HemoVita:
A Context-Aware System for Micronutrient Deficiency Assessment and Recommendation

by

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Contributions

Selma Doganata served as the project lead and backend developer. She designed the system architecture and implemented the backend recommendation engine, including cutoff-based lab interpretation, micronutrient consolidation, interaction-aware supplement scheduling, and food recommendation logic. She developed the demographic risk estimation module using a contextual bandit approach, implemented fallback strategies for sparse data, curated all core datasets, built the FastAPI backend, integrated dynamic report generation, and led system evaluation.

Jubyaid Uddin was responsible for frontend development and system integration. He built the web-based interface using Next.js, integrated frontend workflows with the backend API, and implemented user authentication, request validation, and database interactions to ensure reliable end-to-end operation.

Rahat Rahman contributed to research and nutritional modeling. He reviewed epidemiological literature on micronutrient deficiencies, supported validation of demographic risk outputs, assisted in constructing and validating the nutrient interaction network, and helped frame the system as a decision-support tool grounded in nutritional science.

Abstract

Micronutrient deficiencies affect over two billion people worldwide, yet are often inadequately addressed through routine interpretation of laboratory blood results. Clinical feedback typically identifies isolated deficiencies but offers limited guidance on demographic context or nutrient interactions that influence absorption and effectiveness. This project presents HemoVita, a context-aware decision-support system for micronutrient deficiency assessment and personalized nutritional recommendation. HemoVita evaluates laboratory blood data using clinically grounded, rule-based thresholds combined with demographic and population-level information, including age, biological sex, pregnancy status, and geographic population. To complement deterministic classification, the system incorporates a reinforcement learning–based module that estimates deficiency risk under varying contextual conditions. In addition, HemoVita models known nutrient absorption synergies and conflicts, enabling the generation of interaction-aware supplement schedules and dietary suggestions. Evaluation using representative laboratory profiles demonstrates that HemoVita consistently identifies single and multi-nutrient deficiency patterns and produces interpretable, structured recommendations suitable for integration into a web-based application.

1. Introduction

Micronutrient deficiencies remain a widespread and persistent global health problem, affecting over two billion people worldwide. Deficiencies in essential vitamins and minerals such as iron, zinc, vitamin B12, folate, and vitamin D are linked to anemia, impaired development, weakened immune function, and increased morbidity. Despite this burden, existing blood screening practices largely prioritize disease detection rather than nutritional assessment. When micronutrient data is available, interpretation is often limited to static reference ranges, offering little guidance on how deficiencies should be addressed in practice.

Access to micronutrient screening and actionable nutritional guidance is uneven and frequently lacking in low-income and resource-constrained regions, where deficiency prevalence is highest. In these settings, healthcare infrastructure prioritizes acute disease management, and comprehensive micronutrient testing is rarely routine. As a result, populations most affected by nutritional deficiencies are often those with the least access to contextualized data or informed supplementation guidance. Even in higher-resource settings, individuals who receive laboratory results are commonly advised to supplement isolated deficiencies without consideration of demographic factors or nutrient interactions that influence absorption and effectiveness.

This project addresses these gaps through the design and implementation of HemoVita, a context-aware decision-support system for micronutrient deficiency assessment and personalized nutritional recommendation. HemoVita analyzes laboratory blood data using clinically grounded, rule-based thresholds while incorporating demographic and population-level context, including age, biological sex, pregnancy status, and geographic population. To complement deterministic classification, the system integrates a reinforcement learning–based module to estimate deficiency risk under varying contextual conditions. The project scope is limited to decision support and does not include clinical diagnosis or treatment.

The completed system produces structured, interpretable reports that identify potential micronutrient deficiencies, estimate contextual risk, and generate interaction-aware supplement schedules and dietary suggestions. Nutrient absorption synergies and conflicts are explicitly modeled to inform recommendation timing and composition. Evaluation using representative laboratory profiles demonstrates consistent identification of single and multi-nutrient deficiency patterns and coherent recommendation generation, supporting the feasibility of an explainable, hybrid approach to personalized micronutrient decision support.

2. Literature Review

Previous research and implementation of AI in healthcare and analyzing blood results showed that no current technology delivered the comprehensive analysis and recommendation system that HemoVita provides. Only in the past year, a technology called BloodGPT has emerged, adopting a similar approach to HemoVita. It interprets blood results and is targeted towards clinicians and patients alike. After sampling BloodGPT technology, a key feature that it misses and HemoVita provides is at risk factors based on the individual's ethnic background. Ethnicity has a lot to do with how someone's body works and how they should live their lifestyle, and that is something that HemoVita pays attention to.

A related study titled "Deep forest model for diagnosing COVID-19 from routine blood tests" (AlJame et al 2021) addresses the early and accurate diagnosis of COVID-19. It reviews the techniques used to achieve successful COVID-19 screening, namely, with a method called deep forest. This uses AI as a diagnostic tool, whereas HemoVita leaves diagnosis to the doctors and addresses the issue of micronutrient deficiencies and patient accessibility, under the umbrella of public health. Another paper titled "Artificial intelligence in routine blood tests" (Santos-Silva 2024) explores the integration of artificial intelligence (AI) in routine blood tests for diagnosis, prognosis, and disease monitoring. Traditional clinical decision support systems rely on predefined biomarkers, potentially missing hidden patterns in blood test data. AI has the potential to extract subtle correlations that could improve diagnostic accuracy and enable early detection of various conditions, including anemia, diabetes, and heart disease. HemoVita uses predefined biomarkers and clinically accurate nutrient interactions to flag values outside the threshold for a given micronutrient and factors in the food recommendation engine. Initially, we planned to implement XGBoost and other supervised models, but we pivoted away because of the data accessible to us. HemoVita does have a micronutrient risk predictor; however, to determine the percent at risk an individual is for certain micronutrients based on geography.

