POLIS V12 – A Tensional Diagnostic Software: Architecture, Algorithms, and Clinical Implementation

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Abstract

The POLIS V12 tensional ontology models any system as a polis with three meshes (solid, liquid, gaseous). All real systems satisfy the closure condition $\varepsilon = \sum K_m(2 + K_m) = 0$, quantified by the disequilibrium index $\mathrm{IDT}^* \in [0, 1)$. This paper translates this mathematical framework into a software architecture for diagnostic medicine. The software inputs clinical measurements (blood tests, imaging, physiological signals), normalises each variable to $K_m = (v - T)/(v_{\max} - T)$ with $T = K_{\min}$, computes ε and IDT^*, identifies tensional phases, and recommends tensional interventions. Pseudocode, a modular software architecture, and a clinical validation plan with explicit falsification criteria are provided. The software is not a replacement for physicians but a decision support system grounded in a parameter-free, falsifiable theory.

Contents

1 Introduction

Classical diagnostic medicine relies on reference ranges and pattern recognition without a unified mathematical model of health and disease. POLIS V12 provides such a model: health corresponds to a stable Phase 4 state where all three meshes are coherent, and disease corresponds to local or global deviations from:

$$\varepsilon = \sum_m K_m(2 + K_m) = 0$$

The index $\text{IDT}^* = \varepsilon/(1 + \varepsilon)$ is a single scalar measuring the structural distance from tensional equilibrium. This paper describes how to compute IDT^* from clinical data and use it to build a diagnostic decision support system.

2 Tensional Framework

For any dataset of clinical variables $v_1, v_2, \ldots, v_n$:

- Tensional origin: $T = \min(v_1, \ldots, v_n)$
- Normalised structural value: $K_m = (v_m - T)/(v_{\max} - T) \in [0, 1]$
- Residual: $x_m = K_m(2 + K_m)$
- Sum of residuals: $\varepsilon = \sum_{m=1}^{n} x_m$
- Disequilibrium index: $\text{IDT}^* = \varepsilon/(1 + \varepsilon)$

Phase 4 ($\text{IDT}^* \approx 0.85$) is the normal state for real systems. Disease appears when IDT^* deviates significantly from 0.85, or when one mesh exhibits anomalous K_m distribution.

3 Software Architecture

3.1 System Overview

Four main modules:

1. **Data ingestion**: accepts structured clinical data (CSV, HL7, FHIR) and handles missing values.
2. **Tensional normalisation**: computes T, $v_{\max}$, K_m, x_m, ε, IDT^*.
3. **Mesh attribution**: assigns each variable to solid, liquid, or gaseous mesh.
4. **Diagnostic inference**: compares IDT^* to reference values, identifies mesh anomalies, recommends interventions.

3.2 Data Input Format

Each clinical variable is represented as:

```
{
  "name": "CRP",
  "unit": "mg/L",
  "value": 8.2,
  "reference_min": 0.0,
  "reference_max": 5.0,
  "mesh": "liquid",
  "importance": 1.0
}
```

3.3 Core Algorithm

```
import numpy as np

def tensional_normalization(values):
    T = np.min(values)
    vmax = np.max(values)
    if vmax == T:
        return np.zeros_like(values)
    return (values - T) / (vmax - T)

def compute_idt_star(K_m):
    x = K_m * (2 + K_m)
    epsilon = np.sum(x)
    return epsilon / (1 + epsilon)

def diagnostic_report(clinical_table):
    values_by_mesh = {'solid': [], 'liquid': [], 'gaseous': []}
    for record in clinical_table:
        values_by_mesh[record['mesh']].append(record['value'])

    report = {}
    for mesh in ['solid', 'liquid', 'gaseous']:
        if values_by_mesh[mesh]:
            K_m = tensional_normalization(
                np.array(values_by_mesh[mesh]))
            report[f'IDT*_{mesh}'] = compute_idt_star(K_m)

    all_values = np.array([r['value'] for r in clinical_table])
```

```
    K_m_all = tensional_normalization(all_values)
    report['IDT*_global'] = compute_idt_star(K_m_all)
    idt = report['IDT*_global']
    report['phase'] = '4 (normal)' if 0.70 < idt < 0.95 \
        else ('3 (low tension)' if idt <= 0.70 \
        else '4-explosion risk')
    return report
```

3.4 Reference Thresholds

Table 1: Reference ranges for tensional indices.

