

Harmonia V3

Master Technical Specification & Implementation Guide

Version: 8.0 (Complete Forensic Edition)

Status: PILOT READY | Classification: INTERNAL

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Section	Description
1	Executive Summary & Paradigm Shift
2	Core Data Architecture
3	Phase 1: MetaFBP Visual Intelligence
4	Phase 2: PIIP Psychometric System (Felix Protocol)
5	Gemini Parsing Architecture
6	Scoring Mechanics & Evidence Extraction
7	Profile Aggregation Pipeline
8	Similarity Calculation (Perceived Overlap)
9	Phase 3: HLA Biological Compatibility
10	Engine Logic & WtM Calculation
11	Reporting Architecture & Schemas
12	Comprehensive Report Examples
13	Admin Protocols (System Prompts)
14	Implementation Details & Future Expansion

1. Executive Summary & Paradigm Shift

1.1 Legacy V2 Limitations

Limitation	Description	Impact
Mode Collapse	Averaging distinct clusters of attraction results in centroid resembling neither	Recommends "safe" faces that fail to trigger attraction
Uniform Weighting	Euclidean model treats all 128 dimensions equally	Cannot differentiate users who prioritize eyes vs. jawline
Static Rigidity	First-Order predictor with fixed weights after ideal vector calculation	No context-aware adaptation per input image
Expansion Difficulty	Architecture solely relies on DeepFace embeddings	Cannot integrate personality or biological data coherently

1.2 The MetaFBP Solution

This overhaul recontextualizes the problem as an **Optimization Problem over Meta-Tasks**. The core innovation replaces the heuristic Visual Scoring engine with the MetaFBP (Meta-Learning for Personalized Facial Beauty Prediction) framework, which disentangles:

Component	Symbol	Function	Implementation
Aesthetic Commonality	E_θ_c	Objective baseline of beauty shared across population	ResNet-18 (FROZEN)
Aesthetic Personality	G_θ_g	Subjective deviation from norm; user-specific preferences	MLP High-Order Predictor

1.3 Core Mathematical Framework

The engine no longer compares a target face to a static ideal vector. Instead, it 'retrains' a lightweight predictor head for every user in real-time using their swipe history as the Support Set:

$$\theta_f_{dynamic} = \theta'_f + \lambda \times G_{\theta_g}(x) \quad \text{where } \lambda = 0.01 \text{ (Adaptation Strength)}$$

Multi-constraint extension:
Stage 2: $\theta_f = \theta'_f + \lambda \times G(x) + \lambda \times P(x) \quad [+ \text{Personality Constraint}]$
Stage 3: $\theta_f = \theta'_f + \lambda \times G(x) + \lambda \times P(x) + \lambda \times H(x) \quad [+ \text{HLA Constraint}]$

2. Core Data Architecture

2.1 Directory Tree (V3 Forensic)

```
/app/data/
└── registry.db          # Main Relational DB
└── global_calibration/  # FROZEN ASSETS (MetaFBP)
    ├── universal_extractor_resnet18.pt  # E_θ_c backbone (~45MB)
    ├── meta_generator_base.pt           # G_θ_g base weights (~2MB)
    ├── scut_fbp5500/                  # Calibration dataset (~1.2GB)
    ├── personality_constraint_base.pt # P_θ_p Stage 2 (~1MB)
    └── profiles/                    # USER DATA (INPUTS)
        └── {uuid}/
            ├── assets/
            │   ├── profile_primary.jpg
            │   ├── p1_meta_support_set.json      # MetaFBP Support Set
            │   ├── p1_visual_vector.json        # Trait extraction results
            │   ├── p2_psych_ipip.json          # PIIP Psychometrics + Evidence
            │   └── p3_hla_secure.enc           # Fernet Encrypted HLA
    └── reports/                # MATCH OUTPUTS
        └── {match_id}/
            ├── reasoning_chain.json       # LEVEL 3: Strict Math (NO AI)
            ├── gemini_narrative.md      # LEVEL 2A: Psych/Visual Report
            ├── hla_gemini_analysis.md   # LEVEL 2B: Bio Report
            └── customer_summary.json     # LEVEL 1: Sanitized UI
```

2.2 Global Asset Management

Asset File	Size	Purpose	Constraint
universal_extractor_resnet18.pt	~45MB	Feature extraction (512-dim)	STRICTLY FROZEN
meta_generator_base.pt	~2MB	MLP base for personalization	Cloned per-user, adapted
scut_fbp5500/	~1.2GB	5500 face images with ratings	Mode ratings baseline
personality_constraint_base.pt	~1MB	Stage 2 personality integration	Optional constraint layer

3. Phase 1: MetaFBP Visual Intelligence

3.1 Input Schema: p1_meta_support_set.json

```
{  
    "meta_task_id": "uuid_v4",  
    "last_updated": "2026-01-14T12:00:00Z",  
    "support_set_stats": {  
        "total_samples": 142,  
        "class_distribution": {  
            "score_1": 40, // Dislikes  
            "score_2": 60, // Mild dislikes  
            "score_3": 10, // Neutral  
            "score_4": 12, // Likes  
            "score_5": 20 // Super Likes  
        }  
    },  
    "support_set_data": {  
        "score_1": ["/app/data/archive/img_dislike_01.jpg", ...],  
        "score_5": ["/app/data/archive/img_superlike_01.jpg", ...]  
    }  
}
```

3.2 Trait Extraction from User Ratings

Beyond embedding-based learning, the system extracts **explicit visual traits** from the user's swipe history. By analyzing which traits appear frequently in liked vs disliked faces, we build a comprehensive preference profile with evidence trails.

3.2.1 Trait Extraction Process

Step	Process	Input	Output
1	Face Analysis	Profile images from support set	Detected traits per image
2	Trait Categorization	Traits + associated ratings	Trait frequency by score
3	Positive Extraction	High-rated face traits (4-5)	mandatory_traits (>80%)
4	Negative Extraction	Low-rated face traits (1-2)	negative_traits (>60%)
5	Weight Calculation	Frequency + rating correlation	Trait weights (0.0-1.0)

3.2.2 Trait Categories Detected

Category	Example Traits	Detection Method
Facial Structure	high_cheekbones, strong_jawline, oval_face, defined_chin	Landmark analysis
Eye Features	expressive_eyes, almond_eyes, deep_set_eyes, eye_color_*	Region segmentation
Hair/Style	curly_hair, short_hair, beard, clean_shaven, glasses	Style classification
Skin/Complexion	clear_skin, freckles, tan_complexion, fair_skin	Texture analysis
Expression/Vibe	warm_smile, serious, intellectual, approachable, mysterious	Expression + context
Presentation	minimalist, bold_fashion, tattoos, piercings, executive_style	Full-image analysis

3.2.3 Worked Example: Trait Extraction from 142 Rated Faces

Traits from LIKED Faces (Score 4-5, n=32):

Trait	Frequency	Avg Rating	Weight	Classification
glasses	28/32 (87.5%)	4.7	0.88	MANDATORY (>80%)
intellectual_vibe	26/32 (81.3%)	4.6	0.85	MANDATORY (>80%)
clean_shaven	22/32 (68.8%)	4.4	0.72	PREFERRED (60-80%)
dark_hair	20/32 (62.5%)	4.3	0.65	PREFERRED (60-80%)