Three other projects that we investigated are "Blood Analysis system", "Medgem", and "Hemo-Detect". The purpose of all three of these projects was to parse through blood reports and detect blood-related disorders using AI. It is clear that many projects and technologies exist to analyze blood results and provide a diagnosis for some diseases or predict a future disorder. HemoVita expands the scope to nutrition-based diagnostics and preventative healthcare. HemoVita is a crucial tool that can be used for public health applications around the world.

3. Methods and System Design

This section describes how HemoVita processes laboratory blood data and demographic context to produce micronutrient assessments, recommendations, and risk estimates. The system explicitly separates deterministic, guideline-based logic from learned population-level risk modeling to preserve interpretability, traceability, and robustness under missing data.

3.1 Overall Methodology

HemoVita follows a multi-stage processing pipeline. It takes two main inputs:

(1) a set of laboratory blood values indexed by biomarker name, and

(2) a demographic profile containing age, biological sex, pregnancy status, population group, and country.

The system processes these inputs in the following order:

1. Laboratory values are interpreted using clinical cutoff thresholds.
2. Abnormal markers are mapped to micronutrient targets.
3. Supplements are scheduled using nutrient interaction rules.
4. Food-based recommendations are generated for deficient nutrients.
5. A demographic-only risk model estimates background deficiency risk.
6. All outputs are combined into a structured report.

Each stage produces explicit intermediate outputs, making the pipeline easy to inspect and test.

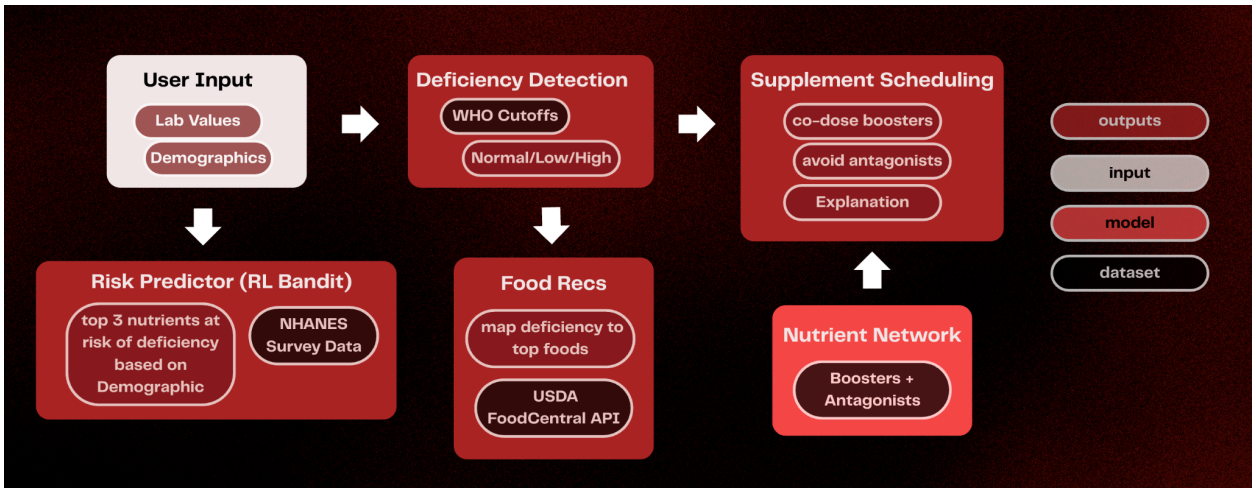


Figure 3.1: Complete HemoVita system workflow, showing how laboratory inputs and demographic context propagate through deficiency detection, risk estimation, nutrient interaction modeling, and recommendation generation.

3.2 System Architecture

HemoVita is implemented as a modular backend system with a web-based frontend. All interpretation and recommendation logic runs on the backend to ensure consistent behavior. The backend is built with FastAPI and exposes two endpoints. The main endpoint, /api/report, runs the full pipeline and returns the final report. A second endpoint, /api/risk-profile, exposes only the demographic risk model and is used for testing and debugging.

All clinical knowledge and nutritional rules are stored in structured datasets rather than hardcoded logic. These include laboratory cutoff tables, nutrient interaction data, food composition data, and population-level deficiency statistics. Updating these datasets does not require changing application code.

The Next.js frontend acts purely as a client: it validates input, forwards requests, and renders results. Authentication and data persistence are handled separately and do not influence recommendation logic.

3.3 Recommendation Engine

The recommendation engine consists of four main components: lab interpretation, nutrient targeting, supplement scheduling, and food recommendations.

3.3.1 Laboratory Interpretation

Each lab value is mapped to a standardized biomarker definition that specifies the associated micronutrient, population group, unit, and cutoff type. Cutoff thresholds come from structured reference tables derived from widely accepted public health sources, including World Health Organization (WHO) guidelines and International Zinc Nutrition Consultative Group (IZiNCG) recommendations.

For each biomarker, the engine selects the appropriate cutoff values based on population and unit. The observed value is then classified as:

- low if below the lower threshold
- high if above the upper threshold
- normal if within range
- unknown if the value or mapping is missing

Discrete labels are used intentionally to avoid false precision and to keep results consistent across laboratories.

3.3.2 Nutrient Targeting and Consolidation

After classification, biomarkers are mapped to micronutrient targets. Multiple biomarkers that reflect the same physiological deficiency are consolidated into a single target. For example, low hemoglobin, low MCV, and low ferritin are treated together as indicators of iron deficiency. This consolidation prevents duplicate recommendations and simplifies later scheduling.

3.3.3 Supplement Scheduling and Fallback Strategy

Supplements are assigned to three fixed time slots: morning, midday, and evening. Each nutrient target must be placed into exactly one slot. Scheduling is guided by nutrient interaction rules derived from a curated interaction dataset. Two types of interactions are used:

- Synergistic interactions ("boosts") encourage co-dosing.
- Antagonistic interactions ("inhibits") prevent nutrients from being scheduled together.

