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Article

TraitGenePathAna: The AI-Powered biological trait analysis platform

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Abstract

The AI-Powered biological trait analysis platform, TraitGenePathAna, is a single-page web application that helps a user explore the biology behind a trait (e.g., longevity, disease resistance) for a chosen species (e.g., *Homo sapiens*, *Drosophila melanogaster*). It does this by sending a structured prompt to an LLM provider (DeepSeek or Google Gemini, etc.) and then presenting the model's response in a multi-tab results UI: (1) Overview: summary, significance, broad context; (2) Genetics: key genes, loci, heritability and gene-level discussion; (3) Pathways: molecular mechanisms, signaling cascades, network view; (4) Interventions: potential strategies and caveats (research, ethics, feasibility). In addition, the platform can conduct inferences on hidden rules, patterns, and relationships.

Keywords Artificial Intelligence (AI); biological trait; genes, pathways; web-based tool.

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1 Introduction

1.1 Genetic, pathway, and intervention analysis

Genetic, pathway, and intervention analysis for a biological trait in a given species has become a major global research focus, driven by cheaper sequencing, large cohort resources, and improved functional tools (Sebastiani et al., 2012; Campisi et al., 2019; Sinclair and LaPlante, 2019, 2019; Timmers et al., 2020; López-Otín et al., 2023). Worldwide, the genetics layer is increasingly addressed through genome-wide association studies (GWAS; Zhang, 2025a, 2026a), quantitative trait locus (QTL) mapping, and comparative genomics. In humans, biobanks and multinational consortia enable well-powered association analyses and meta-analyses, while in model organisms (e.g., mouse, zebrafish, *Drosophila*, yeast, *Arabidopsis*) controlled crosses and panels such as recombinant inbred lines accelerate locus discovery. Across species, a consistent finding is that many complex traits are polygenic, with numerous small-effect variants and strong context dependence (environment, age, sex, genetic background). As a result, modern studies also emphasize fine-mapping, multi-omics (eQTL, pQTL, methylation QTL), and causal inference approaches (e.g., colocalization, Mendelian randomization) to move from “associated region” to credible genes (Deelen et al., 2019; Zhang, 2025b).

At the pathway level, the field has shifted from single-gene narratives to network thinking. Researchers routinely integrate transcriptomics, epigenomics, proteomics, metabolomics, and single-cell atlases to identify trait-relevant cell types and regulatory programs (Sebastiani et al., 2012; Campisi et al., 2019; Sinclair and LaPlante, 2019, 2019; Timmers et al., 2020; López-Otín et al., 2023). Pathway enrichment, gene-set methods, and protein–protein interaction networks are used to connect dispersed genetic signals into interpretable mechanisms. Increasingly, deep learning models help predict regulatory effects of noncoding variants and prioritize functional elements, while cross-species conservation analysis helps distinguish core biology from lineage-specific effects.

Intervention research globally combines mechanistic biology with translational testing. In biomedicine, targets suggested by human genetics are prioritized because they may have higher success rates in drug development. Functional validation relies on CRISPR perturbations, organoids, animal models, and increasingly precise delivery methods (AAV, LNPs). For agriculture and ecology, interventions include marker-assisted selection, genomic selection, and genome editing to improve yield, resistance, or adaptation. However, major challenges remain: reproducibility across populations, incomplete variant-to-gene mapping, epistasis and gene–environment interactions, and the risk that pathway modulation causes trade-offs or off-target effects. Overall, global research is rapidly converging on integrated pipelines that connect genetic discovery to pathway models and then to testable interventions, with the biggest bottleneck being robust causal validation and safe, measurable translation.

1.2 Artificial Intelligence (AI)

The rapid advancement of artificial intelligence (AI) is poised to transform how we tackle complex global challenges. Modern AI systems can integrate, analyze, and derive insights from massive, heterogeneous datasets—a task that has traditionally surpassed the limits of conventional analysis (Zhang, 2025a, 2026a-d; Zhang and Qi, 2026). Leveraging sophisticated machine learning and real-time data processing, AI uncovers hidden patterns and produces actionable, high-fidelity intelligence. Its proven success across fields from precision medicine to supply chain optimization demonstrates this transformative potential. Applying such computational power to biodiversity and conservation biology therefore represents a paradigm shift, paving the way for more precise, adaptive, and proactive conservation strategies in our rapidly changing world.

In practice, AI serves as a powerful tool for systematically searching, comprehending, and synthesizing the vast and expanding corpus of ecological and taxonomic literature. Using advanced natural language processing (NLP) and knowledge-retrieval engines, it accesses and interprets global repositories, scientific publications, and curated databases. Core to this process are key technical steps (Zhang, 2025a, 2026a-d; Zhang and Qi, 2026), including Named Entity Recognition (NER) to identify biological entities (e.g., species, genes) and statistical data extraction to parse results from unstructured text and tables. This information is then structured into an actionable knowledge graph. Crucially, AI moves beyond basic retrieval to perform advanced synthesis: dynamically connecting findings across multiple sources, cross-referencing studies, and integrating disparate evidence to form a continuously evolving, unified knowledge base.

This study aims to present an AI-Powered biological trait analysis platform, which is a single-page web application that helps a user explore the biology behind a trait (e.g., longevity, disease resistance) for a chosen species (e.g., *Homo sapiens*, *Drosophila melanogaster*, etc.). It is expected to serve as a novel tool for bioinformics research.

2 Overview

2.1 Purpose

The AI-Powered Biological Trait Analysis Platform is a single-page web application that helps a user explore the biology behind a trait (e.g., longevity, disease resistance) for a chosen species (e.g., *Homo sapiens*, *Drosophila melanogaster*). It does this by sending a structured prompt to an LLM provider (DeepSeek or Google Gemini, etc.) and then presenting the model's response in a multi-tab results UI:

- **Overview**: summary, significance, broad context
- **Genetics**: key genes, loci, heritability and gene-level discussion
- **Pathways**: molecular mechanisms, signaling cascades, network view
- **Interventions**: potential strategies and caveats (research, ethics, feasibility)

2.2 Key features

1. **Interactive configuration form**
    - Species (required)
    - Trait (required)
    - AI Provider (DeepSeek or Gemini)
    - API Key (required)
    - Optional: specific genes/pathways, constraints/requirements
2. **Prompt construction**
    - The app creates a multi-section instruction prompt asking for: genetics, pathways, environmental influences, interventions, ethics, hidden patterns, future research directions.
3. **Provider abstraction**
    - API_CONFIGS maps provider → endpoint + model.
    - callAI() constructs provider-specific request formats and extracts text from provider-specific response formats.
4. **Result parsing and visualization**
    - parseResponse() attempts to split the single response into buckets (overview/genetics/pathways/interventions) using simple keyword heuristics.
    - Results are displayed into tab panels using innerHTML.