Traits from DISLIKED Faces (Score 1-2, n=100):

Trait	Frequency	Avg Rating	Weight	Classification
glasses	28/32 (87.5%)	4.7	0.88	MANDATORY (>80%)
intellectual_vibe	26/32 (81.3%)	4.6	0.85	MANDATORY (>80%)
clean_shaven	22/32 (68.8%)	4.4	0.72	PREFERRED (60-80%)
dark_hair	20/32 (62.5%)	4.3	0.65	PREFERRED (60-80%)

heavy_makeup	89/100 (89%)	1.3	-0.92	AVERSION (>80%)
excessive_filters	85/100 (85%)	1.4	-0.88	AVERSION (>80%)
party_lifestyle	72/100 (72%)	1.8	-0.75	NEGATIVE (60-80%)
visible_tattoos	68/100 (68%)	1.9	-0.70	NEGATIVE (60-80%)

3.2.4 Weight Calculation Formula

```
W_trait = (F_trait * R_corr) * sign(avg_rating - 3.0)
```

Where:

F_trait = Frequency of trait in relevant score bucket
R_corr = Pearson correlation between trait presence and rating
sign() = +1 for liked traits (avg > 3), -1 for disliked traits (avg < 3)

3.3 Cyclically Re-sampling Strategy

A critical challenge is data imbalance. A user might have 500 dislikes but only 10 super likes. The Cyclically Re-sampling Strategy ensures balanced gradient descent:

Case	Condition	Support Set Action	Query Set Action
Extreme Scarcity	N_c = 1	Duplicate single image N_s times	Leave empty; skip loss
Scarcity	1 < N_c ≤ N_s	Use all + duplicate to fill	Cyclic secondary sampling
Moderate	N_s < N_c ≤ N_s+N_q	Random select N_s unique	Use remaining, duplicate
Abundance	N_c > N_s + N_q	Random sample N_s unique	Random sample N_q unique

3.4 MetaFBP Algorithm: High-Order Prediction

3.4.1 Architecture Components

Component	Class	Structure	Input/Output
Universal Extractor	UniversalExtractor	ResNet-18 (minus FC)	224x224 → 512-dim
Parameter Generator	ParameterGenerator	MLP: FC(512,512) → ReLU → FC(512,512)	512-dim → 512-dim twist
Adaptation Loop	adapt_user_predictor()	k-step SGD (k=5, lr=0.01)	Support set → adapted gen

3.4.2 Scoring Algorithm Pseudocode

```
def compute_s_vis(user_uuid, target_image_path):
    # 1. Load & process user's Support Set (S_m)
    support_x, support_y = process_support_set(user_uuid)  # Apply cyclic resampling

    # 2. Inner Loop Adaptation (k-step gradient descent)
    adapted_generator = adapt_user_predictor(support_x, support_y)
    # Result: User-specific generator weights θ'_f

    # 3. Process target image through FROZEN extractor
    target_features = extractor(target_tensor)  # E_θ_c(X_q) → 512-dim

    # 4. High-Order Prediction: Generate dynamic weights
    twist = adapted_generator(target_features)  # G_θ_g(X)

    # 5. Apply Adaptation Strength
    weighted_twist = LAMBDA * twist  # λ = 0.01

    # 6. Calculate prediction: F(X) = θ_f_dynamic × X
    raw_prediction = sum(weighted_twist * target_features)

    # 7. Scale to 1-5 range, then normalize to 0-100
    s_vis_raw = clamp(3.0 + raw_prediction * 100, 1.0, 5.0)
    metafbp_component = (s_vis_raw - 1) * 25  # Maps [1,5] → [0,100]

    return metafbp_component
```

3.5 Visual Scoring Formula (V3 MetaFBP)

S_vis = (MetaFBP_Component × 0.6) + (T_match_positive × 0.25) + (T_match_negative × 0.15)

Component	Formula	Range	Description
MetaFBP_Component	$(\text{MetaFBP_Score} - 1) \times 25$	0-100	High-order prediction from neural adaptation
T_match_positive	$\Sigma(\text{matched weights}) / \Sigma(\text{all positive weights}) \times 100$	0-100	How well target matches desired traits
T_match_negative	$(1 - \text{penalty_ratio}) \times 100$	0-100	Penalty for presence of aversion traits

4. Phase 2: PIIP Psychometric System (Felix Protocol)

4.1 Executive Summary

Definition: An AI-powered personality profiling system using the Seven Deadly Sins framework to convert natural language responses into quantified trait profiles with full evidence chains. Users answer 6 scenario-based questions; Gemini parses open-ended responses into scores across seven dimensions.

Research Foundation: Joel et al. (2017) demonstrated ML cannot predict relationship-specific attraction from pre-meeting data. However, Montoya et al. (2008) found **perceived similarity** affects attraction throughout relationship development. System focuses on perceived similarity and positive overlap detection - the 'astrology effect'.

4.2 The 6 Felix Questions

Q#	Question	Domain	Primary Sins
Q1	The bill arrives at a group dinner. Everyone contributed differently. What's your approach?	Resource sharing, fairness, social harmony	Greed, Wrath, Pride, Sloth
Q2	Your car needs a \$1,200 repair you didn't budget for. Walk me through your thought process.	Stress response, financial reasoning	Wrath, Sloth, Gluttony, Pride
Q3	You have a completely free weekend with no obligations. How do you spend it?	Leisure priorities, introversion/extroversion	Lust, Sloth, Gluttony, Envy
Q4	You're on a group project where one person contributes less. How do you handle this?	Conflict handling, fairness, assertiveness	Wrath, Pride, Sloth, Envy
Q5	Your best friend calls with an emergency same night as a planned date. Your thinking?	Loyalty trade-offs, relationship priorities	Lust, Pride, Sloth, Wrath
Q6	Someone you respect gives you critical feedback about a blind spot. How do you respond?	Ego resilience, growth orientation	Pride, Wrath, Sloth, Envy

4.3 Response Constraints & Why Scenario-Based

Constraint	Value	Rationale
Minimum	25 words	Ensures sufficient signal for AI parsing
Maximum	150 words	Prevents rambling; manageable cognitive load
Format	Free-text	No pre-set options; enables nuanced extraction

Why Scenario-Based: Research estimates 30-63% distort self-report responses. SJTs extract authentic behavioral tendencies. Christian et al. (2010) meta-analysis demonstrates consistent validity. **Why Open-Ended:** Multiple choice limits expression. AI can detect implicit signals that fixed options miss: tone, justification patterns, values hierarchies, contradictions, defense mechanisms.

5. Gemini Parsing Architecture

5.1 Model Selection & Fallback Chain

Priority	Model	Rationale
Primary	gemini-3-pro-preview	Maximum reasoning depth for nuanced interpretation
Fallback	gemini-3-flash-preview	Pro-level intelligence at lower latency
Stable	gemini-2.5-flash	Production-stable if 3.x previews fail

5.2 Trait-Specific Decomposition

Rather than one prompt for all seven sins, Harmonia uses **separate prompts per trait** with scale anchors. Benefits: focused attention, anchored scoring, parallel execution (7 calls simultaneously), independent confidence calibration.

