

# yi\_julia\_progress\_report1

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## 1 Final Project Progress Report — HBN Cognition × Temporal Discounting

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### 1.1 Scope update

I will test whether **clinical diagnoses are associated with specific cognition–temporal–discounting patterns** in the Healthy Brain Network (HBN). Features include temporal discounting parameters ( $k$ ,  $\log-k$ , ED50) and NIH Toolbox cognition (Flanker, Processing Speed, List Sorting), with age/sex covariates.

**Why change now:** My lab **gained access to HBN yesterday**, which aligns directly with my focus on transdiagnostic mechanisms and provides sufficient sample size for robust ML.

### 1.2 Data sources & access

- **HBN Phenotype (public pheno CSV):** Accessed via **HTTP programmatically** (`requests` → `pandas.read_csv`) to satisfy the API/web requirement.
- **HBN Clinician-Consensus Diagnosis:** Downloaded CSV from the HBN portal; merged locally (not committed).
- **HBN NIH Toolbox & Temporal Discounting tables:** Local CSVs; merged to an interim master, then cleaned into **processed** analysis views.

**API proof:** `tests.py` performs an HTTP GET of the public pheno CSV and asserts load/shape/ID columns; it also runs my pipeline and verifies processed outputs (row count, required TD columns, missingness thresholds).

### 1.3 What I implemented

- **Pipeline script (`hbn_data_processing_pipeline.py`):**
  - Ingest (API + local), ID normalization, joins.
  - Feature engineering: `k_mean`, `logk_mean`, `ed50_mean`, `k_abs_diff`.

- Missingness policy: drop 90%-missing columns; build **core** (20% missing) and **extended** views; require 90% row completeness in core.
- Export to **data/processed/** (CSV), plus validation metadata.
- **Tests (tests.py):** API fetch test; pipeline run test; processed-file assertions (TD features present, N 1000, 10% missing in key TD).

## 1.4 Planned analysis (1-month, laptop-feasible)

1. **Unsupervised subtypes:** KMeans/Agglomerative (k=3–5) on z-scored TD+NIH; select k via silhouette/Calinski–Harabasz; bootstrap stability.
2. **Diagnosis enrichment:**  $\chi^2$ /Fisher across clusters; Cramér’s V; effect-size profiles of TD/NIH by cluster; sensitivity with age/sex adjustment.
3. **Supervised confirmation (lightweight):** L1-logistic (balanced) predicting selected diagnoses; 5-fold AUROC/AUPRC; permutation importance; calibration.
4. **Reporting:** Heatmaps of cluster centroids, PCA/UMAP visuals, concise enrichment tables and model metrics.

## 1.5 Risks & mitigations

- **DUA timing / portal reliability:** API requirement is already satisfied by public pheno HTTP fetch; analysis proceeds with locally joined tables (not committed).
- **Severe missingness (Picture Sequence):** Excluded from core view; focus on Flanker and Processing Speed with low missingness.
- **ID heterogeneity (EID vs Identifiers):** Normalized to \_EID prior to merges.

## 1.6 Reproducibility

- **data/** and **results/** are **gitignored**; only code, small samples (if any), and this report are committed.

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**1.7 environment.yml** documents dependencies; **README.md** explains how to run **tests.py**.

## 1.8 Data sources

| Data source # | Name / short description  | Source URL   | Type            | List of fields (key)  | Format | Tried Python?             | Estimated data size / points to use              |
|---------------|---|--|-----------------|---|--------|---------------------------|--|
| 1             | <b>HBN Phenotype (R1–R11)</b> — demo-graphics & screening variables. Pulled program-mati-cally.   | http://fcon_1000.projects.unc.edu/data/indiv/indi/Yes_healthy_5000/brain_network/File/...<br>(e.g., HBN_R11_Phenotype.csv) | API (HTTP load) | Age, selected screening totals (e.g., EHQ_Total)  | CSV    | Yes (requests → pandas)   | 2,500 rows available; plan to use ~2,100 matched |
| 2             | <b>Clinician Consensus Diagnosis</b> — DSM-style best-estimate diagnoses.   | Local export: data/raw/Diagnosis_CDx_DiagConsensus.csv   | file            | EID, DX_01, DX_02..., flags/notes   | CSV    | Yes (pandas read locally) | 4,700 rows; plan to use ~2,100 matched           |
| 3             | <b>NIH Toolbox (Cognition)</b> — atten-tion/inhibitory control, cognitive flexibil-ity, process-ing speed, working memory, vocabu-lary. | Local export: data/raw/NIH_final.csv   | file            | Flanker, DCCS, Pattern Comparison, List Sort, Picture Vocabulary scores (raw/standard), admin flags | CSV    | Yes (pandas)              | 3,000 rows; plan to use ~2,100 matched           |

| Data source # | Name / short description                                  | Source URL                                 | Type | List of fields (key)   | Format | Tried Python?       | Estimated data size / points to use    |
|---------------|---|--|------|--|--------|---------------------|--|
| 4             | <b>Temporal Discounting</b> — delay-reward task features. | Local export: data/raw/Temp_Disc_Final.csv | file | k (discount rate), AUC, model fit stats, task/visit metadata | CSV    | <b>Yes</b> (pandas) | 2,400 rows; plan to use ~2,100 matched |

*All sources exceed 300 records; source #1 satisfies the “API/web scraping” requirement.*