Parameter	Range	Clinical interpretation
Global IDT*	0.70–0.90	Phase 4 (healthy)
IDT* < 0.70	—	Phase 1–2 (hypometabolic, rare)
IDT* > 0.95	—	Severe disequilibrium; elevated Phase 4 explosion risk
IDT*_solid / IDT*_liquid	≈ 1.0	Mesh coherence
Solid mesh $K_m > 0.9$	—	Structural lesion (fibrosis, tumour)
Liquid mesh $VT = K - T < 0.2$	—	Flow stagnation (ischaemia, inflammation)
Gaseous mesh K_m high (uncorrelated)	—	Psychiatric or functional disorder

4 Mesh Assignment of Clinical Variables

Table 2: Mapping of clinical variables to tensional meshes.

Variable type	Mesh	Examples
Biopsy, histology, imaging (structure)	Solid	CT density, fibrosis score, tumour size
DNA/RNA, epigenetic marks	Solid	Mutation load, methylation status
Complete blood count, coagulation	Liquid	Haemoglobin, platelets, INR

Variable type	Mesh	Examples
Inflammatory markers	Liquid	CRP, IL-6, TNF-alpha
Metabolic panel	Liquid	Glucose, HbA1c, lipids
Hormones	Liquid	TSH, cortisol, insulin
Pulmonary function tests	Gaseous	FEV1, FVC, DLCO
Blood gases	Gaseous	pO2, pCO2, pH
Heart rate variability	Gaseous	LF/HF ratio, SDNN
EEG, fMRI connectivity	Gaseous	Alpha power, network coherence
Psychological questionnaires	Gaseous	HAM-D, GAD-7, PANSS
Sleep parameters	Gaseous	Apnoea-hypopnoea index, sleep efficiency

5 Diagnostic Inference Engine

The engine follows rules derived from POLIS V12 phase transitions:

1. **Global IDT* out of range:**
   - IDT$^* < 0.70$: metabolic depression, hypothyroidism, advanced liver failure.
   - IDT$^* > 0.95$: systemic inflammation, sepsis, acute stress.
2. **Mesh-specific anomalies:**
   - Solid mesh dominant outliers: localised structural disease (tumour, fibrosis).
   - Liquid mesh low $VT = K - T$ (near 0): circulatory or inflammatory block.
   - Gaseous mesh high K_m uncorrelated with other meshes: psychiatric or functional disorder.
3. **Longitudinal change:** ΔIDT$^* > 0.05$/month indicates progressive disease; ΔIDT$^* < -0.05$ indicates treatment response.

5.1 Example Report: Rheumatoid Arthritis (Active)

```
{
  "global_IDT*": 0.92,
  "phase": "4 (high tension)",
  "mesh_IDT*": {
```

```
    "solid": 0.82,
    "liquid": 0.96,
    "gaseous": 0.88
  },
  "alerts": [
    "Liquid mesh IDT* elevated (0.96): systemic inflammation.",
    "Ratio liquid/solid = 1.17 > 1.1: mesh incoherence."
  ],
  "recommendations": [
    "Target liquid mesh: anti-inflammatory therapy (DMARDs,
       biologics).",
    "Monitor CRP, IL-6 as VT proxies.",
    "If IDT* not reduced within 12 weeks: reconsider diagnosis."
  ]
}
```

6 Software Implementation Stack

- **Backend:** Python (FastAPI) or R (Plumber) for tensional calculations.
- **Frontend:** Web dashboard (React/Streamlit) or EHR integration.
- **Data storage:** PostgreSQL with TimescaleDB for longitudinal IDT* tracking.
- **Validation module:** cross-validation against clinical outcomes (mortality, hospitalisation).
- **Falsification module:** if after 1000 cases the model does not outperform random classification, the software signals its own inadequacy.

7 Clinical Validation Protocol

1. Collect clinical data from 500 patients across 5 disease categories.
2. Compute IDT* for each patient at baseline.
3. Blind clinicians to tensional scores.
4. Compare tensional classification with gold-standard diagnosis.
5. Measure sensitivity, specificity, AUC.
6. **Falsification:** If AUC ≤ 0.6 for any major disease category, the tensional diagnostic hypothesis is falsified for that category.

8 Limitations and Future Work

- The software requires normalisation against a reference population or the patient's own longitudinal data. Choosing the correct $v_{\max}$ and T is critical.
- Missing data must be handled carefully; simple imputation may bias K_m.
- Mesh assignment of some variables is domain-dependent and may need local calibration.
- The software does not replace clinical judgement; it is a decision support tool.

Future work includes integration with wearable sensors (continuous K_m monitoring), patient-specific T based on genetic background, and extension to multi-omics data.

9 Conclusion

The POLIS V12 tensional framework is directly translatable into a diagnostic software. By normalising clinical measurements into K_m values, computing IDT*, and interpreting phase deviations, the software alerts clinicians to mesh-specific pathologies and recommends interventions aimed at reducing tensional residuals. The architecture is modular, falsifiable, and ready for pilot implementation. The next step is a collaboration with a clinical institution to collect and test real-world data.

References

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