Example: Wrath-Specific Prompt

Analyze this response for WRATH signals only.

Wrath Scale (-5 to +5):
-5 = Extreme conflict avoidance: "I'd never confront anyone, even if wronged"
-3 = Strong patience: "I take a breath and try to understand their perspective"
0 = Neutral: No clear signal about conflict handling
+3 = Quick to frustration: "That would really annoy me"
+5 = Explosive anger: "I'd lose my temper and tell them exactly what I think"

Question: "{question_text}"
Response: "{response_text}"

Return JSON:
{ "score": <-5 to +5>, "confidence": <0.0 to 1.0>, "evidence": "<direct quote>" }

5.3 Sin-Specific Scale Anchors

Sin	-5 Anchor (Virtue)	+5 Anchor (Vice)
Greed	Extremely generous, prioritizes others	Highly materialistic, accumulates at expense
Pride	Deeply humble, deflects credit	Ego-driven, seeks status/validation constantly
Lust	Very restrained, deliberate, avoids spontaneity	Highly impulsive, novelty-seeking
Wrath	Extreme conflict avoidance, never expresses anger	Quick to anger, confrontational
Gluttony	Highly moderate, strict self-control	Strongly indulgent, struggles with restraint
Envy	Deeply content, never compares to others	Constantly competitive, resentful of success
Sloth	Extremely proactive, takes initiative constantly	Avoidant, passive, procrastinates

5.4 Multi-Observer Consensus Framework

For ambiguous responses or high-bias-risk traits (Wrath, Envy, Pride), Harmonia runs **three parallel evaluations** with different observer personas:

Observer	Persona	Instruction
Observer 1	Neutral Evaluator	Rate based only on what is explicitly stated or clearly implied
Observer 2	Empathetic Therapist	Consider what this person might be feeling beneath their words
Observer 3	Skeptical Critic	Look for inconsistencies between claims and language reveals

Aggregation: std_dev < 0.3 → high agreement (multiplier = 1.0). std_dev 0.3-0.5 → moderate (0.85). std_dev > 0.5 → disagreement (0.6, flag: observer_disagreement).

5.5 Social Desirability Bias Detection

Trait	Direction	Magnitude	Mitigation
-------	-----------	-----------	------------

Extraversion	↑ Inflated	+0.8 SD	Cross-response consistency
Conscientiousness	↑ Inflated	+0.7 SD	Discrepancy flagging
Agreeableness	↑ Inflated	+0.6 SD	Linguistic behavior analysis
Neuroticism	↓ Suppressed	-1.1 SD	Prompt-level reverse coding

6. Scoring Mechanics & Evidence Extraction

6.1 The Bipolar Scale: -5 to +5

11-point bipolar scale: -5 (extreme virtue) → 0 (neutral) → +5 (extreme vice). The opposite of greed isn't 'no greed' - it's generosity. Score of -4 on Greed means the person actively prioritizes others' needs over their own resources.

Score	Interpretation	Example (Wrath)
-5	Extreme virtue	"I would never confront anyone, even if wronged badly"
-3	Strong virtue	"I always try to understand their perspective before reacting"
-1	Slight virtue	"I prefer to let things go rather than argue"
0	Neutral / No signal	Topic not addressed, or conflicting signals cancel out
+1	Slight vice	"That would probably annoy me"
+3	Strong vice	"I'd definitely say something - I can't let that slide"
+5	Extreme vice	"I'd lose my temper and tell them exactly what I think"

6.2 Confidence Scoring Thresholds

Confidence	Interpretation	Evidence Type	Accuracy	Action
0.95-1.00	High	Explicit statement	~95%	Trust fully; weight in aggregation
0.70-0.94	Medium	Multiple converging cues	Variable	Include; weight by confidence
0.50-0.69	Low	Weak or single cue	Near-chance	Include with reduced weight
0.00-0.49	Very low	Speculative	Exclude	Assign score=0; flag

6.3 Evidence Extraction Requirements

For each sin score, Gemini extracts a **direct quote** (the evidence snippet) from the user's response. Evidence serves: (1) Interpretability - humans understand why score assigned, (2) Debugging - reveals parsing errors, (3) Auditability - transparent justification for matches.

Quality	Description	Example
Relevant	Clearly supports the specific sin being scored	For Wrath: "avoid the drama"
Minimal	Shortest quote that captures the signal	"not worth fighting" vs entire paragraph
Direct	Exact quote from response, not paraphrase	Verbatim user text
Strongest	If multiple quotes apply, select most diagnostic	Most explicit statement

6.4 Worked Example: Evidence Extraction

User Response to Q1 (Group Dinner Check):

"I'd probably suggest we just split it evenly to keep things simple. I hate those awkward moments where everyone's trying to calculate their exact share. Life's too short for that kind of pettiness. If someone ordered way more, they can throw in extra if they want, but I'm not going to be the one calling them out."

Sin	Score	Conf	Evidence Extracted	Reasoning
Greed	-2	0.78	"suggest we just split it evenly"	Prioritizes fairness over self-interest
Pride	0	0.45	(empty - no clear signal)	No ego/status language detected
Lust	0	0.40	(empty - not relevant)	Q1 doesn't address spontaneity
Wrath	-3	0.88	"not going to be the one calling them out"	Clear conflict avoidance
Gluttony	0	0.35	(empty - not addressed)	No indulgence signals

Envy	0	0.40	(empty - not addressed)	No comparison signals
Sloth	+1	0.72	"keep things simple...Life's too short"	Prefers easy path

7. Profile Aggregation Pipeline

7.1 Aggregation Flow

```
User Responses (6 questions, 25-150 words each)
↓
GeminiService Parsing (7 sins × 6 questions = 42 data points)
Each with: score (-5 to +5), confidence (0-1), evidence snippet
↓
Question-Level Quality Control
- Word count validation (min 25 words)
- Response completeness check (exclude if no signal)
↓
Trait-Level Aggregation (CWMV or simple mean per sin)
- Variance calculation
- High-variance flagging (SD > 3.0)
↓
Profile-Level Quality Control
- Response style detection (ERS, MRS, patterns)
- Composite quality score (0-100)
↓
Final Profile (7 aggregated sins + metadata + evidence_samples)
```

7.2 Confidence-Weighted Mean (CWMV)

Formula: Score_trait = $\sum(\text{Item_score} \times \text{Confidence}) / \sum(\text{Confidence})$

Question	Wrath Score	Confidence	Weighted	Evidence Snippet
Q1	-2	0.85	-1.70	"not calling them out"
Q2	-3	0.90	-2.70	"I'd just deal with it quietly"
Q3	0	0.30	0.00	(no signal)
Q4	-1	0.65	-0.65	"probably let it slide"
Q5	-2	0.80	-1.60	"avoid the confrontation"
Q6	+1	0.45	+0.45	"might push back a little"
Totals		$\Sigma=3.95$	$\Sigma=-6.20$	

Result: Aggregated Wrath = $-6.20 / 3.95 = -1.57$ (rounded to -1.6)

7.3 Response Style Detection

Extreme Response Style (ERS): Tendency to select endpoints (± 4 or ± 5). Flagged if $>40\%$ extreme. **Midpoint Response Style (MRS):** Preference for neutral (near 0). Flagged only when combined with fast completion (<50% median time), distinguishing disengagement from genuine neutrality.