Before applying rules, interaction nodes are normalized so that biomarker-level identifiers map correctly to supplement targets. The scheduling algorithm works as follows:

1. Nutrient targets are processed one by one.
2. Each target is placed into the earliest slot that does not conflict with nutrients already assigned to that slot.
3. If no conflict-free slot exists, the nutrient is placed into the final slot as a deterministic fallback.
4. After initial placement, synergistic booster nutrients are added to the same slot when possible and safe.

This approach guarantees that all deficiencies are addressed, even when interactions are dense or conflicting.

3.3.4 Interaction-Based Explanations

The same interaction data used for scheduling is also used to generate explanations. When nutrients are co-dosed due to a known synergy, the system explains why. When nutrients are separated due to antagonism, the system explains that separation. Because explanations and scheduling rules come from the same data source, the system avoids inconsistent or post-hoc justifications.

3.3.5 Food Recommendation Module

Food recommendations are generated to complement supplement guidance. Each micronutrient target maps to a nutrient bundle used in a curated food dataset. Foods are selected based on nutrient density and can be filtered by dietary preference. Each recommendation includes the food name, a typical serving size, and a category label. This module is intended to support dietary improvement rather than replace supplementation.

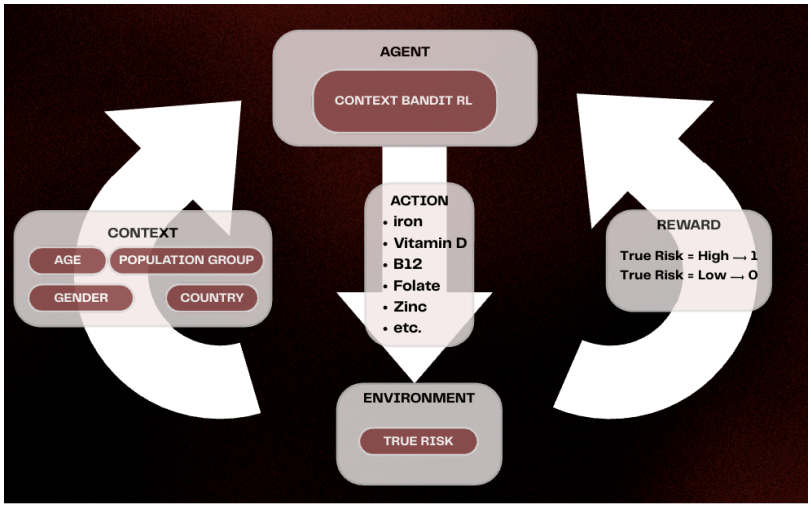
3.4 Demographic Risk Estimation

In addition to laboratory-based interpretation, HemoVita estimates demographic micronutrient deficiency risk to provide population-level context. This component operates independently of laboratory values and does not influence supplement or food recommendations. Its purpose is to provide a background prior indicating which micronutrient deficiencies are more prevalent among individuals with similar demographic profiles.

3.4.1 Contextual Bandit Model (LinUCB)

Demographic risk estimation is implemented using a contextual bandit model based on LinUCB, trained exclusively on population-level data from NHANES. Each micronutrient is treated as an action corresponding to the selection of a deficiency to evaluate, while the context vector consists of demographic attributes including country, population group, gender, and age. Because individual-level deficiency labels are unavailable, population-level prevalence values define the learning environment. During training, deficiency outcomes are simulated by sampling Bernoulli rewards from these prevalence probabilities, where a reward of 1 represents a simulated deficiency and 0 represents no deficiency. This approach converts population statistics into synthetic individual feedback suitable for reinforcement learning. LinUCB selects micronutrient actions using an upper-confidence strategy that balances exploitation of micronutrients with high estimated deficiency risk and exploration of micronutrients with greater uncertainty. Model parameters are updated after each simulated outcome, allowing the model to learn stable associations between demographic context and micronutrient deficiency risk. At inference time, the trained model produces ranked risk scores for micronutrients given the input demographic profile. The model does not use laboratory measurements, does not diagnose deficiencies, and functions strictly as a population-level prior.

Figure 3.4.1: Contextual bandit formulation used for demographic risk estimation, including the context variables, action space, and reward signal derived from population-level prevalence data.



3.4.2 Baseline Risk and Explicit Fallback

When country-specific data is unavailable, HemoVita applies a deterministic fallback strategy using precomputed baseline risk tables derived from the same dataset. If country-level data is missing, population–gender averages are used; if those are unavailable, global averages are applied. All fallback usage is explicitly disclosed in the output.

3.5 Report Synthesis

The final report aggregates all outputs into a structured response returned by the /api/report endpoint. This includes lab classifications, supplement schedules, food recommendations, interaction explanations, a narrative summary, and an optional demographic risk profile. By keeping recommendations deterministic and confining learning-based components to demographic risk estimation, HemoVita remains transparent while still accounting for population-level variation.

4. Web Application Design and Implementation

This section outlines the design and implementation of the HemoVita web application, developed during Semester 2 of the senior project. The functional web app enables users to submit lab data, receive personalized micronutrient risk assessments, and access structured health recommendations through an interactive interface..

4.1 Application Type

HemoVita is a web application with a client-server architecture, featuring a frontend user interface and a backend API. The backend provides RESTful endpoints that process laboratory

biomarker inputs and demographic data, and return structured JSON responses. The frontend uses these responses to display risk summaries, supplement schedules, food recommendations, and historical reports.

4.2 System Modules

4.2.1 Report Submission Module

This module allows users to input laboratory biomarker values (e.g., hemoglobin, ferritin, vitamin levels) along with demographic data such as age, sex, country, and population group. The frontend validates inputs before submitting them to the backend API. Upon submission, the data is persisted in the database and forwarded to the analysis pipeline.

