Article

AI-driven assessment of plant adaptation to climate change: The web tool based on physiological, biological, morphological, and genetic indicators of plant species

WenJun Zhang
School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, China; International Academy of Ecology and Environmental Sciences, Hong Kong
E-mail: wjzhang@iaees.org, zhwj@mail.sysu.edu.cn

Received 30 November 2025; *Accepted 3 December 2025*; *Published online 5 December 2025*; *Published 1 June 2026*

Abstract
A hierarchical indicator system and scoring sytem to assess plant species' adaptation to climate change was constructed in present study. The AI-driven assessment tool based on the systems was developed. It features with (1) Multi-dimensional adaptive capacity analysis. (2) Support for multiple AI providers (DeepSeek, Google Gemini). (3) Real-time progress tracking. (4) Comprehensive scoring system. (5) Actionable recommendations for conservation and management. By integrating physiological, biological, morphological, and genetic perspectives, it offers actionable insights for conservation planning and ecosystem management.

Keywords climate change; plant adaptability; AI; assessment tool.

Computational Ecology and Software
ISSN 2220-721X
URL: http://www.iaees.org/publications/journals/ces/online-version.asp
RSS: http://www.iaees.org/publications/journals/ces/rss.xml
E-mail: ces@iaees.org
Editor-in-Chief: WenJun Zhang
Publisher: International Academy of Ecology and Environmental Sciences

1 Introduction

Plants form the indispensable foundation of Earth's ecosystems. As primary producers, they not only supply the essential foods and oxygen that sustain life but also serve as ecological engineers—regulating water cycles, stabilizing soils, and creating habitats for countless organisms (Podong and Poolsiri, 2013; Zhang, 2014; Zhang et al., 2014; Singh et al., 2016; Farooq et al., 2019; Shobairi et al., 2024). Their role extends beyond mere provision; they are woven into the very fabric of global ecological balance.

Climate change, however, stands as one of the most critical challenges of our era, causing profound disruptions across both human societies and natural systems (Zhang and Liu, 2012; Sundar et al., 2020; Shobairi et al., 2024). This climatic destabilization, unfolding at an unprecedented speed and scale, now severely threatens plant survival worldwide. The manifestations are diverse: shifting temperature zones, altered precipitation patterns, and increased frequency of extreme weather events, all of which compromise plant health, reproduction, and distribution. Yet, the impact is far from uniform. A striking disparity in resilience emerges across species—while some face heightened extinction risks under specific regional and ecological pressures, others demonstrate a remarkable capacity for adaptation. This spectrum of vulnerability, influenced by genetic diversity, phenotypic plasticity, and ecological niche, underscores an urgent scientific and practical necessity: the development of a dynamic, evidence-based evaluation framework. Such a system would be capable of monitoring and assessing the real-time adaptive responses of various species—not only plants but also the animal communities that depend on them—to ongoing climatic shifts.

Constructing this framework, however, presents formidable challenges. Conventional analytical approaches often prove inadequate when navigating the vast, intricate, and rapidly expanding ocean of climatic and ecological data. The critical variables form a dynamic web of interconnected factors: from microclimatic anomalies and habitat fragmentation to phenological shifts, species migration trajectories, and underlying genetic adaptability. This multidimensional puzzle, characterized by feedback loops, time-lagged effects, and regional singularities, exceeds the integrative capacity of traditional modeling tools, which frequently struggle to process such complexity in a timely and actionable manner. Therefore, advancing toward effective ecological forecasting and conservation prioritization will require harnessing novel technologies—such as AI-driven analytics, remote sensing, and integrative multi-omics approaches—to build adaptive systems that can keep pace with the changing planet.

The rapid advancement of Artificial Intelligence (AI) represents a transformative pathway for confronting complex global challenges. Modern AI systems possess unprecedented capabilities in integrating, analyzing, and reasoning across large-scale, heterogeneous datasets—a task that has historically overwhelmed traditional analytical methods (Zhang, 2025, 2026a-b; Zhang and Qi, 2026). By leveraging sophisticated machine learning algorithms, predictive modeling, and real-time data processing architectures, AI can uncover hidden causal relationships, forecast nonlinear ecological trends, and generate high-fidelity, actionable insights. These capabilities are already demonstrating significant success across diverse scientific and industrial domains, from precision medicine to supply chain optimization. Harnessing this computational potential for ecological assessment and conservation biology could therefore enable a paradigm shift toward more precise, dynamically adaptive, and proactively managed strategies to safeguard biodiversity in an era of rapid climate change.

Operationally, AI functions as a powerful and scalable intelligent agent, capable of systematically searching, comprehending, and synthesizing the vast and ever-expanding corpus of published ecological and climatic research. It employs advanced natural language processing (NLP) and knowledge retrieval engines to access and interpret global data repositories, scientific literature, and curated databases. The core of its analytical pipeline involves several key steps (Zhang, 2025, 2026a-b; Zhang and Qi, 2026): Named Entity Recognition (NER) to identify and extract key biological entities (e.g., species names, genes, proteins); relationship extraction to map the complex interactions between these entities (e.g., predation, symbiosis, competition); and statistical data extraction to accurately parse numerical findings, model parameters, and experimental results from unstructured text and tables. The fetched information is subsequently organized into a structured, interoperable knowledge graph.

Crucially, AI can transcend simple information retrieval by performing advanced synthesis. It dynamically connects disparate findings from multiple sources, enabling cross-referencing of studies from different ecosystems or time periods, functional enrichment analysis to infer higher-order biological processes, and automated summarization to distill consensus and identify critical knowledge gaps. This ability to integrate fragmented evidence into a coherent, evolving knowledge framework makes AI an indispensable tool for building the dynamic, evidence-based evaluation systems urgently needed to monitor and forecast ecological adaptation in real time.

Due to the powerful potentiality of AI, this study aims to present a hierarchical indicator system and scoring system to assess plant species' adaptation to climate change, and develop an AI-driven assessment tool.

2 Physiological, Biological, Morphological, and Genetic Indicators of Plant Species' Adaptation to Climate Change

2.1 Hierarchical Indicator System

Here I construct a system of hierarchical indicators to assess plant species' adaptation to climate change:

(1) Physiological Indicators

Adjustments in Photosynthesis: Shifts in photosynthetic pathways (e.g., C3 to C4-like efficiency), changes in photosynthetic optimum temperatures, and altered rates of photorespiration.

Water-Use Efficiency (WUE): Increased WUE measured via carbon isotope discrimination (δ13C); reduced stomatal conductance to conserve water under drought stress.

Thermotolerance of Metabolic Processes: Enhanced stability of key enzymes (e.g., Rubisco activase) and photosynthetic membranes (thylakoids) under heat stress.

Altered Respiration Rates: Acclimation of dark respiration to maintain carbon balance under higher temperatures.

Osmoregulation and Solute Accumulation: Synthesis of compatible solutes (e.g., proline, glycine betaine) to maintain cell turgor under drought or salinity.

Antioxidant Capacity Enhancement: Increased production of antioxidant compounds (e.g., ascorbate, glutathione) and enzymes (e.g., catalase, superoxide dismutase) to scavenge reactive oxygen species (ROS) generated under abiotic stress.

(2) Biological Indicators

Shift in Phenology: Earlier flowering and budburst ("advancement"); altered timing of leaf senescence in autumn.

Changes in Reproductive Strategy: Modified pollinator interactions, increased reliance on self-pollination, or changes in seed dormancy and germination requirements.

Altered Resource Allocation: Shift in biomass partitioning—e.g., increased root-to-shoot ratio under drought, or reduced reproductive effort under stress.

Life Cycle Changes: Shift from perennial to annual life history in some populations to complete cycles during shorter favorable windows.

(3) Morphological Indicators

Leaf Trait Modifications: Smaller, thicker leaves; increased leaf succulence; increased leaf reflectance (pubescence, waxes); more dissected leaves.

Stomatal Morphology and Density: Reduced stomatal density or altered stomatal placement (e.g., sunken stomata) to reduce water loss.

Root Architecture Changes: Deeper root systems to access deeper water tables or more prolific shallow roots to capture sporadic rainfall.

Changes in Plant Architecture: Reduced overall stature, increased branching, or a more compact growth form to reduce transpirative surface and wind stress.

Wood Anatomical Changes: Altered xylem vessel size and density (e.g., narrower vessels to reduce cavitation risk under drought).

(4) Genetic Indicators

Allelic Frequency Shifts: Changes in allele frequencies at loci associated with stress tolerance (e.g., genes for dehydrins, heat-shock proteins, flowering time).

Local Adaptation Signatures: Detection of genomic signatures of selection (via FST scans, GWAS) in populations from warmer/drier parts of the range.

Gene Expression Changes: Differential expression of stress-responsive genes (e.g., upregulation of *DREB*, *AREB*, *HSF* transcription factor families).

Epigenetic Modifications: Heritable changes like DNA methylation that alter gene expression without changing DNA sequence, providing rapid phenotypic plasticity.

Changes in Genetic Diversity: Loss of diversity in marginal populations due to selection and bottlenecks, or increased admixture at leading edges of range shifts.

Adaptive Phenotypic Plasticity: High genetic variation for plasticity itself (e.g., genotype-by-environment interactions) allowing for rapid acclimation within a generation.

Genomic Rearrangements: Presence of copy number variations (CNVs) or transposable element activity linked to adaptive traits.

2.2 Scoring Methodology for Indicator System

2.2.1 Individual Assessment Scores

Each category of indicators (physiological, biological, morphological, genetic) receives an independent score from 0-100 based on:

(1) Stress Tolerance Mechanisms (25 points)

Presence and effectiveness of adaptive traits

Redundancy of protective mechanisms

(2) Environmental Range (25 points)

Breadth of tolerable conditions

Historical exposure to climate variability

(3) Response Capacity (25 points)

Speed of acclimation

Plasticity of responses

(4) Evolutionary Potential (25 points)

Genetic diversity

Historical adaptation evidence

2.2.2 Overall Score Calculation

The overall score is generated through AI synthesis considering:

Weighted average of individual scores

Synergistic effects between categories

Species-specific vulnerabilities

Conservation context

The customize scoring weights:

physiological, weight: 0.30

biological, weight: 0.25

morphological, weight: 0.20

genetic, weight: 0.25

The formula is:

Overall Score = f(

w1 × Physiological_Score,

w2 × Biological_Score,

w3 × Morphological_Score,

w4 × Genetic_Score,

interaction_effects,
vulnerability_adjustments
)
where: w1 + w2 + w3 + w4 = 1.0.