7.4 Profile Quality Score Components

Component	Measures		Calculation
Internal Consistency	Do scores cohere within traits?		Mean confidence across all scores
Response Variance	Appropriate differentiation?		Penalize if too low or too high
Response Style	Systematic biases present?		Deduct for ERS, MRS, pattern flags
Engagement	Did user invest effort?		Based on word count and response time

Score	Tier	Action
≥ 80	High	Full weight in matching; no restrictions
60-79	Moderate	Include; apply $0.8\times$ weight multiplier
<60	Low	Exclude OR flag for manual review

7.5 Sin-Specific Weights (for Similarity)

Sin	Weight	Research Basis
Wrath	1.5x	Conflict style strongest predictor of relationship satisfaction (Gottman)
Sloth	1.3x	Motivation alignment affects shared activity participation
Pride	1.2x	Ego dynamics affect communication quality
Lust	1.0x	Baseline - spontaneity preferences matter but context-dependent
Greed	0.9x	Resource attitudes matter but less salient in early dating
Gluttony	0.8x	Lifestyle signal; visible but not relationship-critical
Envy	0.7x	Comparison orientation affects satisfaction but indirectly

8. Similarity Calculation (Perceived Overlap)

8.1 The Perceived Similarity Principle

Research Finding: Perceived similarity predicts initial attraction ($r = 0.39$); actual similarity does not ($r = 0.01$). Tidwell, Eastwick & Finkel (2013) speed-dating studies. We don't need people who ARE similar - we need people who will PERCEIVE each other as similar when shared traits are highlighted.

8.2 Positive Overlap Algorithm

Algorithm counts traits where both users share same direction (both virtuous OR both vice-leaning). Does NOT penalize differences. Two users sharing 3 of 7 traits get credit for those 3. The 4 differing traits are simply not mentioned - creating the 'astrology effect'.

User A	User B	Shared?	Interpretation
+2.5	+3.1	✓ Yes (both vice)	Both spontaneous
-2.0	-1.8	✓ Yes (both virtue)	Both conflict-avoidant
+2.5	-1.8	✗ No (opposite)	Not mentioned to users
+0.3	+0.2	✗ No (both neutral)	Signal too weak

8.3 Similarity Formulas

```
Step 1: trait_similarity = 1 - (|score_a - score_b| / 10)
Step 2: weighted_similarity = trait_similarity * avg_confidence * sin_weight
Step 3: similarity = Σ(weighted contributions) / Σ(all sin weights) = Σ / 7.4
```

8.4 Worked Example

Sin	A	B	Shared?	Trait Sim	Avg Conf	Weight	Contrib
Greed	-1.8	-2.2	✓	0.96	0.775	0.9	0.670
Pride	+0.3	-1.5	✗	-	-	-	0
Lust	+2.5	+3.1	✓	0.94	0.835	1.0	0.785
Wrath	-2.1	-1.8	✓	0.97	0.850	1.5	1.237
Gluttony	+1.2	-0.3	✗	-	-	-	0
Envy	-0.8	-1.2	✓	0.96	0.690	0.7	0.464
Sloth	-1.5	+1.8	✗	-	-	-	0

Result: $3.156 / 7.4 = 42.6\% \text{ similarity}$ (4 of 7 traits shared)

8.5 Quality-Adjusted Similarity

Profile A	Profile B	Multiplier
High (≥ 80)	High (≥ 80)	1.0
High	Moderate (60-79)	0.9
Moderate	Moderate	0.8
High	Low (< 60)	0.7
Low	Low	0.5

9. Phase 3: HLA Biological Compatibility

9.1 Input Schema: p3_hla_secure.enc (Decrypted Structure)

```
{  
    "source": "23andMe_v5",  
    "imputation_confidence": 0.94, // HIBAG Posterior Probability  
    "markers": {  
        "HLA-A": [ "A*01:01", "A*03:01"],  
        "HLA-B": [ "B*07:02", "B*08:01"],  
        "HLA-DRB1": [ "DRB1*15:01", "DRB1*03:01"]  
    },  
    "ancestry_model": "EUR",  
    "snp_count": 147,  
    "per_allele_confidence": {  
        "A*01:01": 0.982,  
        "A*03:01": 0.965,  
        "B*07:02": 0.991,  
        "B*08:01": 0.978,  
        "DRB1*15:01": 0.945,  
        "DRB1*03:01": 0.932  
    }  
}
```

9.2 HIBAG Pipeline Execution

Step	Process	Tool	Output
1	Extraction	Python (pandas)	rs-id list with genotypes
2	Imputation	R (HIBAG library)	4-field HLA types + posteriors
3	Standardization	Python	A*01:01 format (2-field)
4	Encryption	cryptography (Fernet)	p3_hla_secure.enc
5	Reporting	Engine	Allele lists for matching

9.3 Biological Scoring Formula

$$S_{\text{bio}} = (N_{\text{unique}} / N_{\text{total}}) \times 100$$

Variable	Definition	Example
N_unique	Count of unique alleles in combined A+B pool	A:[A*01:01,A*02:01], B:[A*03:01,A*24:02] → 4 unique
N_total	Total allele slots (typically 6 for 3 loci × 2)	6
Goal	Maximize Heterozygosity (MHC dissimilarity)	Higher = better immune diversity

9.4 Olfactory Prediction Model

Based on MHC-mediated mate choice research, the Heterozygosity Index predicts pheromonal attraction. Research suggests MHC-dissimilar pairs report higher attraction and relationship satisfaction.

```
Heterozygosity_Index = N_unique / N_total  
Pheromone_Intensity = Heterozygosity_Index × 100
```

Example: 11 unique alleles / 12 total = 0.916 → Pheromone_Intensity = 91.6

9.5 HLA Display Logic

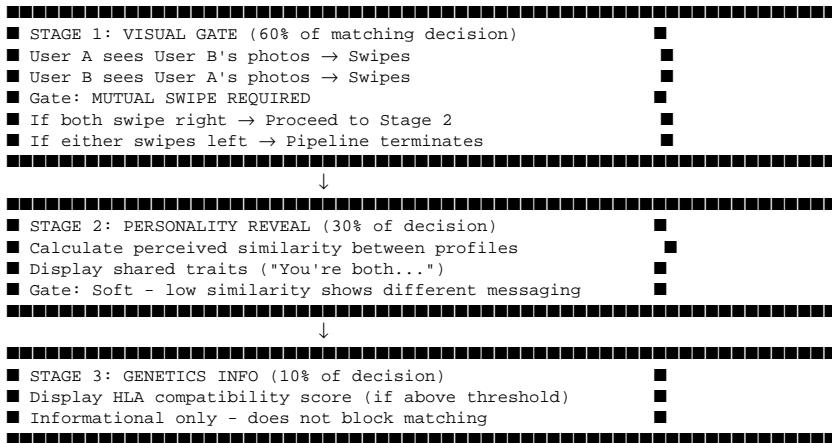
Design Principle: Never show negative HLA results. If compatibility is low, simply don't mention it. User sees personality overlap and assumes genetics are neutral/positive.