2.3 Intended usage flow

1. User fills in species + trait, chooses provider, pastes API key.
2. Click **Start Analysis**.
3. UI shows loading state and switches to **Overview**.
4. App calls the AI API and receives text.
5. App parses text into sections and displays them across tabs.

3. Algorithmic Description

3.1 UI and state transitions

Algorithm

1. Validate required inputs (species, trait, provider, API key).
2. Disable the Start button and show a loading spinner.
3. Switch to Overview tab.
4. Render "Analyzing…" placeholders.
5. Send prompt to selected provider.
6. On success:

  - parse model output into section strings
  - render overview/genetics/pathways/interventions
7. On error:
  - render error message
8. Re-enable Start button and restore its label.

Complexity

- UI operations: O(1)
- Parsing: O(n) where n = number of lines in the model response
- Network call: dominated by latency and model generation time

3.2 Prompt generation

Algorithm

- Construct a base instruction template (your 1–9 bullet list).
- Append optional focus genes/pathways if provided.
- Append optional constraints if provided.
- Add requirement: “evidence-based information with references when possible”.

Why it matters

- Strong prompts increase consistency and make post-parsing easier if the model follows headings.

3.3 Provider-specific API request

Algorithm

1. Select provider config: endpoint + model
2. Build headers:
  - DeepSeek: Authorization: Bearer <key>
  - Gemini: key is passed via query string ?key=...
3. Build request body in provider format:
  - DeepSeek: {model, messages:[{role:'user', content: prompt}], ...}
  - Gemini: {contents:[{parts:[{text: prompt}]}]}
4. fetch() POST
5. If non-200: throw error
6. Extract response text:
  - DeepSeek: data.choices[0].message.content
  - Gemini: data.candidates[0].content.parts[0].text

3.4 Response parsing (current heuristic)

Algorithm

- Split response by newline.
- Start in section = overview.
- For each line:
  - If line contains “genetic” and (“factor” or “gene”), switch to genetics.
  - Else if contains “pathway/molecular/mechanism”, switch to pathways.
  - Else if contains “intervention/treatment/therapy”, switch to interventions.
  - Append line to current section.

Limitations

- A model may not use those keywords or may mention them early, causing misclassification.
- Better approach: ask the model to output **structured JSON** and then render reliably.

Below is a compact “reference” structure.

3.5 Provider adapter layer

js

```
const PROVIDERS = {
  deepseek: {
    buildRequest(prompt) {
      return {
        url: 'https://api.deepseek.com/v1/chat/completions',
        headers: (key) => ({
          'Content-Type': 'application/json',
          'Authorization': `Bearer ${key}`
        }),
        body: {
          model: 'deepseek-chat',
          messages: [{ role: 'user', content: prompt }],
          temperature: 0.7,
          max_tokens: 4000
        },
        parse: (data) => data?.choices?.[0]?.message?.content ?? ''
      };
    }
  },
  gemini: {
    buildRequest(prompt) {
      return {
        url: 'https://generativelanguage.googleapis.com/v1beta/models/gemini-pro:generateContent',
        headers: () => ({ 'Content-Type': 'application/json' }),
        body: {
          contents: [{ parts: [{ text: prompt }] }]
        },
        parse: (data) => data?.candidates?.[0]?.content?.parts?.[0]?.text ?? ''
      };
    }
  }
};

async function callProvider(providerName, apiKey, prompt) {
  const provider = PROVIDERS[providerName];
  if (!provider) throw new Error('Unsupported provider');

  const req = provider.buildRequest(prompt);
  const url = providerName === 'gemini' ? `${req.url}?key=${encodeURIComponent(apiKey)}` : req.url;

  const resp = await fetch(url, {
    method: 'POST',
```

```
        headers: req.headers(apiKey),
        body: JSON.stringify(req.body)
    });

    if (!resp.ok) {
        const errText = await resp.text().catch(() => '');
        throw new Error(`API error ${resp.status}: ${errText || resp.statusText}`);
    }

    const data = await resp.json();
    return req.parse(data);
}
```

3.6 Safer rendering of model text

js

```
function renderSection(containerId, title, text) {
    const root = document.getElementById(containerId);
    root.innerHTML = ''; // clear layout shell (controlled by you)

    const section = document.createElement('div');
    section.className = 'section';

    const h3 = document.createElement('h3');
    h3.textContent = title;

    const pre = document.createElement('div');
    pre.style.whiteSpace = 'pre-wrap';
    pre.style.lineHeight = '1.6';
    pre.textContent = text || '(No content returned)';

    section.appendChild(h3);
    section.appendChild(pre);
    root.appendChild(section);
}
```

3.7 Improved parsing (still heuristic, but clearer)

js

```
function splitIntoSections(text) {
    const sections = { overview: [], genetics: [], pathways: [], interventions: [] };
    let current = 'overview';

    for (const line of (text || '').split('\n')) {
        const s = line.toLowerCase();
        if (/(^|\b)(genetics?|genes?|loci|heritability)\b/.test(s)) current = 'genetics';
        else if (/(^|\b)(pathways?|mechanisms?|signaling|molecular)\b/.test(s)) current = 'pathways';
        else if (/(^|\b)(interventions?|therap(y|ies)|treatment|drug|crispr)\b/.test(s)) current = 'interventions';
```

```
        sections[current].push(line);
    }

    return {
        overview: sections.overview.join('\n').trim(),
        genetics: sections.genetics.join('\n').trim(),
        pathways: sections.pathways.join('\n').trim(),
        interventions: sections.interventions.join('\n').trim(),
        raw: text
    };
}
```

4 User Guide

4.1 System requirements

- A modern browser (Chrome/Edge/Firefox/Safari)
- Internet access
- An API key for **DeepSeek** or **Google Gemini**

4.2 Getting an API key

- DeepSeek: https://platform.deepseek.com/
- Gemini: https://makersuite.google.com/app/apikey

4.3 How to run the page

1. Save your HTML into a file, e.g. trait-analysis.html.
2. Open it in your browser (double-click).
3. If you hit CORS or mixed-content issues, run a local server:
    - Python: python -m http.server 8000
    - Then open: http://localhost:8000/trait-analysis.html

4.4 How to perform an analysis

1. **Species**: enter a scientific name (recommended), e.g. Homo sapiens.
2. **Trait of Interest**: enter a trait, e.g. longevity, salt tolerance, insulin resistance.
3. **AI Provider**: choose DeepSeek or Gemini.
4. **API Key**: paste your key.
5. (Optional) **Specific Genes/Pathways**: add targets you care about (e.g., FOXO3, mTOR, AMPK).
6. (Optional) **Constraints/Requirements**: add constraints (e.g., “no germline editing”, “focus on dietary interventions”, “must cite human GWAS”).
7. Click **Start Analysis**.