2.3 Scoring Methodology for Management Priority

The scoring rules for management priority can be found in Table 1.

Table 1 Scoring rules for for management priority.

Score	Interpretation	Management Priority
80-100	Excellent adaptation potential	Monitor, low intervention
60-79	Good adaptation potential	Moderate conservation priority
40-59	Moderate adaptation potential	Active management recommended
20-39	Poor adaptation potential	High conservation priority
0-19	Very poor adaptation potential	Urgent intervention required

2.4 Conservation Planning

Create a 2D matrix where:
X-axis: Overall adaptation score (score)
Y-axis: Conservation value (rarity, ecological role) (value)
Then
High score + High value: Monitor only
Low score + High value: Immediate intervention
Low score + Low value: Assisted migration candidate

2.5 Key Integrated Concepts

Phenotypic Plasticity: The ability of a single genotype to express different phenotypes under different climates is often the first response.
Adaptive Evolution: Measurable genetic change over generations in response to selection pressures from new climate conditions.
Range Shift: The ultimate geographical indicator—migration to higher latitudes or elevations—driven by the underlying adaptations above.

These indicators are often interconnected and observed in combination, providing evidence of a plant population's ongoing acclimation, adaptation, or migration in response to climate change.

3 System Overview

3.1 Purpose

The Plant Species Climate Adaptation Assessment Tool is an AI-powered web application that evaluates plant species' capacity to adapt to climate change across four scientific dimensions: physiological, biological, morphological, and genetic characteristics.

3.2 Key Features

- Multi-dimensional adaptive capacity analysis
- Support for multiple AI providers (DeepSeek AI, Google Gemini)
- Real-time progress tracking
- Comprehensive scoring system (0-100 scale)

- Actionable recommendations for conservation and management

3.3 Target Users

- Botanists and plant ecologists
- Conservation biologists
- Environmental researchers
- Land managers and restoration specialists
- Climate adaptation planners

4 Algorithmic Architecture

4.1 Overall System Flow

INPUT VALIDATION

- Scientific name validation
- Geographic range verification
- Habitat type selection
- API key authentication

▼

SEQUENTIAL AI ASSESSMENT ENGINE

Phase 1: Physiological Assessment
Progress: 0-25%

▼

Phase 2 Biological Assessment
Progress: 25-50%

▼

Phase 3 Morphological Assessment
Progress: 50-75%

▼

Phase 4 Genetic Assessment
Progress: 75-95%

```
└──────────────────────────────────────────────────────────────┘
                              │
                              ▼
┌──────────────────────────────────────────────────────────────┐
│              SYNTHESIS & SUMMARY GENERATION                   │
│ • Aggregate scoring algorithm                                 │
│ • Strength/weakness identification                            │
│ • Recommendation engine                                       │
│ Progress: 95-100%                                             │
└──────────────────────────────────────────────────────────────┘
                              │
                              ▼
┌──────────────────────────────────────────────────────────────┐
│                 RESULTS PRESENTATION                          │
│ • Multi-panel visualization                                   │
│ • Score displays with context                                 │
│ • Actionable recommendations                                  │
└──────────────────────────────────────────────────────────────┘
```

4.2 Detailed Algorithm Components

4.2.1 Input Processing Algorithm

javascript

```
FUNCTION validateInput():
    INPUT: scientificName, nativeRange, habitatType, apiKey

    STEP 1: Trim whitespace from all inputs

    STEP 2: Validate required fields
        IF scientificName is empty THEN
            RETURN error("Scientific name is required")
        END IF

        IF nativeRange is empty THEN
            RETURN error("Native range is required")
        END IF

        IF habitatType is not selected THEN
            RETURN error("Habitat type must be selected")
        END IF

        IF apiKey is empty THEN
            RETURN error("API key is required")
        END IF

    STEP 3: Format base information string
```

```
        baseInfo = CONCATENATE(
            "Scientific Name: ", scientificName, NEWLINE,
            "Native Range: ", nativeRange, NEWLINE,
            "Habitat Type: ", habitatType, NEWLINE,
            "Additional Traits: ", additionalTraits OR "None provided"
        )

    STEP 4: Initialize UI states
        hideError()
        showProgress()
        hideResults()

    RETURN baseInfo
END FUNCTION
```

4.2.2 AI Provider Configuration Algorithm

javascript

```
FUNCTION configureAIProvider(providerName):

    CONFIGURATIONS = {
        "deepseek": {
            url: "https://api.deepseek.com/v1/chat/completions",
            model: "deepseek-chat",
            temperature: 0.7,
            max_tokens: 1500
        },
       "gemini": {
            url: "https://generativelanguage.googleapis.com/v1beta/models/gemini-pro:generateContent",
            model: "gemini-pro",
            temperature: 0.7,
            max_tokens: 1500
        }
    }

    RETURN CONFIGURATIONS[providerName]
END FUNCTION
```

4.2.3 Sequential Assessment Algorithm

javascript

```
FUNCTION performSequentialAssessment(baseInfo, apiKey):

    // Define assessment phases
    assessmentPhases = [
        {
            name: "physiological",
            weight: 0.25,
```

```
        progressRange: [0, 25]
    },
    {
        name: "biological",
        weight: 0.25,
        progressRange: [25, 50]
    },
    {
        name: "morphological",
        weight: 0.25,
        progressRange: [50, 75]
    },
    {
        name: "genetic",
        weight: 0.25,
        progressRange: [75, 95]
    }
]

results = {}

FOR EACH phase IN assessmentPhases DO

    STEP 1: Update progress indicator
        progressPercent = phase.progressRange[1]
        statusMessage = "Analyzing " + phase.name + " adaptations..."
        updateProgress(progressPercent, statusMessage)

    STEP 2: Generate specialized prompt
        prompt = generatePrompt(phase.name, baseInfo)

    STEP 3: Call AI API
        TRY:
            response = callAI(prompt, apiKey)
        CATCH error:
            THROW "Failed to assess " + phase.name + ": " + error.message
        END TRY

    STEP 4: Parse JSON response
        jsonContent = extractJSON(response)

        IF jsonContent is NULL THEN
            THROW "Failed to parse " + phase.name + " response"
        END IF
```

```
            results[phase.name] = jsonContent

        STEP 5: Rate limiting delay
            WAIT 500 milliseconds

    END FOR

    RETURN results
END FUNCTION
```

4.2.4 Prompt Generation Algorithm

javascript

```
FUNCTION generatePrompt(assessmentType, baseInfo):

    prompts = {
        "physiological": """
            As a plant physiologist, assess the physiological
            adaptations of this plant species to climate change:

            {baseInfo}

            Provide a detailed analysis including:
            1. Water use efficiency and stomatal regulation
            2. Photosynthetic capacity under stress
            3. Thermoregulation mechanisms
            4. Osmotic adjustment capabilities
            5. Overall physiological adaptation score (0-100)

            Format your response as JSON with the following structure:
            {
                "score": <number>,
                "waterUseEfficiency": "<assessment>",
                "photosyntheticCapacity": "<assessment>",
                "thermoregulation": "<assessment>",
                "osmoticAdjustment": "<assessment>"
            }
        """,

        "biological": """
            As a plant biologist, assess the biological characteristics
            affecting climate adaptation of this species:

            {baseInfo}
```

```
        Provide a detailed analysis including:
        1. Life cycle and phenological flexibility
        2. Reproductive strategies under climate stress
        3. Growth rate and resource allocation
        4. Biotic interactions (pollinators, symbionts)
        5. Overall biological adaptation score (0-100)

        Format your response as JSON with the following structure:
        {
            "score": <number>,
            "lifeCycle": "<assessment>",
            "reproductiveStrategies": "<assessment>",
            "growthRate": "<assessment>",
            "bioticInteractions": "<assessment>"
        }
    """,

    "morphological": """
        As a plant morphologist, assess the morphological
        adaptations of this species to climate change:

        {baseInfo}

        Provide a detailed analysis including:
        1. Leaf structure and adaptations
        2. Root system architecture
        3. Stem and bark characteristics
        4. Surface area to volume ratio
        5. Overall morphological adaptation score (0-100)

        Format your response as JSON with the following structure:
        {
            "score": <number>,
            "leafStructure": "<assessment>",
            "rootSystem": "<assessment>",
            "stemBark": "<assessment>",
            "surfaceRatio": "<assessment>"
        }
    """,

    "genetic": """
        As a plant geneticist, assess the genetic potential
        for climate adaptation of this species:
```

```
            {baseInfo}

            Provide a detailed analysis including:
            1. Genetic diversity and population structure
            2. Known stress-responsive genes
            3. Plasticity and adaptive potential
            4. Breeding and conservation considerations
            5. Overall genetic adaptation score (0-100)

            Format your response as JSON with the following structure:
            {
                "score": <number>,
                "geneticDiversity": "<assessment>",
                "stressGenes": "<assessment>",
                "plasticity": "<assessment>",
                "conservation": "<assessment>"
            }
        """
    }

    RETURN prompts[assessmentType].replace("{baseInfo}", baseInfo)
END FUNCTION
```