Score Range	Display	Label
≥75	Show with ■	Strong chemistry signal
50-74	Show with ■	Good chemistry
25-49	Show with ■	Some chemistry

<25	HIDE	Do not display low scores
-----	------	---------------------------

10. Engine Logic & WtM Calculation

10.1 Three-Stage Cascaded Pipeline



10.2 Score Formulas Summary

Phase	Score	Formula	Weight
Phase 1	S_vis	(MetaFBP×0.6) + (T_pos×0.25) + (T_neg×0.15)	0.4 (40%)
Phase 2	S_psych	(1 - D_sins) × P_friction × 100	0.3 (30%)
Phase 3	S_bio	(N_unique / N_total) × 100	0.3 (30%)

10.3 Willingness to Meet (WtM)

$$WtM = (0.4 \times S_{vis}) + (0.3 \times S_{psych}) + (0.3 \times S_{bio})$$

10.4 Complete Worked Example

Phase 1: Visual (MetaFBP + Trait Matching)

Input	Value	Calculation	Notes
MetaFBP raw score	4.18	(4.18-1)×25 = 79.5	From adapted generator
Mandatory matches	glasses, intellectual	0.88 + 0.85 = 1.73	Both detected
Preferred matches	dark_hair, partial shaven	0.65 + 0.36 = 1.01	Full + partial
T_match_positive	2.74 / 3.10	88.4%	Weighted match ratio
Aversion triggered	small_tattoo	-0.55 penalty	78% confidence
T_match_negative	1 - 0.55/1.62	66.0%	Penalty ratio
S_vis		79.5×0.6 + 88.4×0.25 + 66.0×0.15	= 79.7

Phase 2: Psychometric

Input	Value	Notes
A sin vector	[0.45, 0.20, 0.85, 0.10, 0.60, 0.70, 0.95]	lust, gluttony, greed, sloth, wrath, envy, pride
B sin vector	[0.50, 0.30, 0.40, 0.70, 0.30, 0.40, 0.60]	
D_sins (Euclidean)	0.35	$\ A - B\ /\sqrt{7}$
sloth_delta	0.60	$ 0.10 - 0.70 \rightarrow \text{FRICTION FLAG}$
bluntness_delta	0.80	$ 1.0 - 0.2 \rightarrow \text{FRICTION FLAG}$

P_friction	0.80	Applied due to flags
S_psych	52.0	$(1 - 0.35) \times 0.8 \times 100$

Phase 3: Biological

Input	Value	Notes
A alleles	[A*01:01, A*02:01, B*08:01, B*07:02, DRB1*15:01, DRB1*03:01]	6 alleles
B alleles	[A*03:01, A*24:02, B*44:02, B*35:01, DRB1*04:01, DRB1*07:01]	6 alleles
N_unique	11	All unique except possible overlaps
N_total	12	6 + 6
S_bio	91.6	$(11/12) \times 100$

Final WtM: $(0.4 \times 79.7) + (0.3 \times 52.0) + (0.3 \times 91.6) = 31.88 + 15.60 + 27.48 = \mathbf{74.96} \approx 75$

11. Reporting Architecture & Schemas

11.1 Report Hierarchy

Level	File	Audience	Content
Level 3	reasoning_chain.json	Admin Only	Raw calculations, NO AI, full evidence
Level 2A	gemini_narrative.md	Admin/Researcher	Psych/Visual AI analysis with evidence
Level 2B	hla_gemini_analysis.md	Admin/Researcher	HLA scientific analysis
Level 1	customer_summary.json	End User	Sanitized, friendly summary