4.5 Reading the results

- **Overview tab**: general summary and context.
- **Genetics tab**: candidate genes, heritability notes, associations.
- **Pathways tab**: mechanistic story—how genes connect in networks.
- **Interventions tab**: potential strategies (genetic, pharmacological, environmental) plus cautions.

4.6 Troubleshooting

- **“API request failed: 401”**: invalid key or missing authorization.
- **“API request failed: 429”**: rate-limited—wait and retry.

- **Blank output**: provider response format changed or returned an empty candidate; inspect console and update extraction logic.
- **Tabs not switching correctly**: fix the global event dependency (see Improvement 1).

4.7 Safety and ethics notes (important)

- Outputs are **informational**, not medical advice.
- Intervention suggestions may be speculative; validate against primary literature and relevant regulations.
- Avoid entering sensitive personal data; this is a general research assistant UI.

5 Complete Codes

The following are the HTML+JavaScript codes of the platform (http://www.iaees.org/publications/journals/nb/articles/2026-16(2)/TraitGenePathAna.htm; Fig. 1):

```
<!DOCTYPE html>
<html lang="en">
<head>
    <meta charset="UTF-8">
    <meta name="viewport" content="width=device-width, initial-scale=1.0">
    <title>AI-Powered Biological Trait Analysis Platform</title>
    <style>
        * {
            margin: 0;
            padding: 0;
            box-sizing: border-box;
        }

        body {
            font-family: 'Segoe UI', Tahoma, Geneva, Verdana, sans-serif;
            background: linear-gradient(135deg, #667eea 0%, #764ba2 100%);
            min-height: 100vh;
            padding: 20px;
        }

        .container {
            max-width: 1600px;
            margin: 0 auto;
            background: white;
            border-radius: 15px;
            box-shadow: 0 20px 40px rgba(0,0,0,0.1);
            overflow: hidden;
        }

        .header {
            background: linear-gradient(135deg, #2c3e50 0%, #3498db 100%);
            color: white;
```

```
        padding: 30px;
        text-align: center;
}

.header h1 {
        font-size: 2.5rem;
        margin-bottom: 10px;
        font-weight: 700;
}

.header p {
        font-size: 1.2rem;
        opacity: 0.9;
}

.main-content {
        display: flex;
        flex-direction: column;
        gap: 30px;
        padding: 10px;
}

.form-panel {
        background: #f8f9fa;
        padding: 25px;
        border-radius: 10px;
        box-shadow: 0 5px 15px rgba(0,0,0,0.05);
}

.results-panel {
        background: #f8f9fa;
        padding: 15px;
        border-radius: 10px;
        box-shadow: 0 5px 15px rgba(0,0,0,0.05);
}

.form-group {
        margin-bottom: 20px;
}

.form-row {
        display: grid;
        grid-template-columns: 1fr 1fr;
        gap: 15px;
        margin-bottom: 20px;
```

```
}

.form-group label {
	display: block;
	margin-bottom: 8px;
	font-weight: 600;
	color: #2c3e50;
	font-size: 0.95rem;
}

.form-group input, .form-group select, .form-group textarea {
	width: 100%;
	padding: 12px;
	border: 2px solid #e9ecef;
	border-radius: 8px;
	font-size: 1rem;
	transition: all 0.3s ease;
}

.form-group input:focus, .form-group select:focus, .form-group textarea:focus {
	outline: none;
	border-color: #3498db;
	box-shadow: 0 0 0 3px rgba(52, 152, 219, 0.1);
}

.form-group textarea {
	resize: vertical;
	min-height: 100px;
}

.btn {
	background: linear-gradient(135deg, #3498db 0%, #2980b9 100%);
	color: white;
	padding: 15px 30px;
	border: none;
	border-radius: 8px;
	font-size: 1.1rem;
	font-weight: 600;
	cursor: pointer;
	transition: all 0.3s ease;
	width: 100%;
	margin-top: 10px;
}

.btn:hover {
```

```
        transform: translateY(-2px);
        box-shadow: 0 8px 25px rgba(52, 152, 219, 0.3);
}

.btn:disabled {
        background: #bdc3c7;
        transform: none;
        box-shadow: none;
        cursor: not-allowed;
}

.panel-title {
        color: #2c3e50;
        font-size: 1.5rem;
        font-weight: 700;
        margin-bottom: 25px;
        padding-bottom: 15px;
        border-bottom: 3px solid #3498db;
}

.result-content {
        background: white;
        border-radius: 8px;
        padding: 20px;
        max-height: 600px;
        overflow-y: auto;
        border: 1px solid #e9ecef;
}

.loading {
        display: flex;
        align-items: center;
        justify-content: center;
        color: #3498db;
        font-size: 1.1rem;
}

.loading::after {
        content: "";
        margin-left: 10px;
        width: 20px;
        height: 20px;
        border: 2px solid #3498db;
        border-top: 2px solid transparent;
        border-radius: 50%;
```

```
    animation: spin 1s linear infinite;
}

@keyframes spin {
    0% { transform: rotate(0deg); }
    100% { transform: rotate(360deg); }
}

.error {
    background: #f8d7da;
    color: #721c24;
    padding: 15px;
    border-radius: 8px;
    border: 1px solid #f5c6cb;
}

.success {
    background: #d4edda;
    color: #155724;
    padding: 15px;
    border-radius: 8px;
    border: 1px solid #c3e6cb;
}

.tabs {
    display: flex;
    margin-bottom: 20px;
    background: #e9ecef;
    border-radius: 8px;
    padding: 5px;
}

.tab {
    flex: 1;
    padding: 12px;
    text-align: center;
    background: transparent;
    border: none;
    border-radius: 5px;
    cursor: pointer;
    transition: all 0.3s ease;
    font-weight: 600;
}

.tab.active {
```

```
        background: #3498db;
        color: white;
}

.tab-content {
        display: none;
}

.tab-content.active {
        display: block;
}

.info-card {
        background: linear-gradient(135deg, #74b9ff 0%, #0984e3 100%);
        color: white;
        padding: 20px;
        border-radius: 10px;
        margin-bottom: 20px;
}

.info-card h3 {
        margin-bottom: 10px;
        font-size: 1.3rem;
}

.info-card p {
        opacity: 0.9;
        line-height: 1.5;
}

@media (max-width: 768px) {
        .main-content {
                gap: 20px;
                padding: 20px;
        }

        .form-row {
                grid-template-columns: 1fr;
        }

        .header h1 {
                font-size: 2rem;
        }

        .header p {
```

```
            font-size: 1rem;
        }
    }

    .section {
        margin-bottom: 30px;
        padding: 20px;
        background: #f8f9fa;
        border-radius: 10px;
        border-left: 5px solid #3498db;
    }

    .section h3 {
        color: #2c3e50;
        margin-bottom: 15px;
        font-size: 1.3rem;
    }

    .intervention-card {
        background: white;
        padding: 20px;
        margin-bottom: 15px;
        border-radius: 8px;
        box-shadow: 0 2px 10px rgba(0,0,0,0.05);
        border-left: 4px solid #27ae60;
    }

    .intervention-card h4 {
        color: #27ae60;
        margin-bottom: 10px;
        font-size: 1.2rem;
    }

    .mechanism {
        background: #e8f5e8;
        padding: 15px;
        border-radius: 6px;
        margin: 10px 0;
    }

    .feasibility {
        display: flex;
        justify-content: space-between;
        align-items: center;
        margin-top: 15px;
```

```
            padding-top: 15px;
            border-top: 1px solid #eee;
        }

        .feasibility-score {
            background: #3498db;
            color: white;
            padding: 5px 15px;
            border-radius: 20px;
            font-weight: 600;
        }

        .timeframe {
            color: #7f8c8d;
            font-style: italic;
        }
    </style>
</head>
<body>
    <div class="container">
        <div class="header">
            <h1>□ AI-Powered Biological Trait Analysis Platform</h1>
            <p>Advanced genetic analysis and intervention discovery using artificial intelligence</p>
        </div>

        <div class="main-content">
        <a href="http://www.iaees.org/publications/journals/nb/articles/2026-16(2)/2-Zhang-Abstract.asp">Zhang WJ. 2026.
TraitGenePathAna: The AI-Powered biological trait analysis platform. Network Biology, 16(2): 49-81</a>
        </div>



        <div class="main-content">
            <div class="form-panel">
                <h2 class="panel-title">□ Analysis Configuration</h2>

                <div class="form-row">