4.2.5 Summary Synthesis Algorithm

javascript

```
FUNCTION generateSummary(results, baseInfo, scientificName):

    STEP 1: Extract individual scores
        physScore = results.physiological.score
        bioScore = results.biological.score
        morphScore = results.morphological.score
        genScore = results.genetic.score

    STEP 2: Create summary prompt
        summaryPrompt = """
            Based on the following assessments of {scientificName},
            provide a comprehensive summary:

            Physiological Score: {physScore}/100
            Biological Score: {bioScore}/100
            Morphological Score: {morphScore}/100
            Genetic Score: {genScore}/100

            Original Species Data:
            {baseInfo}
```

```
        Provide a comprehensive summary including:
        1. Overall climate adaptation score (0-100)
        2. Executive summary paragraph
        3. Top 3 strengths for climate adaptation
        4. Top 3 weaknesses or vulnerabilities
        5. Top 3 management recommendations

        Format as JSON:
        {
            "overallScore": <number>,
            "summary": "<paragraph>",
            "strengths": ["<strength1>", "<strength2>", "<strength3>"],
            "weaknesses": ["<weakness1>", "<weakness2>", "<weakness3>"],
            "recommendations": ["<rec1>", "<rec2>", "<rec3>"]
        }
    """

    STEP 3: Update progress
        updateProgress(95, "Generating overall summary...")

    STEP 4: Call AI for synthesis
        summaryResponse = callAI(summaryPrompt, apiKey)

    STEP 5: Parse and validate response
        summaryData = extractJSON(summaryResponse)

        IF summaryData is NULL THEN
            THROW "Failed to parse summary response"
        END IF

    STEP 6: Validate summary structure
        ASSERT summaryData.overallScore EXISTS
        ASSERT summaryData.summary EXISTS
        ASSERT summaryData.strengths IS ARRAY OF LENGTH 3
        ASSERT summaryData.weaknesses IS ARRAY OF LENGTH 3
        ASSERT summaryData.recommendations IS ARRAY OF LENGTH 3

    RETURN summaryData
END FUNCTION
```

4.2.6 Results Display Algorithm

javascript

```
FUNCTION displayResults(results):
```

```
STEP 1: Display physiological results
    physContent = """
        <score-display>
            <score>{results.physiological.score}</score>
            <label>Physiological Adaptation Score</label>
        </score-display>

        <metric-items>
            {results.physiological.waterUseEfficiency}
            {results.physiological.photosyntheticCapacity}
            {results.physiological.thermoregulation}
            {results.physiological.osmoticAdjustment}
        </metric-items>
    """

    renderToElement("physiologicalContent", physContent)

STEP 2: Display biological results
    bioContent = """
        <score-display>
            <score>{results.biological.score}</score>
            <label>Biological Adaptation Score</label>
        </score-display>

        <metric-items>
            {results.biological.lifeCycle}
            {results.biological.reproductiveStrategies}
            {results.biological.growthRate}
            {results.biological.bioticInteractions}
        </metric-items>
    """

    renderToElement("biologicalContent", bioContent)

STEP 3: Display morphological results
    morphContent = """
        <score-display>
            <score>{results.morphological.score}</score>
            <label>Morphological Adaptation Score</label>
        </score-display>

        <metric-items>
            {results.morphological.leafStructure}
            {results.morphological.rootSystem}
```

```
                {results.morphological.stemBark}
                {results.morphological.surfaceRatio}
            </metric-items>
        """

        renderToElement("morphologicalContent", morphContent)

    STEP 4: Display genetic results
        genContent = """
            <score-display>
                <score>{results.genetic.score}</score>
                <label>Genetic Adaptation Score</label>
            </score-display>

            <metric-items>
                {results.genetic.geneticDiversity}
                {results.genetic.stressGenes}
                {results.genetic.plasticity}
                {results.genetic.conservation}
            </metric-items>
        """

        renderToElement("geneticContent", genContent)

    STEP 5: Display summary with recommendations
        summaryContent = """
            <score-display>
                <score>{results.summary.overallScore}</score>
                <label>Overall Climate Adaptation Score</label>
            </score-display>

            <summary-text>{results.summary.summary}</summary-text>

            <strengths-section>
                {FOR EACH strength IN results.summary.strengths}
            </strengths-section>

            <weaknesses-section>
                {FOR EACH weakness IN results.summary.weaknesses}
            </weaknesses-section>

            <recommendations-section>
                {FOR EACH recommendation IN results.summary.recommendations}
            </recommendations-section>
```

```
        """

        renderToElement("summaryContent", summaryContent)

    STEP 6: Show results container
        setElementDisplay("resultsContainer", "grid")

    STEP 7: Complete progress
        updateProgress(100, "Analysis complete!")

    STEP 8: Hide progress after delay
        WAIT 2000 milliseconds
        hideProgress()
END FUNCTION
```

4.2.7 Error Handling Algorithm

javascript

```
FUNCTION handleError(error, context):

    STEP 1: Log error details
        console.error("Error in " + context + ":", error)

    STEP 2: Determine error type and user message
        IF error.message CONTAINS "API key" THEN
            userMessage = "Invalid API key. Please check your credentials."
        ELSE IF error.message CONTAINS "rate limit" THEN
            userMessage = "API rate limit exceeded. Please wait and try again."
        ELSE IF error.message CONTAINS "network" THEN
            userMessage = "Network error. Please check your connection."
        ELSE IF error.message CONTAINS "parse" THEN
            userMessage = "Failed to process AI response. Please try again."
        ELSE
            userMessage = "Assessment failed: " + error.message
        END IF

    STEP 3: Display error to user
        showError(userMessage)

    STEP 4: Clean up UI state
        hideProgress()

    STEP 5: Optional: Send telemetry
        // sendErrorTelemetry(error, context, userAgent)
END FUNCTION
```

5 User Guide

Getting Started

Step 1: Obtain an API Key

For DeepSeek AI:

1. Visit https://platform.deepseek.com
2. Create an account or sign in
3. Navigate to API Keys section
4. Generate a new API key
5. Copy the key securely

For Google Gemini:

1. Visit https://makersuite.google.com/app/apikey
2. Create an account or sign in
3. Go to API Keys in your account settings
4. Create a new secret key
5. Copy the key securely

□□ **Security Note**: Never share your API key publicly or commit it to version control.

Step 2: Select Your AI Provider

1. Locate the purple "Select AI Provider" dropdown at the top
2. Choose between:
    - **DeepSeek AI**
    - **Google Gemini**

Step 3: Enter Your API Key

1. Find the yellow "API Key" section
2. Paste your API key into the input field
3. The key is stored locally in your browser session only

Step 4: Fill in Species Information

Required Fields:

Scientific Name

- Enter the Latin binomial name
- Example: Quercus robur (English Oak)
- Example: Pinus ponderosa (Ponderosa Pine)
- Format: *Genus species*

Native Range

- Describe the geographic distribution
- Example: "Europe, Western Asia"
- Example: "Western North America, British Columbia to Mexico"
- Be as specific as possible

Habitat Type

- Select from dropdown:
    - **Forest**: Species primarily in wooded areas
    - **Grassland**: Prairie, savanna, or steppe species
    - **Wetland**: Species in marshes, swamps, or riparian zones
    - **Desert**: Arid-adapted species
    - **Alpine**: High-elevation species

- **Coastal**: Species in coastal environments
- **Agricultural**: Cultivated or field-edge species

Optional Fields:

Additional Traits

- Provide any relevant physiological or morphological information
- Examples:
  - "Deep taproot system, drought-deciduous leaves"
  - "C4 photosynthesis, thick waxy cuticle"
  - "Ectomycorrhizal associations, fire-adapted bark"
  - "Serotinous cones, resprouting capability"

Step 5: Run the Assessment

1. Click the blue "ASSESS CLIMATE ADAPTATION" button
2. Watch the progress bar:
   - **0-25%**: Physiological assessment
   - **25-50%**: Biological assessment
   - **50-75%**: Morphological assessment
   - **75-95%**: Genetic assessment
   - **95-100%**: Summary generation

Expected Duration: 30-90 seconds depending on API response times

Step 6: Review Results

The results display in five sections:

1. Physiological Assessment (Top Left)

- **Overall Score**: 0-100 rating
- **Water Use Efficiency**: Stomatal control and water conservation
- **Photosynthetic Capacity**: Performance under stress
- **Thermoregulation**: Temperature adaptation mechanisms
- **Osmotic Adjustment**: Cellular water balance

2. Biological Assessment (Top Right)

- **Overall Score**: 0-100 rating
- **Life Cycle Flexibility**: Phenological plasticity
- **Reproductive Strategies**: Seed production and dispersal
- **Growth Rate**: Resource allocation patterns
- **Biotic Interactions**: Pollinator and symbiont relationships

3. Morphological Assessment (Bottom Left)

- **Overall Score**: 0-100 rating
- **Leaf Structure**: Anatomical adaptations
- **Root System**: Architecture and depth
- **Stem & Bark**: Structural features
- **Surface Ratio**: Surface area to volume characteristics

4. Genetic Assessment (Bottom Right)

- **Overall Score**: 0-100 rating
- **Genetic Diversity**: Population variation
- **Stress-Responsive Genes**: Known adaptive alleles
- **Plasticity Potential**: Phenotypic flexibility

- **Conservation Status**: Genetic considerations

5. Overall Summary (Full Width at Bottom)

- **Overall Adaptation Score**: Composite 0-100 rating
- **Executive Summary**: Narrative synthesis
- **Strengths**: Top 3 adaptive advantages
- **Weaknesses**: Top 3 vulnerabilities
- **Recommendations**: Top 3 management actions

Interpreting Scores

Score Ranges:

Score	Interpretation	Management Priority
80-100	Excellent adaptation potential	Monitor, low intervention
60-79	Good adaptation potential	Moderate conservation priority
40-59	Moderate adaptation potential	Active management recommended
20-39	Poor adaptation potential	High conservation priority
0-19	Very poor adaptation potential	Urgent intervention required

Example Use Cases

Example 1: Oak Species Assessment

Input:

- Scientific Name: Quercus robur
- Native Range: Europe, Western Asia, North Africa
- Habitat Type: Forest
- Additional Traits: Deep taproot, deciduous, ectomycorrhizal, long-lived

Expected Output:

- Physiological Score: 65-75 (moderate drought tolerance)
- Biological Score: 70-80 (long lifespan, strong ecological interactions)
- Morphological Score: 60-70 (deciduous adaptation)
- Genetic Score: 70-85 (high genetic diversity)
- Overall Score: 68-77

Recommendations Might Include:

- Assisted migration to cooler/wetter sites
- Protection of existing mycorrhizal networks
- Monitoring for drought stress

Example 2: Desert-Adapted Cactus

Input:

- Scientific Name: Carnegiea gigantea
- Native Range: Sonoran Desert, Arizona, California, Mexico
- Habitat Type: Desert
- Additional Traits: CAM photosynthesis, succulent stems, shallow root system, nurse plant dependency

Expected Output:

- Physiological Score: 85-95 (excellent water conservation)
- Biological Score: 55-65 (slow growth, nurse plant dependency)
- Morphological Score: 90-95 (highly adapted structure)
- Genetic Score: 50-60 (limited genetic diversity)

- Overall Score: 70-79

Recommendations Might Include:

- Protect nurse plant populations
- Monitor regeneration success
- Consider ex-situ conservation

Troubleshooting

Problem: "Please enter your API key"

Solution: You must provide a valid API key in the yellow section before running an assessment.