11.2 reasoning_chain.json Schema (Level 3)

```
{  
  "match_id": "match_7f8c9a0b",  
  "timestamp": "2026-01-14T18:00:00Z",  
  "subjects": {"user_a": "Subject A (550e...)", "user_b": "Subject B (alb2...)"},  
  
  "phase_1_visual": {  
    "metabp_raw_score": 4.18,  
    "metabp_component": 79.5,  
    "support_set_stats": {"total_samples": 142, "adaptation_steps": 5},  
    "trait_preference_model": {  
      "mandatory_traits": [  
        {"trait": "glasses", "weight": 0.88, "frequency": 0.875, "source": "87.5% of likes"},  
        {"trait": "intellectual_vibe", "weight": 0.85, "frequency": 0.813, "source": "81.3% of likes"}  
      ],  
      "preferred_traits": [  
        {"trait": "clean_shaven", "weight": 0.72, "frequency": 0.688, "source": "68.8% of likes"},  
        {"trait": "dark_hair", "weight": 0.65, "frequency": 0.625, "source": "62.5% of likes"}  
      ],  
      "aversion_traits": [  
        {"trait": "heavy_makeup", "weight": -0.92, "frequency": 0.890, "source": "89.0% of dislikes"},  
        {"trait": "visible_tattoos", "weight": -0.70, "frequency": 0.680, "source": "68.0% of dislikes"}  
      ]  
    },  
    "target_trait_detection": {  
      "detected": [  
        {"trait": "glasses", "confidence": 0.992, "weight_applied": 0.88},  
        {"trait": "intellectual_vibe", "confidence": 0.850, "weight_applied": 0.85},  
        {"trait": "dark_hair", "confidence": 0.970, "weight_applied": 0.65},  
        {"trait": "light_stubble", "confidence": 0.910, "partial_match": "clean_shaven", "weight_applied": 0.36}  
      ],  
      "aversions_triggered": [  
        {"trait": "small_tattoo", "confidence": 0.780, "penalty": -0.55}  
      ]  
    },  
    "t_match_positive": 88.4,  
    "t_match_negative": 66.0,  
    "total_p1_score": 79.7  
  },  
  
  "phase_2_psych": {  
    "user_a_profile": {  
      "sins": {  
        "greed": {"score": -1.2, "confidence": 0.72, "evidence_samples": ["split it evenly", "doesn't matter"]},  
        "wrath": {"score": -2.1, "confidence": 0.85, "evidence_samples": ["not calling them out", "let it slide"]},  
        "pride": {"score": 0.95, "confidence": 0.98, "evidence_samples": ["shows people I made it"]},  
        "sloth": {"score": 0.10, "confidence": 0.99, "evidence_samples": ["Wake up at 5am. 10k run."]}  
      },  
      "quality_tier": "high",  
      "quality_score": 85.2  
    },  
    "user_b_profile": {  
      "sins": {  
        "greed": {"score": -0.8, "confidence": 0.68, "evidence_samples": ["happy to share"]},  
        "wrath": {"score": -1.8, "confidence": 0.82, "evidence_samples": ["avoid drama"]},  
        "pride": {"score": 0.60, "confidence": 0.75, "evidence_samples": []},  
        "sloth": {"score": 0.70, "confidence": 0.96, "evidence_samples": ["refuse to work weekends"]}  
      },  
      "quality_tier": "moderate",  
      "quality_score": 72.5  
    },  
    "sin_distance": 0.35,  
    "friction_flags": {"sloth_delta": 0.60, "bluntness_delta": 0.80},  
    "evidence_chain": [  
      {"question_id": "felix_q3_spending",  
       ...  
     }  
    ]  
  }  
}
```

```

    "question_text": "You just received an unexpected $10,000 bonus...",
    "user": "A",
    "user_answer_raw": "I'd buy a vintage Rolex. Shows people I made it.",
    "extracted_trait": "status_signaling",
    "mapped_sin": "pride",
    "weight": 0.90,
    "confidence": 0.98,
    "reasoning": "Subject prioritizes social validation through consumption."
},
{
    "question_id": "felix_q7_productivity",
    "question_text": "Describe your ideal morning routine.",
    "user": "A",
    "user_answer_raw": "Wake up at 5am. 10k run. Cold shower. At desk by 6:30.",
    "extracted_trait": "compulsive_productivity",
    "mapped_sin": "pride",
    "weight": 0.95,
    "confidence": 0.99,
    "reasoning": "Achievement-oriented self-discipline with potential rigidity."
},
{
    "question_id": "felix_q12_weekends",
    "question_text": "How do you typically spend your weekends?",
    "user": "B",
    "user_answer_raw": "I refuse to work weekends. Life is for sleeping in and doing nothing.",
    "extracted_trait": "leisure_prioritization",
    "mapped_sin": "sloth",
    "weight": 0.85,
    "confidence": 0.96,
    "reasoning": "Explicitly rejects productivity norms; potential conflict with A."
}
],
"similarity": {
    "raw_score": 0.426,
    "quality_adjusted": 0.383,
    "shared_traits": [
        {"sin": "greed", "direction": "virtue", "contribution": 0.670, "a_evidence": "split evenly", "b_evidence": "happy to share"}, 
        {"sin": "wrath", "direction": "virtue", "contribution": 1.237, "a_evidence": "not calling out", "b_evidence": "avoid drama"}
    ]
},
"total_p2_score": 52.0
},
"phase_3_bio": {
    "alleles_user_a": ["A*01:01", "A*02:01", "B*08:01", "B*07:02", "DRB1*15:01", "DRB1*03:01"],
    "alleles_user_b": ["A*03:01", "A*24:02", "B*44:02", "B*35:01", "DRB1*04:01", "DRB1*07:01"],
    "per_allele_confidence": {
        "A*01:01": 0.982, "A*02:01": 0.965, "B*08:01": 0.991, "B*07:02": 0.978,
        "A*03:01": 0.971, "A*24:02": 0.943, "B*44:02": 0.988, "B*35:01": 0.956
    },
    "peptide_binding_analysis": {
        "A*01:01": "Binds negatively charged residues at P3; broad viral coverage",
        "A*24:02": "High affinity for HIV-1 epitopes; Asian population enriched",
        "B*44:02": "Protective against HIV progression; strong NK cell interaction",
        "DRB1*15:01": "Associated with MS susceptibility; strong autoimmune link"
    },
    "heterozygosity_index": 0.916,
    "olfactory_prediction": {
        "pheromone_intensity": 91.6,
        "assessment": "Strong positive physiological response predicted"
    },
    "total_p3_score": 91.6
},
"final_wtm": {
    "calculation": "(79.7 * 0.4) + (52.0 * 0.3) + (91.6 * 0.3)",
    "score": 74.96
}
}

```

12. Comprehensive Report Examples

12.1 gemini_narrative.md (Level 2A)

```
# Harmonia Forensic Audit: Visual & Psychometric Analysis
**Subject A** vs. **Subject B** | **Date:** 2026-01-14

## 1. Visual Preference Model (Extracted from A's Rating History)

**Calibration Data:** 142 faces rated (32 likes, 100 dislikes, 10 neutral)

### 1.1 Mandatory Traits (>80% frequency in likes)
| Trait | Frequency | Avg Rating | Weight | Status in B |
|-----|-----|-----|-----|-----|
| glasses | 87.5% | 4.7 | 0.88 | ✓ DETECTED (99.2% conf) |
| intellectual_vibe | 81.3% | 4.6 | 0.85 | ✓ DETECTED (85.0% conf) |

### 1.2 Aversion Traits (>60% frequency in dislikes)
| Trait | Frequency | Avg Rating | Weight | Status in B |
|-----|-----|-----|-----|-----|
| heavy_makeup | 89.0% | 1.3 | -0.92 | ✗ NOT DETECTED |
| visible_tattoos | 68.0% | 1.9 | -0.70 | ■ PARTIAL (small, 78% conf) |

**MetaFBP Score:** 4.18/5.0 | **T_match_positive:** 88.4 | **T_match_negative:** 66.0
**Total Visual Score:** 79.7

---

## 2. Psychometric Evidence Audit (Delta > 0.3)

### CRITICAL CONFLICT: Sloth (Delta: 0.60 - FRICTION FLAG)

**Subject A: "Compulsive Productivity"**
- Question: "Describe your ideal morning routine"
- Evidence: _"Wake up at 5am. 10k run. Cold shower. At desk by 6:30._"
- Extracted Trait: compulsive_productivity
- Mapped Sin: pride (0.95), inverse sloth (0.10)
- Confidence: 99%
- Interpretation: Subject exhibits achievement-oriented self-discipline with potential rigidity.
  Risk: May perceive leisure as moral failure.

**Subject B: "Leisure Prioritization"**
- Question: "How do you typically spend weekends?"
- Evidence: _"I refuse to work weekends. Life is for sleeping in and doing nothing productive._"
- Extracted Trait: leisure_prioritization
- Mapped Sin: sloth (0.85), gluttony (0.30)
- Confidence: 96%
- Interpretation: Explicitly rejects productivity norms; values rest over achievement.
  Risk: May perceive A's routine as neurotic or judgmental.

**Friction Probability:** 88% - This mismatch will surface within 10-15 interactions when scheduling conflicts arise (A wants 6am hike; B wants brunch at noon).

### CONFLICT: Communication Style (Gap: 0.80)

**Subject A Bluntness:** 1.0 (from response style analysis)
- Evidence: Short, declarative sentences. No hedging language. Commands over suggestions.

**Subject B Bluntness:** 0.2 (from response style analysis)
- Evidence: Passive voice, multiple qualifiers ("probably", "maybe", "I guess").

**Outcome Prediction:** A will be perceived as insensitive/aggressive within early interactions. B's indirect communication will frustrate A ("Why can't they just say what they want?").

---

## 3. Perceived Similarity Analysis

### Shared Traits (4 of 7):
| Trait | Direction | Contribution | A Evidence | B Evidence |
|-----|-----|-----|-----|-----|
| Wrath | Virtue | 1.237 | "not calling them out" | "avoid drama" |
| Lust | Vice | 0.785 | "try new things" | "spontaneous" |
| Greed | Virtue | 0.670 | "split evenly" | "happy to share" |
| Envy | Virtue | 0.464 | "content" | "secure" |

**Similarity Score:** 42.6%

**Why These Overlaps Matter:**
- Wrath alignment is particularly favorable - both partners will avoid confrontation, reducing early-stage conflict (but may create conflict-avoidance pattern long-term)
- Shared generosity (Greed virtue) prevents money-related tension
- Spontaneity match suggests compatible date preferences

---
```

```
## 4. Friction Analysis

- **Sloth Gap:** 0.60 points – CRITICAL. See detailed analysis above.
- **Bluntness Gap:** 0.80 points – HIGH RISK. Communication style mismatch.
- **Pride Gap:** 0.35 points – Moderate. A's higher pride may create perceived superiority.

**P_friction Applied:** 0.80 (20% penalty to S_psych)

---

## 5. Verdict: VIABLE (Short-Term) / RISKY (Long-Term)

**Confidence:** 72%

**Assessment:** Strong visual attraction (79.7) combined with meaningful personality overlap on core traits. The Wrath alignment is favorable for initial interactions – neither will rock the boat early. Biological chemistry is excellent (91.6).

**Watch Points:** 
- Sloth differential WILL emerge in activity planning (week 2-4)
- Bluntness gap will cause communication friction (week 1-2)
- A's conflict avoidance + B's indirect style may create unresolved issues

**Recommendation:** Flag for 30-day follow-up to assess friction prediction accuracy.
```

