Clinical Nutrition ESPEN xxx (xxxx) xxx

Contents lists available at ScienceDirect

Clinical Nutrition ESPEN

journal homepage: http://www.clinicalnutritionespen.com

Letter to the Editor

Interpreting IDDSI-linked nutrient patterns: From correlations to compositional modules

Keywords:
IDDSI
Oral nutritional supplements
Principal component analysis
Feature clustering
Unsupervised analysis

1. Background and context

Detopoulou et al. systematically profiled 40 available oral nutritional supplements with the standardized International Dysphagia Diet Standardisation Initiative (IDDSI) Flow Test and related IDDSI levels to energy and macronutrients using Spearman's rank correlations and Principal Components Analysis (PCA) [1]. They reported a median energy density of 1.50 kcal/mL, positive associations of residual volume and IDDSI level with energy, protein, fat, and fiber (Table 2), and three rotated components—energy/fat, carbohydrate, and IDDSI level/fiber—explaining 80.5 % of variance (Table 3), with Figures 2–3 supporting IDDSI-aligned product selection. These contributions are substantial and commendable; however, their multivariate interpretation—particularly the reliance on PCA—warrants further discussion.

2. Distributional considerations

First, distributional imbalance can reshape apparent associations. In this sample, IDDSI 0 comprises 21 products (52.5 %) and IDDSI 1 10 products (25 %), so approximately 77.5 % of items cluster in levels 0–1 (Results, Table 1). Under such concentration, within-level homogeneity in viscosity, fiber, fat, and energy density can induce joint variation among multiple nutritional variables; the observed positive correlations of residual volume and IDDSI level with several macronutrients (Table 2) may therefore be partly shaped by a common-cause pattern rather than exclusively reflecting autonomous nutrient–nutrient dependencies. Brief sensitivity checks—e.g., IDDSI-controlled partial correlations or within-level (0 or 1) analyses—could probe this possibility while preserving their framing [2].

3. Multivariate structural limits

Second, when a strong categorical driver organizes formulation choices, reliance on PCA can limit how multivariate structure is represented. They extract three components explaining 80.5 % variance (Table 3), yet PCA's linear, orthogonal projection may underrepresent hierarchical or nonlinear groupings in which IDDSI-linked thickening (e.g., via fiber) shapes multiple variables [3,4]. The joint loading of IDDSI level and fiber is consistent with such a mechanism and suggests value in reframing variables as modules, not as isolated pairs, to align statistical summaries with formulation logic and clinical decision-making. These perspectives highlight the value of viewing compositional and rheological properties through a unified multivariate lens rather than isolated pairwise relations.

4. Proposed analytical refinements

Against this backdrop, we recommend emphasizing unsupervised, feature-centric approaches—specifically, hierarchical Feature Agglomeration and Highly Variable Feature Selection—to complement the pipeline. Feature Agglomeration groups variables by behavioral similarity (e.g., correlation or cosine distance), surfacing coherent nutrient modules that can be directly communicated and actioned clinically; Highly Variable Feature Selection highlights features with the greatest dispersion, reducing redundancy while foregrounding dominant sources of variation [5]. When applied jointly, these strategies shift the emphasis from lists of pairwise correlations toward structured components with shared properties, thereby enriching the interpretation of Tables 1–3 and Figures 2–3 without undue reliance on linear projections.

5. Translational implications

In conclusion, Detopoulou et al. provide a valuable foundation for IDDSI-aligned product selection and for integrating compositional information with texture-based categorization. Accounting for potential common-cause effects tied to category concentration and reframing variables as modules can sharpen reproducibility and clarify clinical decision pathways. Such analytical steps would strengthen the translational value of their findings by linking IDDSI-based texture classification more explicitly to nutritional architecture.

Disclosures

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

https://doi.org/10.1016/j.clnesp.2026.102982

Please cite this article as: S. Oka, K. Yoshida and Y. Takefuji, Interpreting IDDSI-linked nutrient patterns: From correlations to compositional modules, Clinical Nutrition ESPEN, https://doi.org/10.1016/j.clnesp.2026.102982

CRediT authorship contribution statement

Souichi Oka: Writing – original draft, Conceptualization. Kiyo Yoshida: Investigation. Yoshiyasu Takefuji: Writing – review & editing, Supervision, Project administration.

Data availability statement

Data availability: No new data were created or analyzed in this study.

Funding source

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

References

[1] Detopoulou P, Grammatikopoulou MG, Lytra E, et al. Determination of the international dysphagia diet standardization initiative level of commercially available oral nutritional supplements. Clin Nutr ESPEN 2025;67:404–9. https://doi.org/10.1016/j.clnesp.2025.03.022.

[2] Yao Y, Ochoa A. Limitations of principal components in quantitative genetic association models for human studies. eLife 2023;12:e79238. https://doi.org/10.7554/eLife.79238.

[3] Elhaik E. Principal component analyses (PCA)-based findings in population genetic studies are highly biased and must be reevaluated. Sci Rep 2022;12(1):14683. https://doi.org/10.1038/s41598-022-18634-2.

[4] Mohseni N, Elhaik E. Biases of Principal Component Analysis (PCA) in physical anthropology studies require a reevaluation of evolutionary insights. eLife 2024;13. https://doi.org/10.7554/eLife.94685. RP94685.

[5] Xie Y, Jing Z, Pan H, Xu X, Fang Q. Redefining the high variable genes by optimized LOESS regression with positive ratio. BMC Bioinf 2025;26(1):104. https://doi.org/10.1186/s12859-025-05678-9.

Souichi Oka*, Kiyo Yoshida
Science Park Corporation, 3-24-9 Iriya-Nishi, Zama-shi, Kanagawa 252-0029, Japan

Yoshiyasu Takefuji
Faculty of Data Science, Musashino University, 3-3-3 Ariake Koto-ku, Tokyo 135-8181, Japan
E-mail address: takefuji@keio.jp.

* Corresponding author. Science Park Corporation, 3-24-9 Iriya-Nishi, Zama-shi, Kanagawa 252-0029, Japan.
E-mail addresses: souichi.oka@sciencepark.co.jp (S. Oka), kyoshida@sciencepark.co.jp (K. Yoshida).

6 February 2026

Please cite this article as: S. Oka, K. Yoshida and Y. Takefuji, Interpreting IDDSI-linked nutrient patterns: From correlations to compositional modules, Clinical Nutrition ESPEN, https://doi.org/10.1016/j.clnesp.2026.102982