Problem: "API request failed" or "Invalid API key"

Solutions:

- Verify your API key is correct
- Check that you have available credits/quota with your AI provider
- Ensure you selected the correct AI provider matching your key

Problem: "Failed to parse response"

Solutions:

- The AI may have returned an unexpected format
- Try running the assessment again
- If persistent, try switching AI providers

Problem: Assessment takes too long

Solutions:

- Wait up to 2 minutes for complex assessments
- Check your internet connection
- Verify the AI service is not experiencing downtime

Problem: No results appear

Solutions:

- Check the browser console for errors (F12 → Console tab)
- Ensure JavaScript is enabled
- Try refreshing the page and re-entering information

Best Practices

For Accurate Assessments:

1. **Be Specific with Scientific Names**
   - Use accepted binomial nomenclature
   - Include subspecies if relevant
   - Double-check spelling
2. **Provide Detailed Native Range**
   - Include continents, countries, or regions
   - Note elevation ranges if relevant
   - Mention climate zones
3. **Select Appropriate Habitat**
   - Choose the primary habitat type
   - If species spans multiple habitats, select the most common
4. **Add Meaningful Additional Traits**
   - Focus on climate-relevant characteristics
   - Include unique adaptations

- o Mention known stress responses

5. **Compare Multiple Species**
   - o Run assessments on related species
   - o Compare scores across different genera
   - o Identify patterns in adaptation strategies

Data Privacy & Security

Local Storage Only

- API keys are stored only in your browser session
- No data is sent to our servers
- All processing occurs between your browser and the AI provider

API Key Security

- Keys are sent only to the selected AI provider
- Use password-type input (hidden characters)
- Consider using API keys with spending limits

No Data Retention

- Assessment results are not saved permanently
- Refresh the page to clear all data
- No user tracking or analytics

Technical Documentation

System Requirements

Browser Compatibility

- **Chrome/Edge**: Version 90+
- **Firefox**: Version 88+
- **Safari**: Version 14+
- **Opera**: Version 76+

Internet Connection

- Minimum: 1 Mbps
- Recommended: 5+ Mbps for optimal performance

API Requirements

- Valid API key from DeepSeek or Gemini
- Sufficient API quota/credits
- No rate limiting restrictions

API Specifications

DeepSeek AI Configuration

javascript

```
{
    url: "https://api.deepseek.com/v1/chat/completions",
    model: "deepseek-chat",
    temperature: 0.7,
    max_tokens: 1500,
    timeout: 30000ms
}
```

Gemini Configuration

javascript

```
{
    url: "https://generativelanguage.googleapis.com/v1beta/models/gemini-pro:generateContent",
    model: "gemini-pro",
    temperature: 0.7,
    max_tokens: 1500,
    timeout: 30000
}
```

Response Format Specification

Individual Assessment Response

json

```json
{
    "score": 75,
    "metric1": "Detailed assessment text for first metric...",
    "metric2": "Detailed assessment text for second metric...",
    "metric3": "Detailed assessment text for third metric...",
    "metric4": "Detailed assessment text for fourth metric..."
}
```

Summary Response

json

```json
{
    "overallScore": 72,
    "summary": "Comprehensive paragraph summarizing adaptation potential...",
    "strengths": [
        "First major strength description",
        "Second major strength description",
        "Third major strength description"
    ],
    "weaknesses": [
        "First major vulnerability description",
        "Second major vulnerability description",
        "Third major vulnerability description"
    ],
    "recommendations": [
        "First management recommendation",
        "Second management recommendation",
        "Third management recommendation"
    ]
}
```

Performance Metrics

Typical Response Times

- **Per Assessment**: 5-15 seconds
- **Total Analysis**: 30-90 seconds
- **Summary Generation**: 10-20 seconds

Token Usage Estimates

- **Per Assessment**: ~800-1200 tokens
- **Summary**: ~1000-1500 tokens
- **Total per Species**: ~4000-6000 tokens

Cost Estimates

- **DeepSeek**: ~$0.02-0.04 per assessment
- **Google Gemini**: ~ 0.15 cents per assessment

Error Codes & Messages

Error Code	Message	Cause	Solution
VAL_001	"Please fill in all required fields"	Missing input	Complete all * fields
API_001	"Please enter your API key"	No API key	Enter valid key
API_002	"Invalid API key"	Wrong key	Verify key accuracy
API_003	"API rate limit exceeded"	Too many requests	Wait and retry
NET_001	"Network error"	Connection issue	Check internet
PAR_001	"Failed to parse response"	Invalid JSON	Retry assessment
SYS_001	"Assessment failed"	General error	Check console logs

Scoring Methodology

Individual Assessment Scores

Each category (physiological, biological, morphological, genetic) receives an independent score from 0-100 based on:

1. **Stress Tolerance Mechanisms** (25 points)
   - Presence and effectiveness of adaptive traits
   - Redundancy of protective mechanisms
2. **Environmental Range** (25 points)
   - Breadth of tolerable conditions
   - Historical exposure to climate variability
3. **Response Capacity** (25 points)
   - Speed of acclimation
   - Plasticity of responses
4. **Evolutionary Potential** (25 points)
   - Genetic diversity
   - Historical adaptation evidence

Overall Score Calculation

The overall score is generated through AI synthesis considering:

- Weighted average of individual scores
- Synergistic effects between categories
- Species-specific vulnerabilities
- Conservation context

Formula (conceptual):

Overall Score = f(
    w1 × Physiological_Score,
    w2 × Biological_Score,
    w3 × Morphological_Score,

```
    w4 × Genetic_Score,
    interaction_effects,
    vulnerability_adjustments
)
```

where: w1 + w2 + w3 + w4 = 1.0 (equal weighting baseline)

Customization Options

For Developers

Modify Temperature Parameter:

```javascript
// In API_CONFIGS object, adjust temperature
temperature: 0.7    // Default
// Lower (0.3-0.5) = more consistent, conservative
// Higher (0.8-1.0) = more creative, varied
```

Adjust Token Limits:

```javascript
max_tokens:  1500   // Default
// Increase for more detailed responses
// Decrease for faster, more concise responses
```

Add New Habitat Types:

```html
<select id="habitatType">
    <!-- Add new options here -->
    <option value="custom">Custom Habitat Type</option>
</select>
```

Customize Scoring Weights:

```javascript
// Modify assessment phase weights
assessmentPhases = [
    { name: "physiological", weight: 0.30 },    // Increased
    { name: "biological", weight: 0.25 },
    { name: "morphological", weight: 0.20 },    // Decreased
    { name: "genetic", weight: 0.25 }
]
```

Best Practices for Conservation Planning

Using Assessments for Decision-Making

1. Baseline Documentation

- Assess current populations before intervention
- Establish monitoring benchmarks
- Track changes over time

2. Prioritization Matrix

Create a 2D matrix:

- **X-axis**: Overall adaptation score
- **Y-axis**: Conservation value (rarity, ecological role)
- **High score + High value**: Monitor only

- **Low score + High value**: Immediate intervention
- **Low score + Low value**: Assisted migration candidate

3. Comparative Analysis

- Assess multiple species in same ecosystem
- Identify community-level vulnerabilities
- Prioritize keystone species with low scores

4. Scenario Planning

- Run assessments under different climate projections
- Model range shifts
- Identify refugia locations

Integration with Conservation Workflows

Initial Species Selection
- Regional species lists
- Conservation status review

↓

Climate Adaptation Assessment
- Run tool for each species
- Document scores and recommendations

↓

Field Validation
- Verify predicted vulnerabilities
- Collect additional trait data

↓

Management Plan Development
- Implement tool recommendations
- Set monitoring protocols

↓

Adaptive Management
- Re-assess periodically
- Adjust strategies based on results

Frequently Asked Questions (FAQ)

Q1: How accurate are the assessments?

A: Assessments are based on scientific literature and AI analysis, providing expert-level insights. However, they should be validated with field observations and used as one tool among many in conservation planning.

Q2: Can I save my results?

A: Currently, results are not automatically saved. We recommend:

- Taking screenshots of results
- Copying text to a document
- Using your browser's print-to-PDF function

Q3: How often should I re-assess species?

A: We recommend:

- **Annual**: For high-priority species
- **Every 3-5 years**: For moderate-priority species
- **After major events**: Post-drought, fire, or climate anomalies

Q4: Can I assess subspecies or varieties?

A: Yes, enter the full trinomial name (e.g., *Quercus robur* subsp. *pedunculiflora*) and provide subspecies-specific information in the additional traits field.

Q5: What if my species has limited published research?

A: The AI will work with available information but may provide more general assessments. Providing detailed additional traits helps significantly.

Q6: Can I use this for agricultural crops?

A: Yes, select "Agricultural" as the habitat type and focus on cultivated varieties. The tool assesses wild-type adaptation potential.

Q7: How do I interpret conflicting scores?

A: High variance between categories indicates:

- Specialized adaptations in some areas
- Significant vulnerabilities in others
- Need for targeted management strategies

Q8: Can this tool predict extinction risk?

A: No. This tool assesses adaptive capacity to climate change, which is one component of extinction risk. Use in conjunction with population viability analysis and threat assessments.