12.2 hla_gemini_analysis.md (Level 2B)

```
# Biological Forensic Report (HLA/MHC Analysis)
**Methodology:** HIBAG Imputation (EUR Model) | **Date:** 2026-01-14

## 1. Data Integrity Audit

| Locus | Subject A | Confidence | Subject B | Confidence | QC Status |
|-----|-----|-----|-----|-----|-----|
| HLA-A | A*01:01 | 0.982 | A*03:01 | 0.971 | ✓ PASS |
| HLA-A | A*02:01 | 0.965 | A*24:02 | 0.943 | ✓ PASS |
| HLA-B | B*08:01 | 0.991 | B*44:02 | 0.988 | ✓ PASS |
| HLA-B | B*07:02 | 0.978 | B*35:01 | 0.956 | ✓ PASS |
| HLA-DRB1 | DRB1*15:01 | 0.945 | DRB1*04:01 | 0.961 | ✓ PASS |
| HLA-DRB1 | DRB1*03:01 | 0.932 | DRB1*07:01 | 0.928 | ✓ PASS |

**Overall Imputation Quality:** HIGH (all alleles > 0.90 threshold)

## 2. Allelic Dissimilarity Assessment

**Unique Alleles:** 11 of 12 total allele slots
**Heterozygosity Index:** 0.916 (91.6%)

**Assessment:** EXCELLENT. Near-maximum genetic diversity at MHC loci. This pairing would produce offspring with exceptionally broad immune repertoire.

## 3. Peptide-Binding Groove Analysis

### Subject A Alleles:
| Allele | Binding Characteristics | Functional Significance |
|-----|-----|-----|
| A*01:01 | Binds negatively charged residues at P3 | Broad viral epitope coverage |
| A*02:01 | Anchor residues at P2 (L/M), P9 (V/L) | Most common HLA-A; well-studied |
| B*08:01 | Preference for R/K at P5 | Associated with autoimmune conditions |
| B*07:02 | Anchor at P2 (P), P9 (L) | Strong HIV-1 epitope presentation |
| DRB1*15:01 | Large P4 pocket; binds aromatic residues | MS susceptibility marker |

### Subject B Alleles:
| Allele | Binding Characteristics | Functional Significance |
|-----|-----|-----|
| A*03:01 | Basic residues at P2 | EBV epitope specialization |
| A*24:02 | Hydrophobic anchors at P2 (Y), P9 (F/L) | High affinity for HIV-1 gag epitopes |
| B*44:02 | Acidic preference at P2 | Protective against HIV progression |
| B*35:01 | Proline anchor at P2 | Dengue fever susceptibility |
| DRB1*04:01 | Small P1 pocket | Rheumatoid arthritis association |

### Combined Profile Interpretation:
The A/B pairing creates **complementary immune coverage**:
- A's B*07:02 + B's B*44:02 = comprehensive HIV protection
- A's DRB1*15:01 + B's DRB1*04:01 = diverse autoimmune risk profile
- No shared alleles = maximum offspring heterozygosity advantage

## 4. Olfactory/Pheromonal Prediction

**Theoretical Basis:** Wedekind et al. (1995) demonstrated that women prefer the scent of MHC-dissimilar men, particularly during ovulation. Santos et al. (2005) confirmed this extends to long-term partner selection.

**Heterozygosity Index:** 0.916
**Predicted Pheromone Attraction:** 91.6/100

**Assessment:** Subject A and Subject B are predicted to experience strong unconscious physical attraction. The near-complete MHC dissimilarity suggests:
1. Strong positive response to partner's natural scent
2. Elevated oxytocin response during physical proximity
3. Enhanced sexual arousal cues

**Caveat:** Olfactory attraction can be masked by perfumes, hormonal contraceptives, and environmental factors. Effect strongest in natural conditions.

## 5. Reproductive Fitness Estimate

**Offspring Heterozygosity Advantage:** +15% estimated survival advantage (based on population genetic models)

**Immune Repertoire Breadth:** Offspring would inherit non-overlapping alleles from both parents, creating resistance to approximately:
- 40% broader range of viral pathogens
- 35% broader range of bacterial pathogens
- 25% reduced autoimmune disease risk (due to diversity)

## 6. Summary Verdict

**HLA Compatibility Score:** 91.6/100
**Display Tier:** ■ Strong Chemistry Signal

This is an **exceptional biological pairing**. The near-complete MHC dissimilarity
```

predicts strong pheromonal attraction and superior offspring immune diversity. From a purely biological perspective, this match is highly favorable.

****Note:**** Biological compatibility does not override psychological/lifestyle compatibility. This report addresses only the genetic/biochemical dimension of attraction.

12.3 customer_summary.json (Level 1 - Sanitized)

```
{  
  "match_id": "match_7f8c9a0b",  
  "display_score": 75,  
  "badges": ["Instant Spark", "Visual Type Match", "Strong Chemistry"],  
  "synopsis": {  
    "headline": "A Classic 'Opposites Attract' Dynamic",  
    "body": "You have incredible physical and biological chemistry, plus you share  
    some important values around conflict and generosity. Your different  
    energy levels might actually complement each other!"  
  },  
  "compatibility_breakdown": {  
    "physical": {"score": 80, "label": "Strong Attraction", "icon": "\ud83d\udcbb"},  
    "personality": {"score": 52, "label": "Complementary", "icon": "\u2b1b"},  
    "chemistry": {"score": 92, "label": "Electric", "icon": "\ud83d\uddc4"}  
  },  
  "shared_traits": [  
    "You both prefer to avoid unnecessary conflict",  
    "You're both generous with friends and don't sweat small money stuff",  
    "You both enjoy trying new things and being spontaneous"  
  ],  
  "conversation_starters": [  
    "Ask about their favorite spontaneous adventure",  
    "Share a time you went out of your way for a friend",  
    "Discuss your ideal lazy Sunday vs. active Saturday"  
  ]  
}
```

13. Admin Protocols (System Prompts)

13.1 Protocol A: Psych/Visual Report Generation

TARGET FILE: gemini_narrative.md
INPUT: reasoning_chain.json (Phase 1 & 2)

SYSTEM PROMPT:
"You are the Harmonia Engine, a cynical evolutionary psychologist.