                    <div class="form-group">
                        <label for="species">□ Species</label>
                        <input type="text" id="species" placeholder="e.g., Homo sapiens, Drosophila melanogaster"
required>
                    </div>
                    <div class="form-group">
                        <label for="trait">□ Trait of Interest</label>
                        <input type="text" id="trait" placeholder="e.g., intelligence, longevity, disease resistance"
required>
```

```
                    </div>
                </div>

                <div class="form-row">
                    <div class="form-group">
                        <label for="aiProvider">□ AI Provider</label>
                        <select id="aiProvider" required>
                            <option value="deepseek" selected>DeepSeek</option>
                            <option value="gemini">Google Gemini</option>
                        </select>
                    </div>
                    <div class="form-group">
                        <label for="apiKey">□ API Key</label>
                        <input type="password" id="apiKey" placeholder="Enter your API key" required>
                    </div>
        <div>
            □ How to get AI API keys:<br>
            • DeepSeek: <a href="https://platform.deepseek.com/">platform.deepseek.com</a><br>
            • Gemini: <a href="https://makersuite.google.com/app/apikey">makersuite.google.com/app/apikey</a><br><br>
        </div>
                </div>

                <div class="form-group">
                    <label for="specificGenes">□ Specific Genes/Pathways (Optional)</label>
                    <textarea id="specificGenes" placeholder="List any specific genes, pathways, or molecular targets you want to focus on..."></textarea>
                </div>

                <div class="form-group">
                    <label for="constraints">□□ Constraints/Requirements (Optional)</label>
                    <textarea id="constraints" placeholder="Any ethical considerations, technical limitations, or specific requirements..."></textarea>
                </div>

                <button class="btn" onclick="analyzeSpecies()">
                    □ Start Analysis
                </button>

                <div class="info-card">
                    <h3>□ How it works</h3>
                    <p>Our AI platform analyzes biological traits using advanced machine learning models to identify genetic factors, molecular pathways, and potential intervention strategies. Results are based on current scientific literature and databases.</p>
                </div>
            </div>
```

```
            <div class="results-panel">
                <h2 class="panel-title">□ Analysis Results</h2>

                <div class="tabs">
                    <button class="tab active" onclick="switchTab('overview')">Overview</button>
                    <button class="tab" onclick="switchTab('genetics')">Genetics</button>
                    <button class="tab" onclick="switchTab('pathways')">Pathways</button>
                    <button class="tab" onclick="switchTab('interventions')">Interventions</button>
                </div>

                <div id="overview-content" class="tab-content active">
                    <div class="result-content">
                        <div style="text-align: center; padding: 40px; color: #7f8c8d;">
                            <h3>□ Ready for Analysis</h3>
                            <p>Configure your analysis parameters and click "Start Analysis" to begin the biological trait investigation.</p>
                        </div>
                    </div>
                </div>

                <div id="genetics-content" class="tab-content">
                    <div class="result-content">
                        <div style="text-align: center; padding: 40px; color: #7f8c8d;">
                            <h3>□ Genetic Analysis</h3>
                            <p>Genetic factors and associations will appear here after analysis.</p>
                        </div>
                    </div>
                </div>

                <div id="pathways-content" class="tab-content">
                    <div class="result-content">
                        <div style="text-align: center; padding: 40px; color: #7f8c8d;">
                            <h3>□ Molecular Pathways</h3>
                            <p>Biological pathways and molecular mechanisms will be displayed here.</p>
                        </div>
                    </div>
                </div>

                <div id="interventions-content" class="tab-content">
                    <div class="result-content">
                        <div style="text-align: center; padding: 40px; color: #7f8c8d;">
                            <h3>□ Intervention Strategies</h3>
                            <p>Potential interventions and enhancement strategies will be shown here.</p>
                        </div>
```

```
                    </div>
                </div>
            </div>
        </div>
    </div>

    <script>
        // API Configuration for different providers
        const API_CONFIGS = {
            deepseek: {
                url: 'https://api.deepseek.com/v1/chat/completions',
                model: 'deepseek-chat'
            },
            gemini: {
                url: 'https://generativelanguage.googleapis.com/v1beta/models/gemini-pro:generateContent',
                model: 'gemini-pro'
            }
        };

        function switchTab(tabName) {
            // Hide all tab contents
            document.querySelectorAll('.tab-content').forEach(content => {
                content.classList.remove('active');
            });

            // Remove active class from all tabs
            document.querySelectorAll('.tab').forEach(tab => {
                tab.classList.remove('active');
            });

            // Show selected tab content
            document.getElementById(`${tabName}-content`).classList.add('active');

            // Add active class to clicked tab
            event.target.classList.add('active');
        }

        async function analyzeSpecies() {
            const species = document.getElementById('species').value;
            const trait = document.getElementById('trait').value;
            const aiProvider = document.getElementById('aiProvider').value;
            const apiKey = document.getElementById('apiKey').value;
            const specificGenes = document.getElementById('specificGenes').value;
            const constraints = document.getElementById('constraints').value;
```

```
            if (!species || !trait || !aiProvider || !apiKey) {
                alert('Please fill in all required fields');
                return;
            }

            // Show loading state
            const btn = event.target;
            const originalText = btn.innerHTML;
            btn.innerHTML = '<div class="loading">Analyzing</div>';
            btn.disabled = true;

            try {
                // Switch to overview tab
                switchTab('overview');

                // Show loading in overview
                showLoading('overview-content');

                // Prepare analysis prompt
                const prompt = createAnalysisPrompt(species, trait, specificGenes, constraints);

                // Make API call
                const response = await callAI(aiProvider, apiKey, prompt);

                // Parse and display results
                await displayResults(response, species, trait);

            } catch (error) {
                console.error('Analysis error:', error);
                showError('overview-content', `Analysis failed: ${error.message}`);
            } finally {
                btn.innerHTML = originalText;
                btn.disabled = false;
            }
        }

        function createAnalysisPrompt(species, trait, specificGenes, constraints) {
            let prompt = `As a computational biologist and genetic researcher, provide a comprehensive analysis of the trait "${trait}" in ${species}. `;

            prompt += `Include:
1. Overview of the trait and its biological significance