Advanced Topics

Multi-Species Comparative Analysis

Workflow for Ecosystem-Level Assessment:

1. **Select Representative Species**
    - Dominant canopy species (if forest)
    - Keystone species
    - Indicator species
    - Rare/endemic species
2. **Batch Assessment**
    - Run tool for each species
    - Record all scores in spreadsheet
    - Calculate community averages
3. **Identify Patterns**

- o Species with consistently low scores
- o Categories with widespread vulnerability
- o Functional groups at risk

4. **Prioritize Interventions**

- o Focus on species with lowest scores
- o Address systematic vulnerabilities
- o Leverage species with high scores as climate refugia

Integration with Climate Models

Connecting Assessments to Climate Projections:

1. **Obtain Local Climate Projections**

- o Temperature changes
- o Precipitation changes
- o Extreme event frequency

2. **Match to Trait Vulnerabilities**

- o Low water use efficiency + decreased precipitation = high risk
- o Limited thermoregulation + increased temperature = high risk
- o Poor phenological flexibility + shifted seasons = high risk

3. **Calculate Risk Scores**

Risk = (Climate Change Magnitude) × (1 - Adaptation Score/100)

4. **Map Spatial Risk**

- o Overlay species distributions
- o Apply risk scores
- o Identify high-risk populations

Genetic Conservation Planning

Using Genetic Scores for Conservation:

High Genetic Scores (70-100):

- **Strategy**: In-situ conservation
- **Action**: Protect diverse populations
- **Priority**: Maintain gene flow

Moderate Genetic Scores (40-69):

- **Strategy**: Genetic rescue
- **Action**: Facilitate gene flow between populations
- **Priority**: Monitor genetic diversity trends

Low Genetic Scores (0-39):

- **Strategy**: Ex-situ conservation
- **Action**: Seed banking, botanical gardens
- **Priority**: Assisted gene flow or breeding programs

Conclusion

The Plant Species Climate Adaptation Assessment Tool provides a comprehensive, AI-powered analysis of species' capacity to adapt to climate change. By integrating physiological, biological, morphological, and genetic perspectives, it offers actionable insights for conservation planning and ecosystem management.

Key Takeaways:

1. Holistic Assessment: Four-dimensional analysis provides comprehensive understanding

2. Actionable Recommendations: Specific management guidance for each species

3. Scalable Application: From individual species to ecosystem-level analysis
4. Evidence-Based: Grounded in scientific literature and expert knowledge
5. Adaptive Tool: Regular re-assessment supports adaptive management

Recommended Workflow:

Assess → Validate → Plan → Implement → Monitor → Re-assess

Support & Resources:

- **API Documentation**:
  - DeepSeek: https://platform.deepseek.com/docs
  - Gemini: https://ai.google.dev/gemini-api/docs
- **Scientific Background**:
  - IPCC Reports on Climate Change
  - Conservation Biology literature
  - Plant Ecology journals

Future Enhancements:

Planned features include:

- Result export to CSV/PDF
- Historical assessment comparison
- Integration with species distribution models
- Collaborative annotation and field validation
- Mobile-responsive design improvements

Version: 1.0
Last Updated: 2025

This tool is designed to support conservation decision-making but should not be the sole basis for management actions. Always integrate multiple sources of information, local expertise, and field validation.

6 Codes

The following are the HTML+JavaScript codes of the AI assessment tool (http://www.iaees.org/publications/journals/ces/articles/2026-16(2)/plantAdaptAI.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>Plant Species Climate Adaptation Assessment</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: 20px;
        box-shadow: 0 20px 60px rgba(0,0,0,0.3);
        overflow: hidden;
    }

    .header {
        background: linear-gradient(135deg, #2ecc71 0%, #27ae60 100%);
        color: white;
        padding: 30px;
        text-align: center;
    }

    .header h1 {
        font-size: 2.5em;
        margin-bottom: 10px;
        text-shadow: 2px 2px 4px rgba(0,0,0,0.2);
    }

    .header p {
        font-size: 1.2em;
        opacity: 0.95;
    }

    .main-content {
        padding: 30px;
    }

    .input-section {
        background: #f8f9fa;
        padding: 25px;
        border-radius: 15px;
        margin-bottom: 30px;
        border: 2px solid #e9ecef;
    }

    .section-title {
```

```
        font-size: 1.5em;
        color: #2c3e50;
        margin-bottom: 20px;
        display: flex;
        align-items: center;
        gap: 10px;
    }

    .form-row {
        display: grid;
        grid-template-columns: repeat(auto-fit, minmax(250px, 1fr));
        gap: 20px;
        margin-bottom: 20px;
    }

    .form-group {
        display: flex;
        flex-direction: column;
    }

    .form-group label {
        font-weight: 600;
        color: #34495e;
        margin-bottom: 8px;
        font-size: 0.95em;
    }

    .form-group input,
    .form-group select,
    .form-group textarea {
        padding: 12px;
        border: 2px solid #dfe6e9;
        border-radius: 8px;
        font-size: 1em;
        transition: all 0.3s ease;
        font-family: inherit;
    }

    .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;
}

.ai-selector {
    background: linear-gradient(135deg, #667eea 0%, #764ba2 100%);
    padding: 20px;
    border-radius: 12px;
    margin-bottom: 20px;
}

.ai-selector label {
    color: white;
    font-weight: 600;
    margin-bottom: 10px;
    display: block;
    font-size: 1.1em;
}

.ai-selector select {
    width: 100%;
    padding: 12px;
    border: none;
    border-radius: 8px;
    font-size: 1em;
    background: white;
    cursor: pointer;
}

.api-key-group {
    background: #fff3cd;
    padding: 20px;
    border-radius: 12px;
    border: 2px solid #ffc107;
    margin-bottom: 20px;
}

.api-key-group label {
    color: #856404;
    font-weight: 600;
    margin-bottom: 10px;
    display: block;
}
```

```
.api-key-group input {
    width: 100%;
    padding: 12px;
    border: 2px solid #ffc107;
    border-radius: 8px;
    font-size: 1em;
}

.api-key-info {
    font-size: 0.9em;
    color: #856404;
    margin-top: 8px;
}

.button-group {
    display: flex;
    gap: 15px;
    margin-top: 25px;
}

.btn {
    flex: 1;
    padding: 15px 30px;
    font-size: 1.1em;
    font-weight: 600;
    border: none;
    border-radius: 10px;
    cursor: pointer;
    transition: all 0.3s ease;
    text-transform: uppercase;
    letter-spacing: 1px;
}

.btn-primary {
    background: linear-gradient(135deg, #3498db 0%, #2980b9 100%);
    color: white;
    box-shadow: 0 4px 15px rgba(52, 152, 219, 0.4);
}

.btn-primary:hover {
    transform: translateY(-2px);
    box-shadow: 0 6px 20px rgba(52, 152, 219, 0.6);
}
```

```
.btn-secondary {
    background: linear-gradient(135deg, #95a5a6 0%, #7f8c8d 100%);
    color: white;
}

.btn-secondary:hover {
    transform: translateY(-2px);
    box-shadow: 0 4px 15px rgba(149, 165, 166, 0.4);
}

.btn:disabled {
    opacity: 0.6;
    cursor: not-allowed;
    transform: none !important;
}

.progress-section {
    background: #e8f5e9;
    padding: 20px;
    border-radius: 12px;
    margin-bottom: 30px;
    display: none;
}

.progress-section.active {
    display: block;
}

.progress-bar {
    width: 100%;
    height: 30px;
    background: #c8e6c9;
    border-radius: 15px;
    overflow: hidden;
    margin-bottom: 15px;
    box-shadow: inset 0 2px 4px rgba(0,0,0,0.1);
}

.progress-fill {
    height: 100%;
    background: linear-gradient(90deg, #4caf50 0%, #66bb6a 100%);
    transition: width 0.5s ease;
    display: flex;
    align-items: center;
    justify-content: center;
```

```
        color: white;
        font-weight: 600;
    }

    .progress-status {
        text-align: center;
        color: #2e7d32;
        font-weight: 600;
        font-size: 1.1em;
    }

    .results-grid {
        display: grid;
        grid-template-columns: repeat(2, 1fr);
        gap: 25px;
        margin-bottom: 30px;
    }

    .result-section {
        background: white;
        border-radius: 15px;
        padding: 25px;
        box-shadow: 0 4px 15px rgba(0,0,0,0.1);
        border: 2px solid #e9ecef;
    }

    .result-section h3 {
        color: #2c3e50;
        margin-bottom: 20px;
        padding-bottom: 15px;
        border-bottom: 3px solid #3498db;
        font-size: 1.4em;
    }

    .summary-section {
        grid-column: 1 / -1;
        background: linear-gradient(135deg, #fff9e6 0%, #ffe6cc 100%);
        border: 2px solid #ff9800;
    }

    .summary-section h3 {
        border-bottom-color: #ff9800;
    }

    .metric-item {
```

```
        background: #f8f9fa;
        padding: 15px;
        margin-bottom: 12px;
        border-radius: 8px;
        border-left: 4px solid #3498db;
}

.metric-label {
        font-weight: 600;
        color: #2c3e50;
        margin-bottom: 5px;
}

.metric-value {
        color: #7f8c8d;
        font-size: 0.95em;
}

.score-display {
        display: flex;
        align-items: center;
        gap: 15px;
        background: linear-gradient(135deg, #e3f2fd 0%, #bbdefb 100%);
        padding: 20px;
        border-radius: 12px;
        margin-bottom: 20px;
}

.score-number {
        font-size: 3em;
        font-weight: bold;
        color: #1976d2;
}

.score-label {
        font-size: 1.2em;
        color: #1565c0;
}

.summary-text {
        background: white;
        padding: 20px;
        border-radius: 10px;
        margin-bottom: 20px;
        line-height: 1.8;
```

```
        color: #2c3e50;
        border-left: 4px solid #ff9800;
    }

    .recommendations {
        margin-top: 20px;
    }

    .recommendations h4 {
        color: #2c3e50;
        margin-bottom: 12px;
        font-size: 1.2em;
    }

    .recommendation-item {
        background: white;
        padding: 12px 15px;
        margin-bottom: 10px;
        border-radius: 8px;
        border-left: 4px solid #4caf50;
        line-height: 1.6;
    }