4.2.2 Risk Evaluation Endpoint

The risk evaluation endpoint processes demographic information and biomarker data to estimate micronutrient deficiency risks. It leverages population-level statistics and normalization logic derived from curated datasets. The output includes:

- An overall risk score
- A categorical risk bucket (low, moderate, high)
- Per-micronutrient predicted risk values
- A natural-language summary explaining the results

4.2.3 Network Graph Endpoint

This module generates nutrient interaction relationships using graph-based representations. Nutrients are modeled as nodes, while biological or absorption-related interactions form edges. Although the current implementation uses NetworkX for backend graph logic, the system is designed to support future visualization enhancements, including interactive and 3D network displays.

4.2.4 Report Rendering Module

The report rendering module converts backend JSON responses into structured UI components. These include:

- Marker classification tables (normal, low, high)
- Supplement schedules grouped by time of day
- Food recommendations per micronutrient
- Risk summaries and historical lab reports

4.3 Technology Stack:

4.3.1 Backend

- Python as the primary backend language
- FastAPI for building high-performance REST APIs
- Pydantic for request and response validation
- Pandas and NumPy for data preprocessing, normalization, and statistical analysis

4.3.2 Frontend

- Next.js for server-side rendering and routing
- React for building reusable UI components
- TypeScript for improved type safety and maintainability

4.3.3 Data and Visualization

- Pandas and NumPy for structured data handling
- NetworkX for modeling micronutrient interaction graphs
- Interactive or 3D network visualization

4.4 Implementation Challenges:

4.4.1 Data Normalization Across Sources

Micronutrient data came from various sources with inconsistent naming, units, and population categories, necessitating extensive preprocessing. This was resolved by creating standardized schemas and mapping layers to align all datasets before analysis.

4.4.2 JSON Serialization for Frontend Integration

Serialization issues with complex Python objects, like NumPy types and graph structures, were resolved by converting outputs to JSON-safe formats and using Pydantic models for response schemas.

5. Results and Evaluation

HemoVita was evaluated using three scenarios targeting distinct system components: (1) an end-to-end multi-deficiency case, (2) a normal control case to verify non-overrecommendation, and (3) a demographic-only query to qualitatively assess the reinforcement learning–based risk model. All tests were executed through the FastAPI backend using curl requests (Listings 1–3).

5.1 End-to-End Recommendation Behavior

Setup. A 21-year-old female (United States, population: Women) with low hemoglobin, MCV, ferritin, vitamin B12, and vitamin D, and normal calcium and magnesium.

```
(base) selmadoganata@Selmas-Air hemovita % curl -X POST http://127.0.0.1:8000/api/report \
  -H "Content-Type: application/json" \
  -d '{
    "labs": {
      "Hemoglobin": 11.2,
      "MCV": 78.0,
      "ferritin": 10.0,
      "vitamin_B12": 150.0,
      "vitamin_D": 25.0,
      "calcium": 2.3,
      "magnesium": 0.8
    },
    "patient": {
      "age": 21,
      "sex": "female",
      "pregnant": false,
      "country": "United States",
      "population": "Women"
    }
  }'
```

Results.

Biomarker	Value	Classification
Hemoglobin	11.2	Low
MCV	78.0	Low
Ferritin	10.0	Low
Vitamin B12	150.0	Low
Vitamin D	25.0	Low
Calcium	2.3	Normal
Magnesium	0.8	Normal

Time of Day	Supplements	Notes
Morning	Iron, Vitamin B12, Vitamin C	Vitamin C enhances non-heme iron absorption
Midday	Vitamin D, Magnesium	Magnesium required for vitamin C activation.

Evening	-	-

Nutrient	Top Ranked Food	Typical Serving
Iron	Beef Liver	85 g
Vitamin B12	Clams	100 g
Vitamin D	Salmon	85 g

All abnormal markers were correctly classified as low, and anemia-related biomarkers were consolidated into a single iron deficiency target. The supplement plan scheduled iron, vitamin C, and vitamin B12 together in the morning, and vitamin D with magnesium at midday. These decisions followed interaction rules: vitamin C enhances iron absorption, magnesium supports vitamin D activation, and iron was separated from vitamin D to avoid interference. Each placement was accompanied by a network-based explanation. Food recommendations matched the identified deficiencies and prioritized nutrient-dense sources, demonstrating coherent, interaction-aware guidance grounded in clinical cutoffs.

5.2 Control Case: Non-Overrecommendation

Setup. The same demographic profile with all laboratory values within normal ranges.

```
(base) selmadoganata@Selmas-Air hemovita % curl -X POST http://127.0.0.1:8000/api/report \
  -H "Content-Type: application/json" \
  -d '{
    "labs": {
      "Hemoglobin": 13.2,
      "MCV": 89.0,
      "ferritin": 45.0,
      "vitamin_B12": 420.0,
      "vitamin_D": 75.0,
      "calcium": 2.35,
      "magnesium": 0.85
    },
    "patient": {
      "age": 21,
      "sex": "female",
      "pregnant": false,
      "country": "United States",
      "population": "Women"
    }
  }'
```

Results.

Biomarker	Value	Classification
Hemoglobin	13.2	Normal
MCV	89.0	Normal
Ferritin	45.0	Normal

Vitamin B12	420.0	Normal
Vitamin D	75.0	Normal
Calcium	2.35	Normal
Magnesium	0.85	Normal

All biomarkers were labeled normal, no supplements were scheduled, and no food recommendations were produced. The report explicitly stated that no intervention was required, confirming that HemoVita does not over-prescribe.

5.3 Demographic Risk Model Validation

Setup. A demographic-only query representing a 21-year-old woman in Bangladesh, evaluated using the /api/risk-profile endpoint.

```
(base) selmadoganata@Selmas-Air hemovita % curl -X POST http://127.0.0.1:8000/api/risk-profile \
  -H "Content-Type: application/json" \
  -d '{
    "country": "Bangladesh",
    "population": "Women",
    "gender": "Female",
    "age": 21
  }'
```

Results.