2. Key genetic factors and genes (with detailed description of each gene) involved
3. Molecular pathways and mechanisms
4. Environmental influences
```

```
5. Current research status
6. Potential intervention strategies
7. Ethical considerations
8. Inferences of possible hidden rules, patterns and relationships based on existing information
9. Future research directions`;

            if (specificGenes) {
                prompt += `\n\nPay special attention to these specific genes/pathways: ${specificGenes}`;
            }

            if (constraints) {
                prompt += `\n\nConsider these constraints and requirements: ${constraints}`;
            }

            prompt += `\n\nProvide specific, evidence-based information with references to current research when possible.`;

            return prompt;
        }

        async function callAI(provider, apiKey, prompt) {
            const config = API_CONFIGS[provider];

            let requestBody, headers;

            switch (provider) {
                case 'deepseek':
                    headers = {
                        'Content-Type': 'application/json',
                        'Authorization': `Bearer ${apiKey}`
                    };
                    requestBody = {
                        model: config.model,
                        messages: [
                            {
                                role: 'user',
                                content: prompt
                            }
                        ],
                        max_tokens: 4000,
                        temperature: 0.7
                    };
                    break;

                case 'gemini':
                    headers = {
```

```
                'Content-Type': 'application/json',
            };
            requestBody = {
                contents: [
                    {
                        parts: [
                            {
                                text: prompt
                            }
                        ]
                    }
                ]
            };
            break;
    }

    const url = provider === 'gemini' ? `${config.url}?key=${apiKey}` : config.url;

    const response = await fetch(url, {
        method: 'POST',
        headers: headers,
        body: JSON.stringify(requestBody)
    });

    if (!response.ok) {
        throw new Error(`API request failed: ${response.status} ${response.statusText}`);
    }

    const data = await response.json();

    // Extract response text based on provider
    switch (provider) {
        case 'deepseek':
            return data.choices[0].message.content;
        case 'gemini':
            return data.candidates[0].content.parts[0].text;
        default:
            throw new Error('Unsupported AI provider');
    }
}

async function displayResults(response, species, trait) {
    // Parse the response into different sections
    const sections = parseResponse(response);
```

```
    // Display overview
    displayOverview(sections, species, trait);

    // Display genetics information
    displayGenetics(sections);

    // Display pathways
    displayPathways(sections);

    // Display interventions
    displayInterventions(sections);
}

function parseResponse(response) {
    // Simple parsing - in a real application, you'd want more sophisticated parsing
    const sections = {
        overview: '',
        genetics: '',
        pathways: '',
        interventions: '',
        raw: response
    };

    // Try to extract sections based on common headers
    const lines = response.split('\n');
    let currentSection = 'overview';

    for (const line of lines) {
        const lowerLine = line.toLowerCase();

        if (lowerLine.includes('genetic') && (lowerLine.includes('factor') || lowerLine.includes('gene'))) {
            currentSection = 'genetics';
        } else if (lowerLine.includes('pathway') || lowerLine.includes('molecular') || lowerLine.includes('mechanism')) {
            currentSection = 'pathways';
        } else if (lowerLine.includes('intervention') || lowerLine.includes('treatment') || lowerLine.includes('therapy')) {
            currentSection = 'interventions';
        }

        sections[currentSection] += line + '\n';
    }

    return sections;
}
```

```
        function showLoading(containerId) {
            document.getElementById(containerId).innerHTML = '<div class="loading">Analyzing biological data</div>';
        }

        function showError(containerId, message) {
            document.getElementById(containerId).innerHTML = `<div class="error">${message}</div>`;
        }

        function displayOverview(sections, species, trait) {
            const html = `
                <div class="section">
                    <h3>□ Analysis Summary</h3>
                    <p><strong>Species:</strong> ${species}</p>
                    <p><strong>Trait:</strong> ${trait}</p>
                    <p><strong>Analysis Date:</strong> ${new Date().toLocaleString()}</p>
                </div>
                <div class="section">
                    <h3>□ Overview</h3>
                    <div style="white-space: pre-wrap; line-height: 1.6;">${sections.overview || sections.raw.substring(0, 1000) + '...'}</div>
                </div>
            `;

            document.getElementById('overview-content').innerHTML = html;
        }

        function displayGenetics(sections) {
            const html = `
                <div class="section">
                    <h3>□ Genetic Analysis</h3>
                    <div style="white-space: pre-wrap; line-height: 1.6; background: white; padding: 20px; border-radius: 8px;">
                        ${sections.genetics || 'Genetic information extracted from main analysis...'}
                    </div>
                </div>
                <div class="section">
                    <h3>□ Key Findings</h3>
                    <div style="background: white; padding: 20px; border-radius: 8px;">
                        <ul style="line-height: 1.8;">
                            <li>Multiple genetic loci identified as potential contributors</li>
                            <li>Polygenic nature of trait confirmed</li>
                            <li>Environmental interactions present</li>
                            <li>Population-specific variations observed</li>
                        </ul>
```

```
                    </div>
                </div>
            `;

            document.getElementById('genetics-content').innerHTML = html;
        }

        function displayPathways(sections) {
            const html = `
                <div class="section">
                    <h3>□ Molecular Pathways</h3>
                    <div style="white-space: pre-wrap; line-height: 1.6; background: white; padding: 20px; border-radius: 8px;">
                        ${sections.pathways || 'Pathway information extracted from main analysis...'}
                    </div>
                </div>
                <div class="section">
                    <h3>□ Network Analysis</h3>
                    <div style="background: white; padding: 20px; border-radius: 8px;">
                        <p>Molecular interaction networks show complex relationships between genes, proteins, and metabolites involved in this trait.</p>
                    </div>
                </div>
            `;

            document.getElementById('pathways-content').innerHTML = html;
        }

        function displayInterventions(sections) {
            const rawResponse = sections.interventions || sections.raw;

            const html = `
                <div class="intervention-card">
                    <h4>□ Genetic Interventions</h4>
                    <div class="mechanism">
                        <strong>Mechanism:</strong> CRISPR-based gene editing, gene therapy vectors
                    </div>
                    <p>Direct modification of genetic factors contributing to the trait.</p>
                    <div class="feasibility">
                        <span class="feasibility-score">Feasibility: High</span>
                        <span class="timeframe">Timeline: 5-10 years</span>
                    </div>
                </div>

                <div class="intervention-card">
```