    .error-message {
        background: #ffebee;
        color: #c62828;
        padding: 15px;
        border-radius: 10px;
        border-left: 4px solid #c62828;
        margin-bottom: 20px;
        display: none;
    }

    .error-message.active {
        display: block;
    }

    @media (max-width: 768px) {
        .results-grid {
            grid-template-columns: 1fr;
        }

        .header h1 {
            font-size: 1.8em;
        }
```

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

            .button-group {
                flex-direction: column;
            }
        }
    </style>
</head>

<body>
    <div class="container">
        <div class="header">
            <h1>□ Plant Species Climate Adaptation Assessment</h1>
            <p>AI-Powered Analysis of Plant Resilience to Climate Change</p>
        </div>
    <div class="main-content">
    <a href="http://www.iaees.org/publications/journals/ces/articles/2026-16(2)/1-Zhang-Abstract.asp">Zhang WJ. 2026. AI-driven assessment of plant adaptation to climate change: The web tool based on physiological, biological, morphological, and genetic indicators of plant species. Computational Ecology and Software, 16(2): 99-153</a>
    </div>

        <div class="main-content">
            <!-- AI Selection -->
            <div class="ai-selector">
                <label for="aiProvider">□ Select AI:</label>
                <select id="aiProvider">
                    <option value="deepseek" selected>DeepSeek AI</option>
                    <option value="gemini">Google Gemini</option>
                </select>
            </div>

            <!-- API Key Input -->
            <div class="api-key-group">
                <label for="apiKey">□ AI API Key:</label>
                <input type="password" id="apiKey" placeholder="Enter your API key">
                <div class="api-key-info">Your API key is stored locally and never sent to our servers.</div>
            </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>
        </div><br>
```

```
<!-- Input Section -->
<div class="input-section">
    <h2 class="section-title">□ Plant Species Information</h2>

    <div class="form-row">
        <div class="form-group">
            <label for="scientificName">Scientific Name *</label>
            <input type="text" id="scientificName" placeholder="e.g., Quercus robur" required>
        </div>
    </div>

    <div class="form-row">
        <div class="form-group">
            <label for="nativeRange">Native Range *</label>
            <input type="text" id="nativeRange" placeholder="e.g., Europe, Western Asia" required>
        </div>
        <div class="form-group">
            <label for="habitatType">Habitat Type *</label>
            <select id="habitatType" required>
                <option value="">Select habitat...</option>
                <option value="forest">Forest</option>
                <option value="grassland">Grassland</option>
                <option value="wetland">Wetland</option>
                <option value="desert">Desert</option>
                <option value="alpine">Alpine</option>
                <option value="coastal">Coastal</option>
                <option value="agricultural">Agricultural</option>
            </select>
        </div>
    </div>

    <h2 class="section-title">□ Additional Traits</h2>

    <div class="form-group">
        <label for="additionalTraits">Additional Physiological/Morphological Traits</label>
        <textarea id="additionalTraits" placeholder="Enter any additional relevant information about the species' adaptive traits, such as leaf structure, root system, phenology, etc."></textarea>
    </div>

    <div class="button-group">
        <button class="btn btn-primary" onclick="assessAdaptation()">
            □ Assess Climate Adaptation
        </button>
        <button class="btn btn-secondary" onclick="resetForm()">
            □ Reset Form
```

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

<!-- Error Message -->
<div id="errorMessage" class="error-message"></div>

<!-- Progress Section -->
<div id="progressSection" class="progress-section">
    <div class="progress-bar">
        <div id="progressFill" class="progress-fill" style="width: 0%">0%</div>
    </div>
    <div id="progressStatus" class="progress-status">Initializing...</div>
</div>

<!-- Results Grid -->
<div id="resultsContainer" class="results-grid" style="display: none;">
    <!-- Physiological Results -->
    <div class="result-section" id="physiologicalResults">
        <h3>□ Physiological Assessment</h3>
        <div id="physiologicalContent"></div>
    </div>

    <!-- Biological Results -->
    <div class="result-section" id="biologicalResults">
        <h3>□ Biological Assessment</h3>
        <div id="biologicalContent"></div>
    </div>

    <!-- Morphological Results -->
    <div class="result-section" id="morphologicalResults">
        <h3>□ Morphological Assessment</h3>
        <div id="morphologicalContent"></div>
    </div>

    <!-- Genetic Results -->
    <div class="result-section" id="geneticResults">
        <h3>□ Genetic Assessment</h3>
        <div id="geneticContent"></div>
    </div>