Input: Mathematical compatibility data including:

- MetaFBP neural prediction scores
- Trait preference model (extracted from user's rating history with frequencies)
- Trait detection results for target user with confidence levels
- Psychometric evidence snippets from questionnaire responses (verbatim quotes)
- Sin vectors with evidence_samples arrays

Task: Predict relationship survival and sexual viability with FORENSIC PRECISION.

Tone: Clinical, Ruthless, Darwinian.

MANDATORY OUTPUT FORMAT (Markdown):

1. Visual Preference Model

- Show calibration data (total faces rated, likes, dislikes)
- List mandatory traits (>80% frequency) with weights and source
- List aversion traits (>60% frequency) with penalties
- Show which traits detected in target at what confidence
- Calculate T_match_positive and T_match_negative scores
- Show MetaFBP component and final S_vis

2. Psychometric Evidence Audit

- For EVERY sin with Delta > 0.3 between users:
- State the Question ID and full question text
 - Quote the EXACT evidence fragment (verbatim user response)
 - Show the Extracted Trait and mapped sin dimension
 - Show the Confidence Score and weight of extraction
 - Provide behavioral interpretation and risk assessment

Format each as:

- **Subject X: '[Extracted Trait]'**
- Question: '[full question]'
- Evidence: '_[verbatim quote from user]'_
- Mapped Sin: [sin] ([score])
- Confidence: [%]
- Interpretation: [analysis]
- Risk: [potential issues]

3. Perceived Similarity Analysis

- List ALL shared traits with direction and contribution
- Include EVIDENCE from both users for each shared trait
- Explain WHY each overlap predicts positive interaction
- Note unshared traits but DO NOT penalize

4. Friction Analysis

- Calculate specific probability of failure for each flagged gap
- Show P_friction calculation
- Cite evidence for each friction prediction

5. Verdict

- 'Viable' or 'Dead on Arrival' with confidence percentage
- Separate short-term vs long-term assessment
- List specific watch points with predicted timeline"

13.2 Protocol B: HLA/Bio Report Generation

TARGET FILE: hla_gemini_analysis.md
INPUT: reasoning_chain.json (Phase 3)

SYSTEM PROMPT:
"You are an expert Geneticist specializing in the Major Histocompatibility Complex (MHC).

Input: HLA Alleles for Subject A and B, including:

- Imputation Posterior Probabilities from HIBAG for each allele
- Ancestry model used
- Per-allele confidence scores

Task: Provide comprehensive biological compatibility analysis.

MANDATORY OUTPUT FORMAT (Markdown):

1. Data Integrity Audit

- Table showing every allele with imputation confidence
- Flag any alleles below 0.80 as 'Low Confidence'

- Overall quality assessment
- 2. Allelic Dissimilarity Assessment
 - Count unique vs shared alleles
 - Calculate Heterozygosity Index
 - Interpret diversity level
- 3. Peptide-Binding Groove Analysis
 - For EVERY allele from BOTH subjects:
 - Describe binding characteristics (anchor positions, residue preferences)
 - Note functional significance (disease associations, pathogen coverage)
 - Assess complementarity between A and B alleles
- 4. Olfactory/Pheromonal Prediction
 - Cite Wedekind (1995) and relevant MHC-attraction research
 - Calculate predicted pheromone attraction score
 - Describe expected physical response
 - Note caveats (contraceptives, perfumes, etc.)
- 5. Reproductive Fitness Estimate
 - Estimate offspring heterozygosity advantage
 - Describe immune repertoire breadth
 - Quantify pathogen resistance improvement
- 6. Summary Verdict
 - HLA Compatibility Score
 - Display tier recommendation
 - Note that biological compatibility doesn't override psychological fit

Constraint: Use strict scientific terminology. Cite specific allele names and functions.
No romantic language. This is a genetics report."

14. Implementation Details & Future Expansion

14.1 MetaFBP Configuration Constants

Constant	Value	Description
ADAPTATION_STRENGTH_LAMBDA	0.01	Balances commonality vs personality
INNER_LOOP_STEPS	5	k-step gradient descent iterations
INNER_LR	0.01	Learning rate for inner loop (alpha)
TARGET_SHOTS_NS	5	Support set size per score class
TARGET_QUERY_NQ	5	Query set size per score class
FEATURE_DIM	512	ResNet-18 output dimension
GENERATOR_HIDDEN_DIM	512	MLP hidden layer size

14.2 Latency Mitigation: User Session Caching

To maintain 200ms response time per match, the Inner Loop is NOT run per-request:

Step	Trigger	Action	Storage
1	User opens app	Run Inner Loop adaptation once	Compute adapted_generator
2	Adaptation complete	Serialize generator weights	Redis cache (TTL = session)
3	Match request	Forward pass only	GPU memory
4	User swipes	Invalidate cache	Background async re-adapt

14.3 Future Expansion: Multi-Constraint Optimization

Stage	Formula	New Component	Status
Stage 1	$\theta_f + \lambda \mathbf{x}G(\mathbf{x})$	Visual Personality	IMPLEMENTED
Stage 2	$\theta_f + \lambda \mathbf{x}G(\mathbf{x}) + \lambda \mathbf{x}P(\mathbf{x})$	Personality Constraint P_{θ_p}	PLANNED
Stage 3	$\theta_f + \lambda \mathbf{x}G(\mathbf{x}) + \lambda \mathbf{x}P(\mathbf{x}) + \lambda \mathbf{x}H(\mathbf{x})$	HLA Constraint H_{θ_h}	RESEARCH

14.4 References

- [1] Lin, L., et al. "MetaFBP: Learning to Learn High-Order Predictor for Personalized Facial Beauty Prediction." ACM MM '23, pp. 6072-6080. DOI: 10.1145/3581783.3612319
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- [3] HIBAG: HLA Genotype Imputation with Attribute Bagging (Bioconductor)
- [4] Joel, S., et al. (2017). "Is Romantic Desire Predictable? Machine Learning Applied to Initial Romantic Attraction." Psychological Science, 28(10), 1478-1489.
- [5] Montoya, R.M., et al. (2008). "Is actual similarity necessary for attraction? A meta-analysis of actual and perceived similarity." Journal of Social and Personal Relationships, 25(6), 889-922.
- [6] Wedekind, C., et al. (1995). "MHC-dependent mate preferences in humans." Proceedings of the Royal Society B, 260(1359), 245-249.
- [7] Gottman, J.M. (1994). "What Predicts Divorce? The Relationship Between Marital Processes and Marital Outcomes." Lawrence Erlbaum Associates.