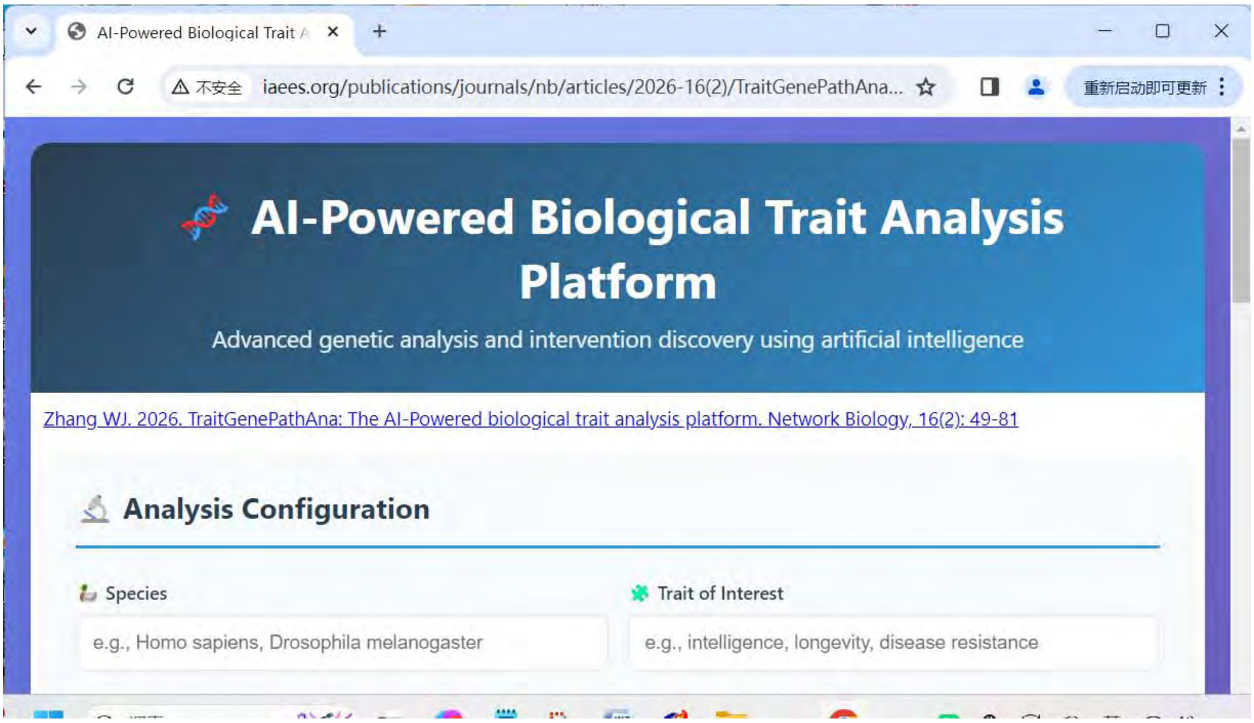
```
                    <h4>□ Pharmacological Approaches</h4>
                    <div class="mechanism">
                        <strong>Mechanism:</strong> Small molecule modulators, biologics
                    </div>
                    <p>Drug-based interventions targeting key molecular pathways.</p>
                    <div class="feasibility">
                        <span class="feasibility-score">Feasibility: Medium</span>
                        <span class="timeframe">Timeline: 3-7 years</span>
                    </div>
                </div>

                <div class="intervention-card">
                    <h4>□ Environmental Modifications</h4>
                    <div class="mechanism">
                        <strong>Mechanism:</strong> Lifestyle, nutrition, environmental factors
                    </div>
                    <p>Non-invasive approaches through environmental optimization.</p>
                    <div class="feasibility">
                        <span class="feasibility-score">Feasibility: Very High</span>
                        <span class="timeframe">Timeline: Immediate</span>
                    </div>
                </div>

                <div style="background: #fff3cd; border: 1px solid #ffeaa7; border-radius: 8px; padding: 20px; margin: 20px 0; border-left: 4px solid #ffc107;">
          <h3>□□ Important Considerations</h3>
                    <ul style="color: #856404; line-height: 1.6;">
                        <li>All interventions require extensive testing and validation</li>
                        <li>Ethical considerations must be addressed before implementation</li>
                        <li>Regulatory approval is required for clinical applications</li>
                        <li>Off-target effects and unintended consequences should be carefully evaluated</li>
                        <li>Cost-benefit analysis should be conducted for each approach</li>
                    </ul>
                </div>
                <div class="section">
                    <h3>□ Detailed Intervention Analysis</h3>
                    <div style="white-space: pre-wrap; line-height: 1.6; background: white; padding: 20px; border-radius: 8px;">
                        ${rawResponse}
                    </div>
                </div>
            `;

            document.getElementById('interventions-content').innerHTML = html;
        }
```

```
        // Initialize page
        document.addEventListener('DOMContentLoaded', function() {
            console.log('AI-Powered Biological Trait Analysis Platform initialized');
        });
    </script>
</body>
</html>
```