    <!-- Summary Results -->
    <div class="result-section summary-section" id="summaryResults">
        <h3>□ Overall Climate Adaptation Summary</h3>
        <div id="summaryContent"></div>
```

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

<script>
    // API Configuration
    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'
        }
    };

    async function callAI(prompt, category) {
        const aiProvider = document.getElementById('aiProvider').value;
        const apiKey = document.getElementById('apiKey').value;

        if (!apiKey) {
            throw new Error('Please enter your API key');
        }

        const config = API_CONFIGS[aiProvider];

        if (aiProvider === 'gemini') {
            // Gemini API format
            const response = await fetch(`${config.url}?key=${apiKey}`, {
                method: 'POST',
                headers: {
                    'Content-Type': 'application/json'
                },
                body: JSON.stringify({
                    contents: [{
                        parts: [{
                            text: prompt
                        }]
                    }],
                    generationConfig: {
                        temperature: 0.7,
                        maxOutputTokens: 1500
                    }
```

```
                })
            });

            if (!response.ok) {
                const error = await response.json();
                throw new Error(error.error?.message || 'API request failed');
            }

            const data = await response.json();
            return data.candidates[0].content.parts[0].text;
        } else {
            // DeepSeek API format
            const response = await fetch(config.url, {
                method: 'POST',
                headers: {
                    'Content-Type': 'application/json',
                    'Authorization': `Bearer ${apiKey}`
                },
                body: JSON.stringify({
                    model: config.model,
                    messages: [{
                        role: 'user',
                        content: prompt
                    }],
                    temperature: 0.7,
                    max_tokens: 1500
                })
            });

            if (!response.ok) {
                const error = await response.json();
                throw new Error(error.error?.message || 'API request failed');
            }

            const data = await response.json();
            return data.choices[0].message.content;
        }
    }

    async function assessAdaptation() {
        // Validate required fields
        const scientificName = document.getElementById('scientificName').value.trim();
        const nativeRange = document.getElementById('nativeRange').value.trim();
        const habitatType = document.getElementById('habitatType').value;
```

```
        if (!scientificName || !nativeRange || !habitatType) {
            showError('Please fill in all required fields marked with *');
            return;
        }

        const apiKey = document.getElementById('apiKey').value.trim();
        if (!apiKey) {
            showError('Please enter your API key');
            return;
        }

        // Hide error and show progress
        hideError();
        showProgress();
        hideResults();

        try {
            const additionalTraits = document.getElementById('additionalTraits').value.trim();

            const baseInfo = `
Scientific Name: ${scientificName}
Native Range: ${nativeRange}
Habitat Type: ${habitatType}
Additional Traits: ${additionalTraits || 'None provided'}
            `.trim();

            // Assessment categories
            const assessments = [
                {
                    category: 'physiological',
                    prompt: `As a plant physiologist, assess the physiological adaptations of this plant species to
climate change:

${baseInfo}

Provide a detailed analysis including:
1. Water use efficiency and stomatal regulation
2. Photosynthetic capacity under stress
3. Thermoregulation mechanisms
4. Osmotic adjustment capabilities
5. Overall physiological adaptation score (0-100)

Format your response as JSON with the following structure:
{
    "score": <number>,
```

```
    "waterUseEfficiency": "<assessment>",
    "photosyntheticCapacity": "<assessment>",
    "thermoregulation": "<assessment>",
    "osmoticAdjustment": "<assessment>"
}`
                },
                {
                    category: 'biological',
                    prompt: `As a plant biologist, assess the biological characteristics affecting climate adaptation of this species:

${baseInfo}

Provide a detailed analysis including:
1. Life cycle and phenological flexibility
2. Reproductive strategies under climate stress
3. Growth rate and resource allocation
4. Biotic interactions (pollinators, symbionts)
5. Overall biological adaptation score (0-100)

Format your response as JSON with the following structure:
{
    "score": <number>,
    "lifeCycle": "<assessment>",
    "reproductiveStrategies": "<assessment>",
    "growthRate": "<assessment>",
    "bioticInteractions": "<assessment>"
}`
                },
                {
                    category: 'morphological',
                    prompt: `As a plant morphologist, assess the morphological adaptations of this species to climate change:

${baseInfo}

Provide a detailed analysis including:
1. Leaf structure and adaptations
2. Root system architecture
3. Stem and bark characteristics
4. Surface area to volume ratio
5. Overall morphological adaptation score (0-100)

Format your response as JSON with the following structure:
{
```

```
	"score": <number>,
	"leafStructure": "<assessment>",
	"rootSystem": "<assessment>",
	"stemBark": "<assessment>",
	"surfaceRatio": "<assessment>"
}`
					},
					{
						category: 'genetic',
						prompt: `As a plant geneticist, assess the genetic potential for climate adaptation of this species:

${baseInfo}

Provide a detailed analysis including:
1. Genetic diversity and population structure
2. Known stress-responsive genes
3. Plasticity and adaptive potential
4. Breeding and conservation considerations
5. Overall genetic adaptation score (0-100)

Format your response as JSON with the following structure:
{
	"score": <number>,
	"geneticDiversity": "<assessment>",
	"stressGenes": "<assessment>",
	"plasticity": "<assessment>",
	"conservation": "<assessment>"
}`
					}
				];

				const results = {};

				// Process each assessment
				for (let i = 0; i < assessments.length; i++) {
					const assessment = assessments[i];
					updateProgress(
						((i + 1) / (assessments.length + 1)) * 100,
						`Analyzing ${assessment.category} adaptations...`
					);

					const response = await callAI(assessment.prompt, assessment.category);

					// Parse JSON response
					const jsonMatch = response.match(/\{[\s\S]*\}/);
```

```
                if (jsonMatch) {
                    results[assessment.category] = JSON.parse(jsonMatch[0]);
                } else {
                    throw new Error(`Failed to parse ${assessment.category} response`);
                }

                // Small delay to avoid rate limiting
                await new Promise(resolve => setTimeout(resolve, 500));
            }

            // Generate summary
            updateProgress(95, 'Generating overall summary...');

            const summaryPrompt = `Based on the following assessments of ${scientificName}, provide a comprehensive summary:

Physiological Score: ${results.physiological.score}/100
Biological Score: ${results.biological.score}/100
Morphological Score: ${results.morphological.score}/100
Genetic Score: ${results.genetic.score}/100

Original Species Data:
${baseInfo}

Provide a comprehensive summary including:
1. Overall climate adaptation score (0-100)
2. Executive summary paragraph
3. Top 3 strengths for climate adaptation
4. Top 3 weaknesses or vulnerabilities
5. Top 3 management recommendations

Format as JSON:
{
    "overallScore": <number>,
    "summary": "<paragraph>",
    "strengths": ["<strength1>", "<strength2>", "<strength3>"],
    "weaknesses": ["<weakness1>", "<weakness2>", "<weakness3>"],
    "recommendations": ["<rec1>", "<rec2>", "<rec3>"]
}`;

            const summaryResponse = await callAI(summaryPrompt, 'summary');
            const summaryMatch = summaryResponse.match(/\{[\s\S]*\}/);
            if (summaryMatch) {
                results.summary = JSON.parse(summaryMatch[0]);
            } else {
```

```
                throw new Error('Failed to parse summary response');
            }

            updateProgress(100, 'Analysis complete!');

            // Display results
            displayResults(results);

        } catch (error) {
            console.error('Assessment error:', error);
            showError(`Assessment failed: ${error.message}`);
            hideProgress();
        }
    }

    function displayResults(results) {
        // Display Physiological Results
        const physContent = document.getElementById('physiologicalContent');
        physContent.innerHTML = `
            <div class="score-display">
                <div class="score-number">${results.physiological.score}</div>
                <div class="score-label">Physiological<br>Adaptation Score</div>
            </div>
            <div class="metric-item">
                <div class="metric-label">□ Water Use Efficiency</div>
                <div class="metric-value">${results.physiological.waterUseEfficiency}</div>
            </div>
            <div class="metric-item">
                <div class="metric-label">☀□ Photosynthetic Capacity</div>
                <div class="metric-value">${results.physiological.photosyntheticCapacity}</div>
            </div>
            <div class="metric-item">
                <div class="metric-label">□□ Thermoregulation</div>
                <div class="metric-value">${results.physiological.thermoregulation}</div>
            </div>
            <div class="metric-item">
      <div class="metric-label">□□ Osmotic Adjustment</div>
                <div class="metric-value">${results.physiological.osmoticAdjustment}</div>
            </div>
        `;

        // Display Biological Results
        const bioContent = document.getElementById('biologicalContent');
        bioContent.innerHTML = `
            <div class="score-display">
```

```
        <div class="score-number">${results.biological.score}</div>
        <div class="score-label">Biological<br>Adaptation Score</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Life Cycle Flexibility</div>
        <div class="metric-value">${results.biological.lifeCycle}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Reproductive Strategies</div>
        <div class="metric-value">${results.biological.reproductiveStrategies}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Growth Rate</div>
        <div class="metric-value">${results.biological.growthRate}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Biotic Interactions</div>
        <div class="metric-value">${results.biological.bioticInteractions}</div>
    </div>
`;

// Display Morphological Results
const morphContent = document.getElementById('morphologicalContent');
morphContent.innerHTML = `
    <div class="score-display">
        <div class="score-number">${results.morphological.score}</div>
        <div class="score-label">Morphological<br>Adaptation Score</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Leaf Structure</div>
        <div class="metric-value">${results.morphological.leafStructure}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Root System</div>
        <div class="metric-value">${results.morphological.rootSystem}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Stem & Bark</div>
        <div class="metric-value">${results.morphological.stemBark}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label"> Surface Ratio</div>
        <div class="metric-value">${results.morphological.surfaceRatio}</div>
    </div>
`;
```

```
// Display Genetic Results
const genContent = document.getElementById('geneticContent');
genContent.innerHTML = `
    <div class="score-display">
        <div class="score-number">${results.genetic.score}</div>
        <div class="score-label">Genetic<br>Adaptation Score</div>
    </div>
    <div class="metric-item">
        <div class="metric-label">□ Genetic Diversity</div>
        <div class="metric-value">${results.genetic.geneticDiversity}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label">□ Stress-Responsive Genes</div>
        <div class="metric-value">${results.genetic.stressGenes}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label">□ Plasticity Potential</div>
        <div class="metric-value">${results.genetic.plasticity}</div>
    </div>
    <div class="metric-item">
        <div class="metric-label">□ Conservation Status</div>
        <div class="metric-value">${results.genetic.conservation}</div>
    </div>
`;

// Display Summary Results
const summaryContent = document.getElementById('summaryContent');
const summary = results.summary;
summaryContent.innerHTML = `
    <div class="score-display">
        <div class="score-number">${summary.overallScore}</div>
        <div class="score-label">Overall Climate<br>Adaptation Score</div>
    </div>

    <div class="summary-text">${summary.summary}</div>

    <div class="recommendations">
        <h4>□ Strengths:</h4>
        ${summary.strengths.map(s => `
            <div class="recommendation-item">${s}</div>
        `).join('')}
    </div>

    <div class="recommendations">
```

```
    <h4>□□ Weaknesses:</h4>
        ${summary.weaknesses.map(w => `
            <div class="recommendation-item">${w}</div>
        `).join('')}
    </div>

    <div class="recommendations">
        <h4>□ Recommendations:</h4>
        ${summary.recommendations.map(r => `
            <div class="recommendation-item">${r}</div>
        `).join('')}
    </div>
`;

// Show results container
document.getElementById('resultsContainer').style.display = 'grid';
hideProgress();
}

function updateProgress(percent, status) {
    document.getElementById('progressFill').style.width = percent + '%';
    document.getElementById('progressFill').textContent = Math.round(percent) + '%';
    document.getElementById('progressStatus').textContent = status;
}

function showProgress() {
    document.getElementById('progressSection').classList.add('active');
    updateProgress(0, 'Starting assessment...');
}

function hideProgress() {
    setTimeout(() => {
        document.getElementById('progressSection').classList.remove('active');
    }, 2000);
}

function hideResults() {
    document.getElementById('resultsContainer').style.display = 'none';
}

function showError(message) {
    const errorDiv = document.getElementById('errorMessage');
    errorDiv.textContent = '□ ' + message;
    errorDiv.classList.add('active');
}
```

```
        function hideError() {
            document.getElementById('errorMessage').classList.remove('active');
        }

        function resetForm() {
            document.getElementById('scientificName').value = '';
            document.getElementById('nativeRange').value = '';
            document.getElementById('habitatType').value = '';
            document.getElementById('additionalTraits').value = '';

            hideError();
            hideProgress();
            hideResults();
        }
    </script>
</body>
</html>
```

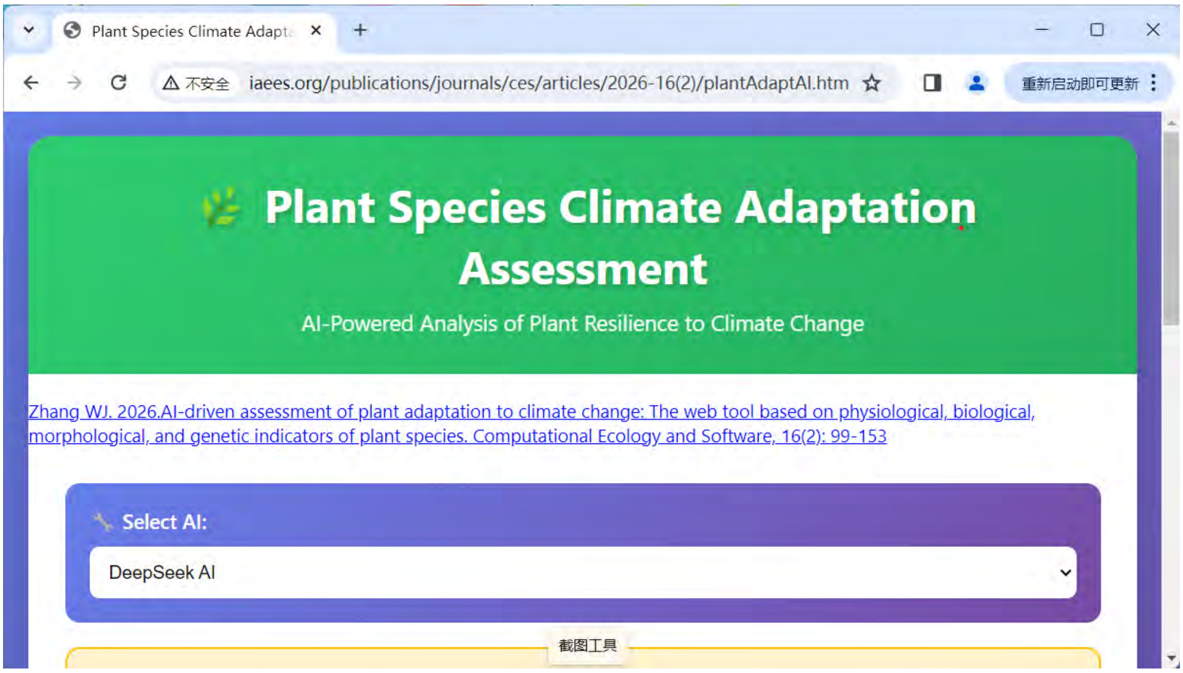

Fig. 1 The web tool page.