Micronutrient	Predicted Risk
Vitamin A	~64.0%
Zinc	~32.3%
Vitamin D	~27.9%

The model ranked vitamin A (~64.0%), zinc (~32.3%), and vitamin D (~27.9%) as the highest predicted deficiency risks. These rankings align with well-documented epidemiological trends among Bangladeshi women. Metadata confirmed that country-specific data was used without fallback. Because the model is trained on population-level prevalence rather than individual clinical labels, evaluation is based on alignment with known public health patterns and stable behavior across contexts rather than supervised accuracy metrics. The model functions strictly as a contextual prior and does not override lab-based recommendations.

5.4 Summary

Across all scenarios, HemoVita demonstrated accurate cutoff-based classification, conservative recommendation triggering, interaction-aware supplement scheduling, aligned food suggestions, and a demographic risk model whose outputs reflect known population trends.

6. Discussion

HemoVita's goal was to create an interpretable, context-aware system for micronutrient deficiency assessment and nutritional recommendation. This goal was met through a hybrid design combining deterministic, guideline-based laboratory interpretation with demographic risk estimation. The system consistently identified deficiencies, avoided overrecommendation in normal cases, and produced interaction-aware recommendations suitable for web deployment.

Initial plans to use supervised models such as XGBoost were abandoned due to data limitations. Available datasets provide population-level prevalence rather than individual-level labels, making supervised classification unreliable and poorly aligned with the project's emphasis on interpretability. The pivot to a reinforcement learning–based contextual bandit allowed demographic risk to be modeled as a population-level prior without relying on unsupported individual predictions.

A key strength of the final system is the strict separation between transparent recommendation logic and learning-based risk estimation. Laboratory cutoffs and nutrient interaction rules remain fully interpretable, while the risk model provides context without influencing recommendations. Limitations include dependence on available laboratory testing and population-level data.

HemoVita is intentionally positioned as a decision-support tool rather than a diagnostic system, with conservative triggering, explicit explanations, and fallback disclosures supporting responsible use. Future work may expand data coverage, incorporate additional micronutrients, and explore uncertainty-aware extensions if suitable individual-level data becomes available. Overall, the final design meets the project objectives more effectively than the originally proposed supervised approach under real-world data constraints.

7. Conclusion

With over two billion people suffering from micronutrient deficiencies worldwide, HemoVita addresses a critical gap between micronutrient testing and actionable guidance. While blood tests can identify abnormal values, they rarely explain how deficiencies interact, how recommendations should be timed, or how demographic context influences nutritional risk. HemoVita demonstrates that these questions can be answered with a transparent, context-aware decision-support system grounded in clinical guidelines rather than opaque prediction models. By combining cutoff-based laboratory interpretation, explicit nutrient interaction modeling, and a reinforcement learning–based demographic risk estimator, HemoVita transforms isolated lab results into coherent, interpretable recommendations. The system consistently identifies meaningful deficiency patterns, avoids overrecommendation, and produces supplement and food guidance aligned with biological mechanisms and public health trends. Positioned explicitly as a decision-support tool, HemoVita supports both patients and clinicians by making nutritional insights understandable, explainable, and actionable. As micronutrient deficiencies remain widespread and under-addressed globally, systems like HemoVita are necessary to move beyond passive lab reporting toward equitable, context-sensitive nutritional care.

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9. Appendix


```
{
  "labels": {
    "Hemoglobin": "low",
    "MCV": "low",
    "ferritin": "low",
    "vitamin_B12": "low",
    "vitamin_D": "low",
    "calcium": "normal",
    "magnesium": "normal"
  },
  "supplement_plan": {
    "morning": [
      "iron",
      "vitamin_B12",
      "vitamin_C"
    ],
    "midday": [
      "vitamin_D",
      "magnesium"
    ],
    "evening": []
  },
  "foods": {
    "iron": [
      { "name": "Beef liver", "serving_g": 85, "category": "Meat" },
      { "name": "Oysters", "serving_g": 85, "category": "Fish/Shellfish" },
      { "name": "Beef (lean)", "serving_g": 85, "category": "Meat" },
      { "name": "Lentils (cooked)", "serving_g": 100, "category": "Legume" },
      { "name": "Chickpeas (cooked)", "serving_g": 100, "category": "Legume" }
    ],
    "vitamin_B12": [
      { "name": "Clams", "serving_g": 100, "category": "Other" },
      { "name": "Beef liver", "serving_g": 85, "category": "Meat" },
      { "name": "Trout", "serving_g": 85, "category": "Fish/Shellfish" },
      { "name": "Salmon", "serving_g": 85, "category": "Fish/Shellfish" },
      { "name": "Tuna", "serving_g": 85, "category": "Fish/Shellfish" }
    ],
    "vitamin_D": [
      { "name": "Salmon", "serving_g": 85, "category": "Fish/Shellfish" },
      { "name": "Trout", "serving_g": 85, "category": "Fish/Shellfish" },
      { "name": "Sardines", "serving_g": 85, "category": "Fish/Shellfish" },
      { "name": "Egg yolks", "serving_g": 100, "category": "Other" },
      { "name": "Fortified milk", "serving_g": 240, "category": "Dairy" }
    ]
  },
  "network_notes": [
    "Vitamin C and iron are scheduled together in the morning to enhance non-heme iron absorption (high confidence).",
    "Magnesium and vitamin D are co-dosed at midday because magnesium is required for vitamin D activation (moderate confidence).",
    "Iron is separated from vitamin D to avoid potential interference with iron utilization (low confidence)."
  ]
```

Figure 5.1: *Output of end-to-end multi-deficiency case curl command*


```
{
  "labels": {
    "Hemoglobin": "normal",
    "MCV": "normal",
    "ferritin": "normal",
    "vitamin_B12": "normal",
    "vitamin_D": "normal",
    "calcium": "normal",
    "magnesium": "normal"
  },

  "supplement_plan": {
    "morning": [],
    "midday": [],
    "evening": []
  },

  "foods": {},

  "report_note":
    "No supplements recommended based on current laboratory values."
}
```