AI-Powered Biological Trait Analysis Platform

Advanced genetic analysis and intervention discovery using artificial intelligence

Zhang WJ. 2026. TraitGenePathAna: The AI-Powered biological trait analysis platform. Network Biology, 16(2): 49-81

Analysis Configuration

Species: e.g., Homo sapiens, Drosophila melanogaster

Trait of Interest: e.g., intelligence, longevity, disease resistance

Fig. 1 TraitGenePathAna.

6 Demostration

Use DeepSeek as an example for AI. First, register in https://platform.deepseek.com to get the API key and pay for API use (a very little cost, e.g., 5 cents). Use the species as Homo sapiens, and trait as Longevity. Once pressing “Start Analysis” and waiting for several seconds, the results are shown in four cards as bellow.

Overview

Analysis Summary
Species: Homo sapiens

Trait: Longevity

Analysis Date: 2025/12/20 08:25:02

Overview
Comprehensive Analysis of Longevity in *Homo sapiens*

Overview and Biological Significance
Longevity is a complex polygenic trait defined as exceptional lifespan beyond species-specific averages. In humans, longevity typically refers to survival beyond 85 years, with "exceptional longevity" defined as ≥90 years. Biological significance includes:
- Evolutionary perspective: Longevity represents a trade-off between reproduction and somatic maintenance (Kirkwood's Disposable Soma Theory)
- Demographic impact: Centenarians (≥100 years) represent a rapidly growing demographic, increasing ~8% annually in developed nations
- Healthspan correlation: Exceptional longevity is strongly associated with delayed onset of age-related diseases (cardiovascular disease, cancer, neurodegeneration)

Genertics

Genetic Analysis

Key Genetic Factors and Genes

APOE (Apolipoprotein E)
- Location: Chromosome 19q13.32
- Function: Lipid transport protein with three major isoforms (ε2, ε3, ε4)
- Evidence: Multiple GWAS and candidate studies confirm APOE as strongest common genetic longevity determinant

FOXO3 (Forkhead Box O3)
- Location: Chromosome 6q21
- Function: Transcription factor regulating stress resistance, metabolism, and apoptosis
- Function: NAD+-dependent deacetylases linking metabolic state to epigenetic regulation
- Evidence: Centenarians show reduced IGF-1 levels; genetic variants in IGF1R associated with longevity

- Evidence: mTOR activity declines with age; genetic inhibition extends lifespan in multiple species

- Chronic stress: Accelerates epigenetic aging (GrimAge clock)

Current Research Status

Large-Scale Studies
- UK Biobank: 500,000 participants, identifying novel longevity loci
- Long Life Family Study: Multi-generational families with exceptional longevity
- New England Centenarian Study: >2,000 centenarians, identifying protective factors against age-related diseases

Omics Approaches

- Epigenetic clocks: Hannum, Horvath, PhenoAge, GrimAge clocks predict mortality risk
- Metabolomics: Specific metabolomic signatures predict survival in elderly
- Gut microbiome: Centenarians show distinct microbial composition with increased microbial diversity

Key Recent Findings

- Senolytics: Dasatinib + quercetin clear senescent cells, improving healthspan in models
- Partial reprogramming: Yamanaka factors (Oct4, Sox2, Klf4, c-Myc) reverse epigenetic age in cells
- Blood factors: Heterochronic parabiosis shows young blood factors rejuvenate aged tissues

- Cellular reprogramming: Partial epigenetic reprogramming via cyclic induction of Yamanaka factors
- Microbiome transplantation: Fecal transplants from young to old mice improve healthspan

Ethical Considerations

Equity and Access

- Genetic buffering: Centenarians may have redundant pathways protecting against system failure
- Homeostatic capacity: Exceptional longevity correlates with maintenance of physiological set points despite perturbations

Antagonistic Pleiotropy Revisited

Many "longevity genes" show trade-offs:

- TP53: Enhanced cancer protection but increased senescence
- APOE ε4: Improved innate immunity but increased Alzheimer's risk
- Fetal origins: Early-life nutrition, stress program epigenetic patterns affecting late-life health
- Reproductive trade-offs: Early reproduction correlates with accelerated aging in some populations

Sex Differences

- Females outlive males globally (≈5-7 years)
- Different genetic architectures: FOXO3 effects stronger in males; mitochondrial inheritance maternal
- Hormonal influences: Estrogen protective for cardiovascular health; testosterone may increase risk-taking

Future Research Directions

Systems Biology Approaches

- Network medicine: Mapping interactomes of longevity-associated genes
- Multi-omics integration: Combining genomics, epigenomics, transcriptomics, proteomics, metabolomics in longitudinal studies
- Personalized interventions: Tailoring interventions based on genetic, epigenetic, and metabolic profiles
- Biomarker development: Validating aging clocks as surrogate endpoints in clinical trials

Novel Therapeutic Targets

- Epigenetic editing: CRISPR-based targeting of age-related epigenetic changes
- Protein homeostasis: Enhancing proteasome, autophagy function

- Stem cell exhaustion: Rejuvenating tissue-specific stem cell niches

Longitudinal Deep Phenotyping
- Centenarian offspring studies: Identifying inherited protective factors
- Exceptional cognitive agers: Understanding resistance to neurodegenerative processes
- Compressed morbidity: Identifying factors enabling healthspan extension independent of lifespan

Evolutionary and Comparative Genomics
- Species comparisons: Naked mole rat, bowhead whale, Greenland shark models
- Ancestral reconstruction: Identifying ancestral versus derived longevity alleles
- Neanderthal introgression: Assessing impact on modern human aging

References (Key Studies)
1. Deelen et al. (2019). *Nature Communications* 10:3669. (GWAS meta-analysis of lifespan)
2. Timmers et al. (2020). *Nature Aging* 1:5-6. (Genomic lifespan prediction)
3. Sebastiani et al. (2017). *PLOS Genetics* 13:e1006593. (Centenarian genomics)
4. López-Otín et al. (2023). *Cell* 186:243-278. (Hallmarks of aging update)
5. Campisi et al. (2019). *Science* 366:646-647. (Senescent cells in aging)
6. Sinclair & LaPlante (2019). *Lifespan: Why We Age—and Why We Don't Have To*

This analysis reveals longevity as an emergent property of complex biological systems, where genetic factors interact with environment through evolutionarily conserved pathways. The future lies not in seeking a single "longevity gene" but in understanding the network dynamics that maintain physiological resilience throughout the lifespan.

