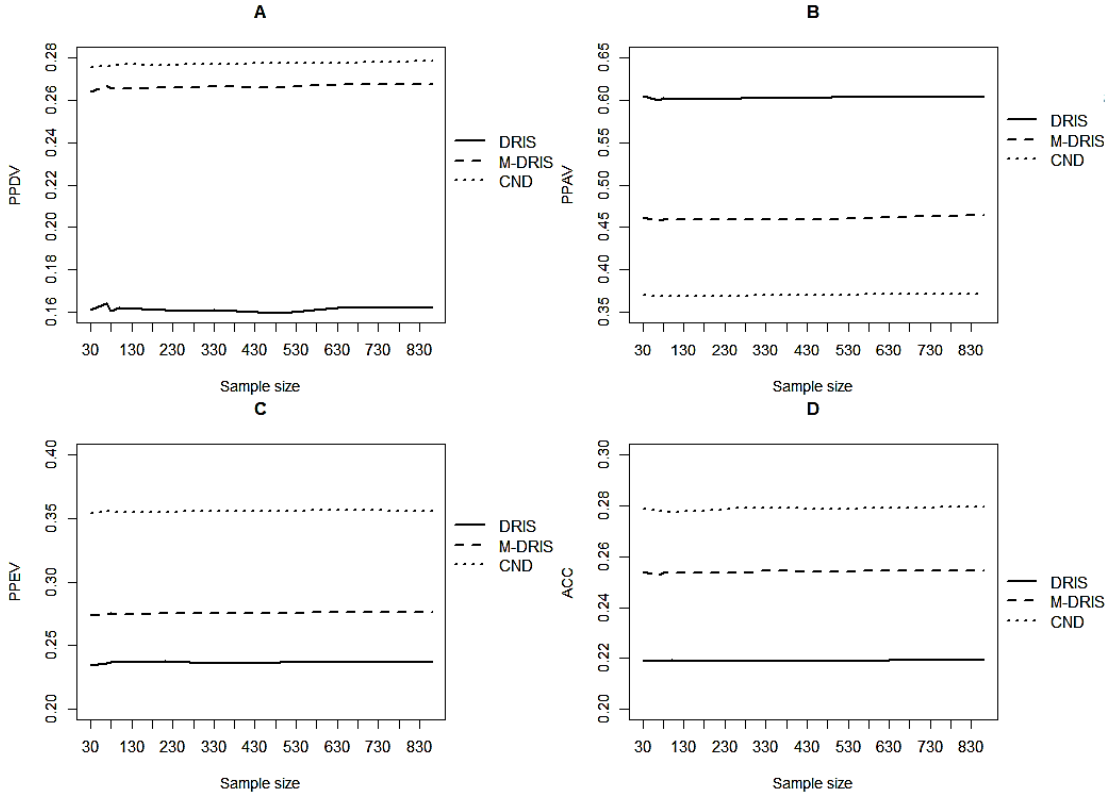

Figure 4. Positive predictive values and accuracy of DRIS, M-DRIS and CND models.
A = Positive Predictive Deficiency Value of the models, B = Positive Predictive Adequate Value of the models, C = Positive Predictive Excess Value of the models and D = Accuracy of the models.

From this figure, we saw that, for all sample sizes considered, the CND model was the most accurate (average accuracy of 27.86%) for diagnosing N, P, and K nutrients in pineapple leaves, followed by the M-DRIS method (average accuracy of 25.39%) and finally the DRIS method (average accuracy of 21.91%). The DRIS and M-DRIS methods were reportedly inferior CND in diagnosing imbalances as they assumed additivity of dual ratios (Parent & Dafir, 1992). The performance of the models varied with sample size. But, from the data size of 330, there was no higher variation in the DRIS, M-DRIS, and CND models' accuracy. The nutrient status of interest when we have low agricultural productivity is nutrient deficiency and to identify this situation, the CND model was the most appropriate, sensitive, accurate, and efficient, compared to the other models. Thes findings are consistent with the work of Tadayon et al. (2023) who conclude that CND is a better technique for assessing nutrient excesses, deficits, or balance in plant tissue. It is a multivariate approach and feneficial over the bivariate Diagnosis and Recommendation Integrated System (DRIS) techniques and conventional univariate critical value (CV) methodologies (Lisboa et al., 2024). Multivariate CND technique is superior for increased diagnostic precision for diagnosing mineral disorders when multiple nutrients are expected to limit yield simultaneously (Savita et al., 2016). Thus, in comparison to DRIS, the CND approach offers a stronger foundation for future advancements in foliar diagnostics.

CONCLUSIONS

This study compared the performance of three different systems, DRIS, M-DRIS, and CND, for diagnosing pineapple leaf nutrient levels while varying the sample size. When compared to DRIS and M-DRIS, CND performed better overall in terms of sensitivity, positive predictive value, and accuracy. Although the DRIS and M-DRIS models demonstrated certain advantages, especially in establishing nutritional balances, the CND method was more successful in detecting nutrient excess and deficiencies. Future works may focus on the comparison of the diagnosis methods for the micronutrients such as zinc, Br also essential for plant growth.

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