Figure 5.2:*Output of Control Case Curl Command*


```
{
  "micronutrient_risks": [
    { "micronutrient": "vitamin_A", "predicted_risk": 0.64 },
    { "micronutrient": "zinc", "predicted_risk": 0.32 },
    { "micronutrient": "vitamin_D", "predicted_risk": 0.28 },
    { "micronutrient": "MCV", "predicted_risk": 0.27 },
    { "micronutrient": "magnesium", "predicted_risk": 0.20 },
    { "micronutrient": "vitamin_E", "predicted_risk": 0.19 }
  ],

  "summary_text":
    "Highest predicted deficiency risks from demographics alone: vitamin A, zinc, and vitamin D.",

  "meta": {
    "country": "Bangladesh",
    "population": "Women",
    "gender": "Female",
    "age": 21,
    "country_known": true,
    "fallback_used": false
  }
}
```

Figure 5.3: *Output of Demographic Risk Curl Command*

Figure 4.1:

Screenshot of the lab entry form displaying biomarker fields and demographic inputs.

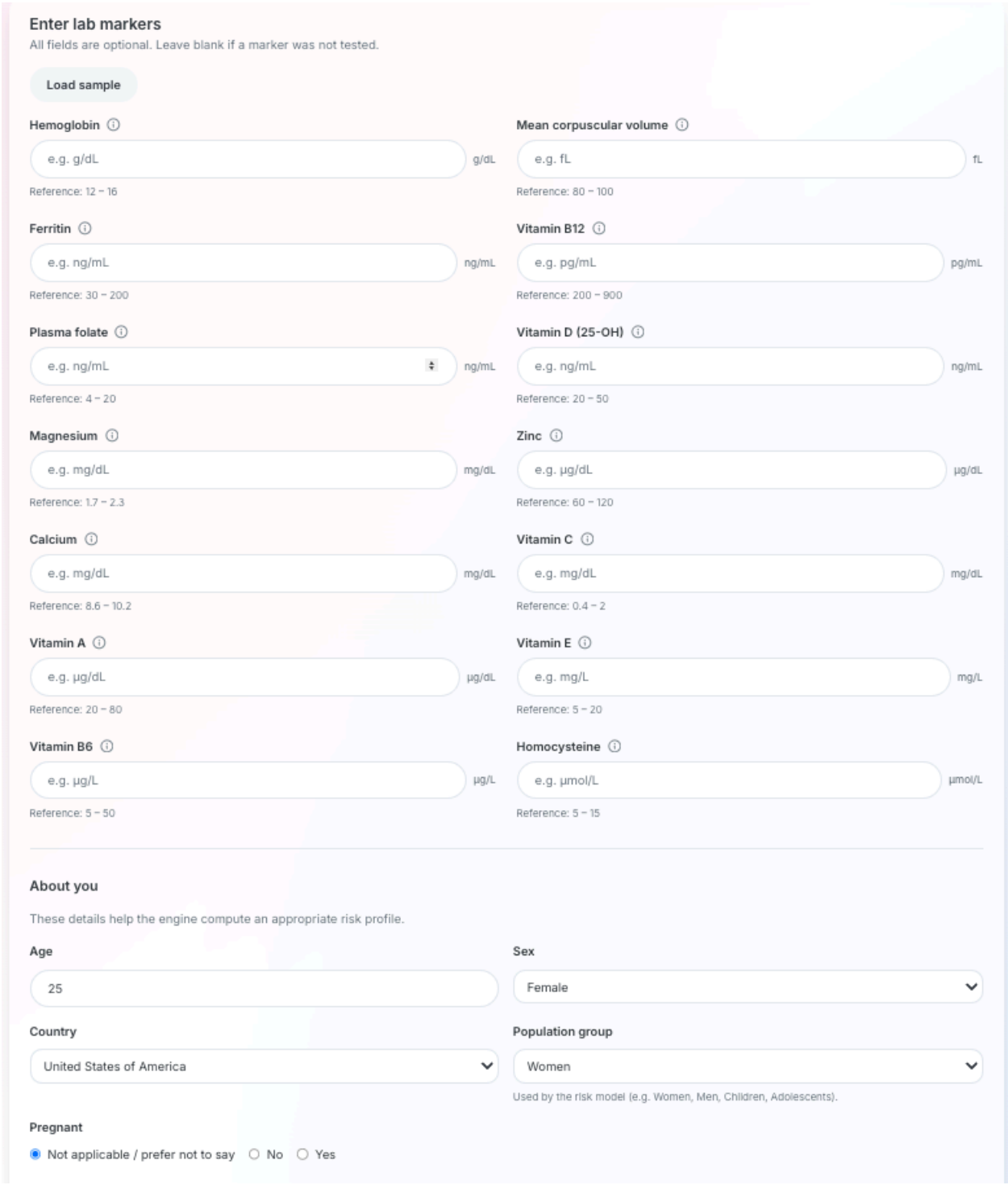


Figure 4.2:

Micronutrient risk overview displaying overall risk percentage and highest-risk nutrients.

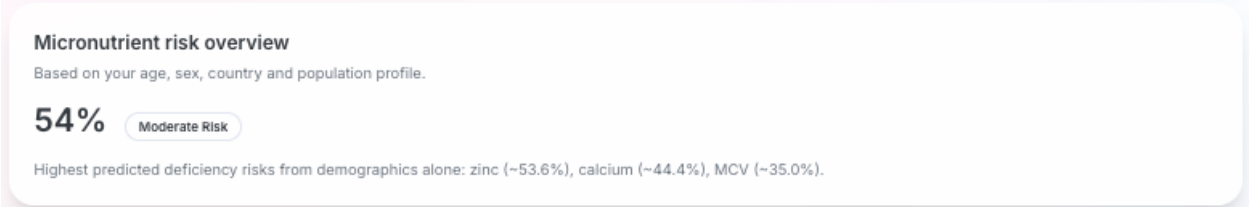


Figure 4.3:

Dashboard view showing marker classification table and supplement schedule.