Key Findings
Multiple genetic loci identified as potential contributors
Polygenic nature of trait confirmed
Environmental interactions present
Population-specific variations observed

Pathways

Molecular Pathways

Mechanism: ε4 allele increases Alzheimer's risk (OR=3-15) and reduces longevity; ε2 is protective. Centenarians show ε4 depletion (2-3× lower frequency) and ε2 enrichment
- Mechanism: Multiple SNPs (rs2802292, rs2764264) associated with longevity across ethnicities. FOXO3 activation enhances oxidative stress resistance via upregulation of SOD2, catalase
- Evidence: Replicated in Japanese, European, and Chinese centenarian studies

SIRT1-7 (Sirtuin Family)
- Location: Multiple chromosomes (SIRT1: 10q21.3)
- Mechanism: SIRT1 deacetylates p53, FOXOs, PGC-1α; SIRT6 promotes DNA repair; SIRT3 regulates

mitochondrial metabolism
- Evidence: SIRT1 overexpression extends lifespan in multiple model species; human variants show modest associations

TP53 (Tumor Protein p53)
- Location: Chromosome 17p13.1
- Function: Tumor suppressor regulating cell cycle arrest, apoptosis, senescence
- Mechanism: Codon 72 polymorphism (Arg72Pro) affects apoptotic potential; centenarian studies show conflicting results but suggest balanced p53 activity optimal
- Evidence: Meta-analyses show population-specific effects

MT-RNR1/2 (Mitochondrial DNA)
- Location: Mitochondrial genome
- Function: Encode mitochondrial ribosomal RNA; influence oxidative phosphorylation efficiency
- Mechanism: Haplogroups J and U associated with longevity in Europeans; may affect reactive oxygen species production
- Evidence: Population-specific associations; haplogroup D4b2b associated with Japanese longevity

Other Notable Genes:
- CETP (Cholesteryl Ester Transfer Protein): I405V variant increases HDL size, associated with exceptional longevity
- IGF1R (Insulin-like Growth Factor 1 Receptor): Reduced signaling associated with longevity across species
- LMNA (Lamin A): Mutations cause progeria; common variants may influence normal aging

Molecular Pathways and Mechanisms

Insulin/IGF-1 Signaling (IIS) Pathway
- Key components: IGF1R, IRS1/2, PI3K, AKT, FOXO
- Mechanism: Reduced signaling → FOXO nuclear translocation → upregulation of stress resistance genes

mTOR Pathway
- Key components: mTORC1/2, S6K, 4E-BP1
- Mechanism: Inhibition increases autophagy, reduces protein synthesis; rapamycin extends lifespan in models

AMPK Pathway
- Key components: AMPK, LKB1, SIRT1
- Mechanism: Energy sensor activating catabolic processes, inhibiting anabolic processes
- Evidence: Metformin (AMPK activator) shows potential lifespan extension effects

DNA Damage Response
- Key components: ATM, ATR, p53, PARP1, SIRT6
- Mechanism: Accumulated DNA damage→ cellular senescence, apoptosis; enhanced repair capacity in long-lived individuals
- Evidence: Centenarians show superior DNA repair capacity; PARP1 activity correlates with species lifespan

Mitochondrial Function

- Mechanism: Reduced electron leak, enhanced mitophagy, optimized oxidative phosphorylation efficiency
- Evidence: Long-lived individuals show lower mitochondrial ROS production despite similar oxidative damage

Environmental Influences

Dietary Factors
- Caloric restriction: 10-40% reduction extends lifespan in models; human data shows improved biomarkers (NIA CALERIE trial)
- Mediterranean diet: Associated with 20% reduced mortality in elderly
- Intermittent fasting: Improves metabolic health, may mimic caloric restriction effects

Lifestyle Factors
- Physical activity: 150+ min/week moderate activity reduces all-cause mortality by 31%
- Cognitive engagement: Associated with reduced dementia risk
- Social integration: Strong social networks reduce mortality risk comparable to smoking cessation

Toxin Exposure
- Smoking: Reduces lifespan by ~10 years
- Air pollution: PM2.5 exposure reduces telomere length
- Exercise mimetics: Compounds activating AMPK/PGC-1α pathway
- Heat/cold exposure: Activate stress response pathways (HSPs, UCP1)

Emerging Approaches
- Optimal aging may require balanced, moderate activity of stress response pathways

Early-Life Programming

Network Analysis
Molecular interaction networks show complex relationships between genes, proteins, and metabolites involved in this trait.

Interventions

Genetic Interventions
Mechanism: CRISPR-based gene editing, gene therapy vectors
Direct modification of genetic factors contributing to the trait.

Feasibility: High
Timeline: 5-10 years
Pharmacological Approaches
Mechanism: Small molecule modulators, biologics
Drug-based interventions targeting key molecular pathways.

Feasibility: Medium
Timeline: 3-7 years
Environmental Modifications
Mechanism: Lifestyle, nutrition, environmental factors
Non-invasive approaches through environmental optimization.

Feasibility: Very High
Timeline: Immediate
Important Considerations
All interventions require extensive testing and validation
Ethical considerations must be addressed before implementation
Regulatory approval is required for clinical applications
Off-target effects and unintended consequences should be carefully evaluated
Cost-benefit analysis should be conducted for each approach
Detailed Intervention Analysis

Potential Intervention Strategies

Pharmacological
- Rapamycin analogs (rapalogs): mTOR inhibitors showing promise in clinical trials for age-related conditions
- Metformin: TAME (Targeting Aging with Metformin) trial underway
- Senolytics: Multiple clinical trials for osteoarthritis, IPF, diabetic kidney disease
- NAD+ boosters: NR, NMN supplements increase NAD+ levels, improve mitochondrial function

Lifestyle Interventions
- Time-restricted eating: 8-10 hour feeding window improves metabolic health
- Gene therapy: AAV delivery of telomerase, Klotho, or FOXO3 in animal models
- Potential for longevity interventions to exacerbate existing health disparities
- Cost of therapies likely initially prohibitive for most populations

Societal Impact
- Demographic shifts: Increased proportion of elderly, strain on pension systems
- Intergenerational equity: Resource allocation between young and old

Philosophical Questions
- Definition of "natural" lifespan versus medical extension
- Potential psychological impacts of significantly extended lifespan

Regulatory Challenges
- FDA does not recognize aging as indication; trials must target specific age-related diseases
- Long trial durations required for lifespan studies

Inferences of Hidden Rules, Patterns, and Relationships

Network Resilience Hypothesis
Longevity may depend less on individual gene variants and more on network properties:
- Digital twins: Creating computational models of aging for personalized interventions

Precision Longevity
- Polygenic risk scores: Developing clinically useful longevity predictors

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