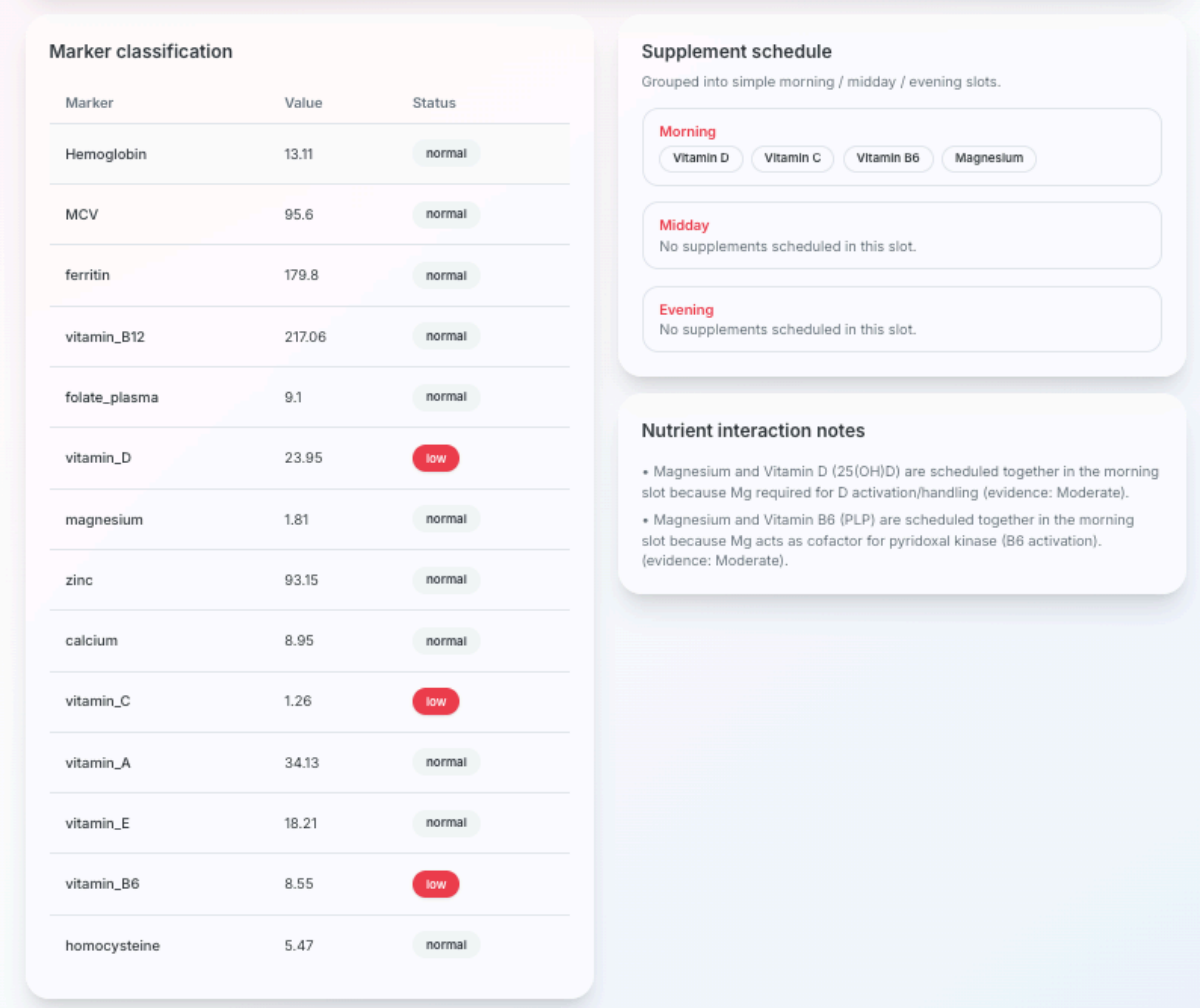


Figure 4.4:

Recommendation for food with highest micronutrient/mineral content per serving.

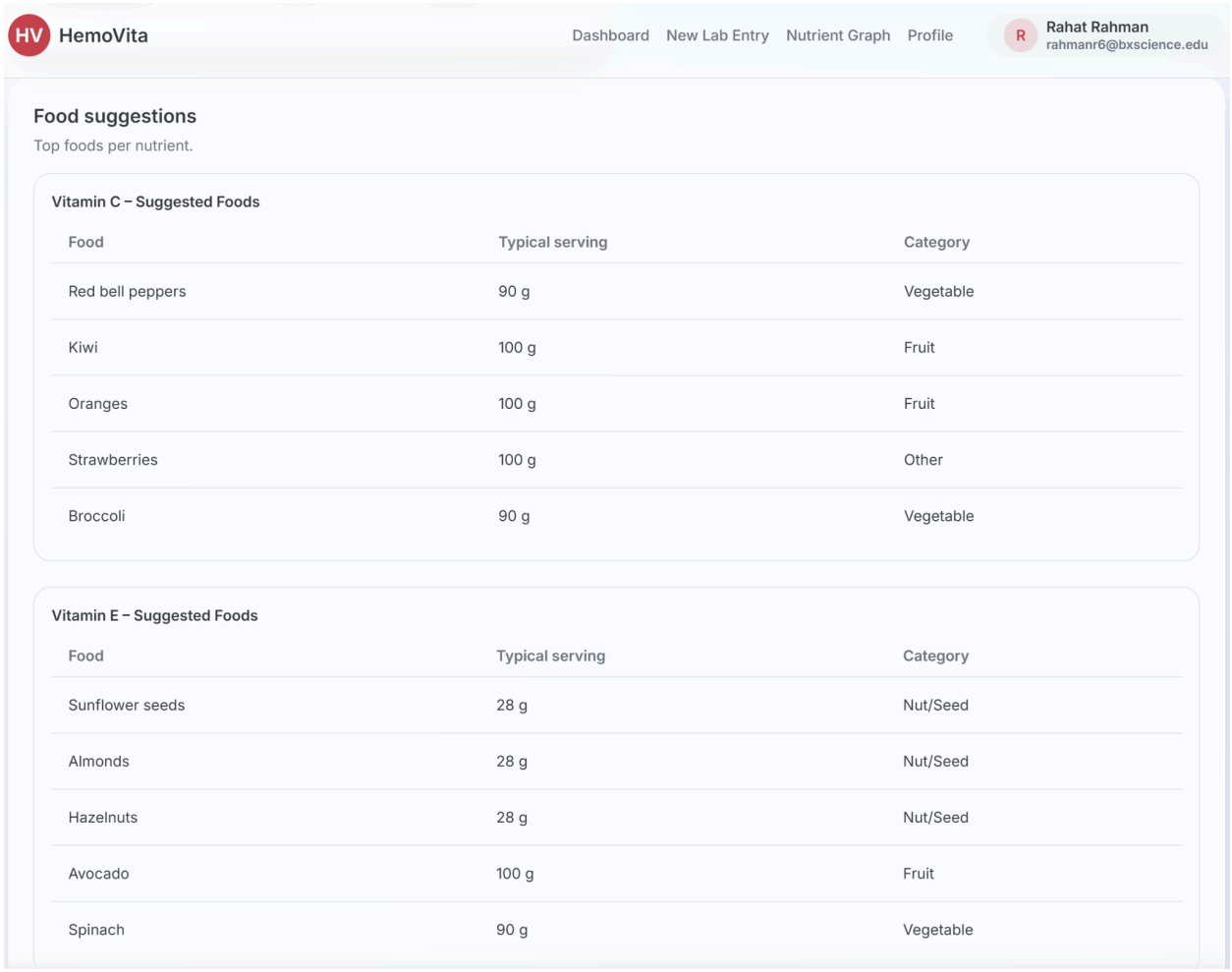
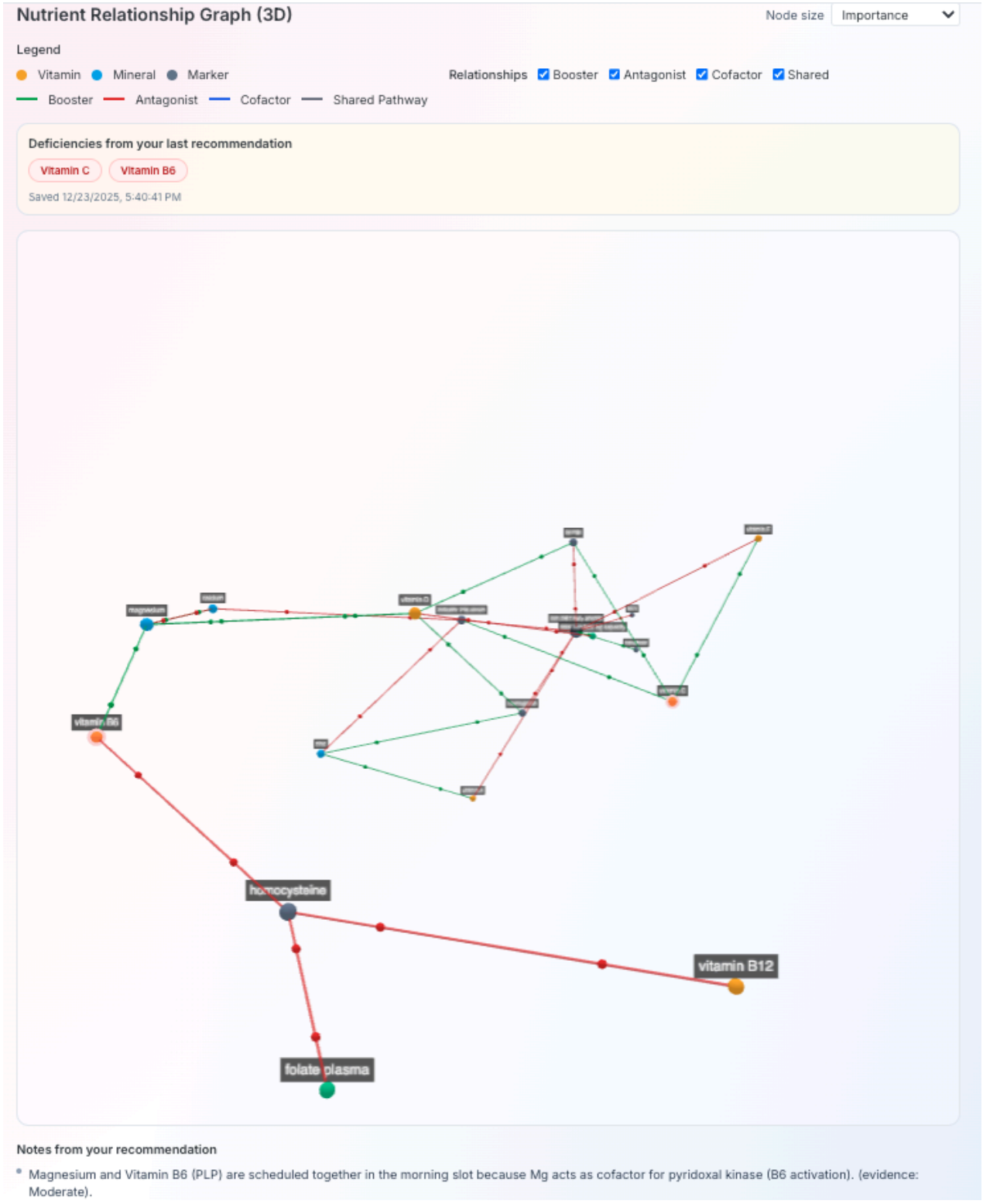


Figure 4.5 :

Conceptual diagram of nutrient relationships.