7 A Demo

In present demo, the Plant Species Scientific Name is Pinus ponderosa, Habitat Type is forest, Native Range is Mediterranean region. Use DeepSeek for AI assessment. Before using this tool, we need to obtain an AI API key. For DeepSeek, for example, log in to https://platform.deepseek.com/, register for an account, and prepay a very small fee to use the assigned API key. The results are as follows (Fig. 2):

(1) Physiological Assessment

Physiological Adaptation Score: 78

Water Use Efficiency

Pinus ponderosa exhibits high water use efficiency (WUE) through conservative stomatal regulation. It possesses stomata that are highly sensitive to vapor pressure deficit (VPD) and soil moisture, closing rapidly to minimize transpirational water loss during drought. Its deep taproot system allows access to deeper soil water reserves. However, as a Mediterranean-origin species, it is adapted to seasonal drought but may face challenges under prolonged, intense megadroughts and increased atmospheric aridity, which can push its hydraulic safety margins.

Photosynthetic Capacity

Photosynthetic capacity is moderately resilient to climate stress. P. ponderosa utilizes a conservative strategy, downregulating photosynthesis during water stress to protect its hydraulic system from cavitation. It can maintain positive carbon gain during moderate drought but experiences significant declines under severe, prolonged stress. Its evergreen habit allows for year-round photosynthesis when conditions permit, but it is not a highly heat-tolerant photosynthetic apparatus; photoinhibition can occur under combined high temperature and high light stress.

Thermoregulation

Thermoregulation relies primarily on evaporative cooling via transpiration and morphological adaptations. Needle morphology (reduced surface area-to-volume ratio) minimizes heat load. Under moderate stress, transpirational cooling is effective. However, under severe drought, stomatal closure to conserve water eliminates this cooling mechanism, leading to increased needle temperature and risk of thermal damage. Its thick bark provides insulation against fire, a climate-change-intensified stressor in its habitat. Overall, its thermoregulation is effective under normal Mediterranean climate variability but vulnerable to extreme heatwaves coupled with drought.

Osmotic Adjustment

Osmotic adjustment capability is moderate. P. ponderosa can accumulate compatible solutes (e.g., proline, soluble sugars) to a certain extent to lower osmotic potential, maintain turgor, and protect cellular structures during drought. This is a key adaptation for enduring seasonal dry periods. However, its capacity for osmotic adjustment is not as pronounced as in some highly drought-tolerant desert or chaparral species. Under extreme or rapid-onset drought, this mechanism may be insufficient to prevent severe water deficits and tissue damage.

(2) Biological Assessment

Biological Adaptation Score: 75

Life Cycle Flexibility

Pinus ponderosa is a long-lived, late-successional conifer with a life cycle adapted to predictable seasonal patterns. Its phenology is relatively inflexible; bud break and cone development are heavily cued by photoperiod and accumulated chilling hours, which may become misaligned with earlier springs and warmer winters under climate change. However, its long lifespan (centuries) and high genetic diversity within populations provide a buffer, allowing for selection over generations. Its deep taproot system aids in drought survival, a key trait for Mediterranean-type climates.

Reproductive Strategies

The species employs a conservative, masting reproductive strategy. It produces large, heavy, wind-dispersed seeds at irregular intervals, which is efficient in stable environments but risky under rapid change. Seed germination requires specific moisture and temperature conditions, and establishment is vulnerable to drought and heat stress. Under climate stress, its low annual reproductive output and slow seedling growth could limit migration or adaptation. However, serotinous cones (in some populations) protect seeds from fire, and its wind pollination allows for long-distance gene flow, which may aid genetic adaptation.

 Growth Rate

Pinus ponderosa exhibits a moderate to fast growth rate for a pine, especially in open conditions, allowing it to compete effectively. Resource allocation prioritizes a deep and extensive root system for water access and a thick, fire-resistant bark. This comes at the cost of reduced investment in rapid height growth under drought stress. Its plasticity in leaf-level physiology (e.g., stomatal control) provides some resilience to intermittent drought, but prolonged aridification or extreme heat can lead to reduced growth, increased mortality, and competitive disadvantage against more drought-tolerant species.

 Biotic Interactions

Biotic interactions are complex and may become destabilizing. It is obligately dependent on wind for pollination, which is reliable but inefficient. It forms ectomycorrhizal associations critical for nutrient and water uptake; these fungal symbionts have their own climate sensitivities, creating a potential vulnerability. Major biotic threats include increased herbivory (e.g., bark beetles) whose outbreaks are exacerbated by drought-weakened trees, and competition with more drought-adapted grasses and shrubs in a warming climate. Its role as a foundation species means changes to its health have cascading ecosystem effects.

(3) Morphological Assessment

Morphological Adaptation Score: 78

 Leaf Structure

Pinus ponderosa exhibits classic xeromorphic needle adaptations. Its long, thick, cylindrical needles (10-25 cm) have a low surface area to volume ratio, reducing water loss. Needles are covered in a thick, waxy cuticle, with sunken stomata arranged in rows, which minimizes transpiration. The hypodermis is sclerenchymatous, providing structural support against wilting. These traits are highly advantageous for increased temperatures, drought, and atmospheric aridity. However, the species' native range is not the Mediterranean (it is western North America), so its adaptations are for continental climates with seasonal drought, not classic summer-dry Mediterranean regimes.

 Root System

Pinus ponderosa develops a deep, extensive taproot system, especially in well-drained soils, allowing access to deep soil water during prolonged drought—a critical trait for climate change. Mature trees also develop a widespread lateral root system, enhancing stability and resource foraging. This dual strategy provides resilience against increasing drought frequency and severity. However, in shallow or compacted soils, root development may be restricted, limiting this adaptation.

 Stem & Bark

The stem and bark show significant adaptations. Mature trees develop exceptionally thick (up to 10 cm), plate-like, fire-resistant bark with a high insulating capacity, protecting the vascular cambium from increased wildfire intensity and frequency associated with climate change. The bark's orange-red color may reflect some solar radiation. The species exhibits a degree of phenotypic plasticity in growth, but its monopodial, tall form can be a liability in extreme wind events and may limit carbon allocation flexibility.

 Surface Ratio

The overall plant morphology, from cylindrical needles to a tall, conical crown, is optimized for a low surface area to volume ratio. This minimizes water loss and heat load per unit of living tissue. The open crown architecture reduces self-shading and allows air circulation, mitigating some heat stress. However, the large size of a mature tree represents a massive, fixed carbon investment with high maintenance respiration costs, which could become a liability under rapidly shifting conditions where resource allocation needs to be more dynamic.

(4) Genetic Assessment

Genetic Adaptation Score: 72

□ Genetic Diversity

Moderate to high. Pinus ponderosa (ponderosa pine) exhibits substantial genetic variation across its extensive native range in western North America (not the Mediterranean as stated in the query, which is a critical data discrepancy). Population structure is primarily shaped by geography and climate, with distinct varieties (e.g., var. ponderosa, var. scopulorum) showing local adaptation to temperature and moisture gradients. High outcrossing and wind dispersal promote gene flow, but isolation-by-distance is common. This broad genetic base provides raw material for adaptation.

□ Stress-Responsive Genes

Well-characterized for conifer stress responses. Known gene families involved include: 1) Dehydrins and aquaporins for drought tolerance, 2) Heat shock proteins (HSPs) for thermal stress, 3) Antioxidant enzymes (e.g., superoxide dismutase, peroxidases) for oxidative damage from multiple stresses, 4) Terpene synthases for defense against insects (increased under climate stress), and 5) Photoprotective pigments/genes for high light/UV stress. Expression plasticity in these pathways is documented, but specific allelic variants tied to climate adaptation are still being mapped.

□ Plasticity Potential

High phenotypic plasticity is a key asset. Ponderosa pine exhibits significant plasticity in traits like root-to-shoot ratio, stomatal conductance, needle morphology, and bud phenology in response to water availability and temperature. This allows individual genotypes to acclimate to moderate environmental shifts. However, plasticity has limits, and extreme or chronic stress may exceed its capacity, requiring genetic adaptation via selection.

□ Conservation Status

Priority actions include: 1) Protecting genetic diversity across its range, especially rear-edge populations that may harbor pre-adapted alleles for drought/heat. 2) Assisted gene flow—moving seed from warmer/drier provenances to cooler/wetter ones facing future climate change. 3) Breeding programs selecting for enhanced drought tolerance and pest resistance (e.g., to bark beetles exacerbated by warming). 4) Monitoring for maladaptation as climate decouples from local genotypes. The species' wide planting in forestry offers opportunities for climate-smart reforestation.

(5) Overall Climate Adaptation Summary

Overall Climate Adaptation Score: 76

Pinus ponderosa demonstrates a moderately high level of climate adaptation potential, with an overall score of 76/100. This score reflects a generally robust physiological and morphological constitution, suggesting good inherent resilience to environmental stressors. However, its genetic score indicates a potential vulnerability, possibly related to limited adaptive genetic diversity or specific genetic constraints. As a forest species native to the Mediterranean region, it is likely pre-adapted to warm, dry summers and periodic drought, but its long-term success under accelerating climate change may be challenged by its genetic profile and specific biological tolerances.

□ Strengths:

Strong physiological resilience to abiotic stressors like drought and heat, as indicated by the high physiological score.

Robust morphological traits that support survival and function in its native habitat type, contributing to its solid morphological score.

Good overall biological fitness and ecological function within forest ecosystems, reflected in the above-average biological score.

□ Weaknesses:

Relatively lower genetic score suggests potential limitations in adaptive genetic diversity or high genetic specificity, which could constrain rapid adaptation to novel climates.

As a Mediterranean species, it may have vulnerabilities to climate extremes outside its historical range, such as intense, prolonged droughts or novel pest/disease pressures.

The lack of specified 'Additional Traits' in the data may indicate an absence of notable specialized adaptations (e.g., fire resilience, specific symbioses) that could enhance climate adaptation.

□ **Recommendations:**

Implement genetic conservation and assisted migration strategies to enhance genetic diversity and introduce pre-adapted genotypes to new areas, mitigating the identified genetic vulnerability.

Focus silvicultural management on reducing stand density and competition to lower water stress, leveraging its physiological drought tolerance while minimizing its weaknesses.

Establish long-term monitoring programs specifically for pest and disease outbreaks, as climate change may expose the species to new biotic threats that its biological score does not fully account for.

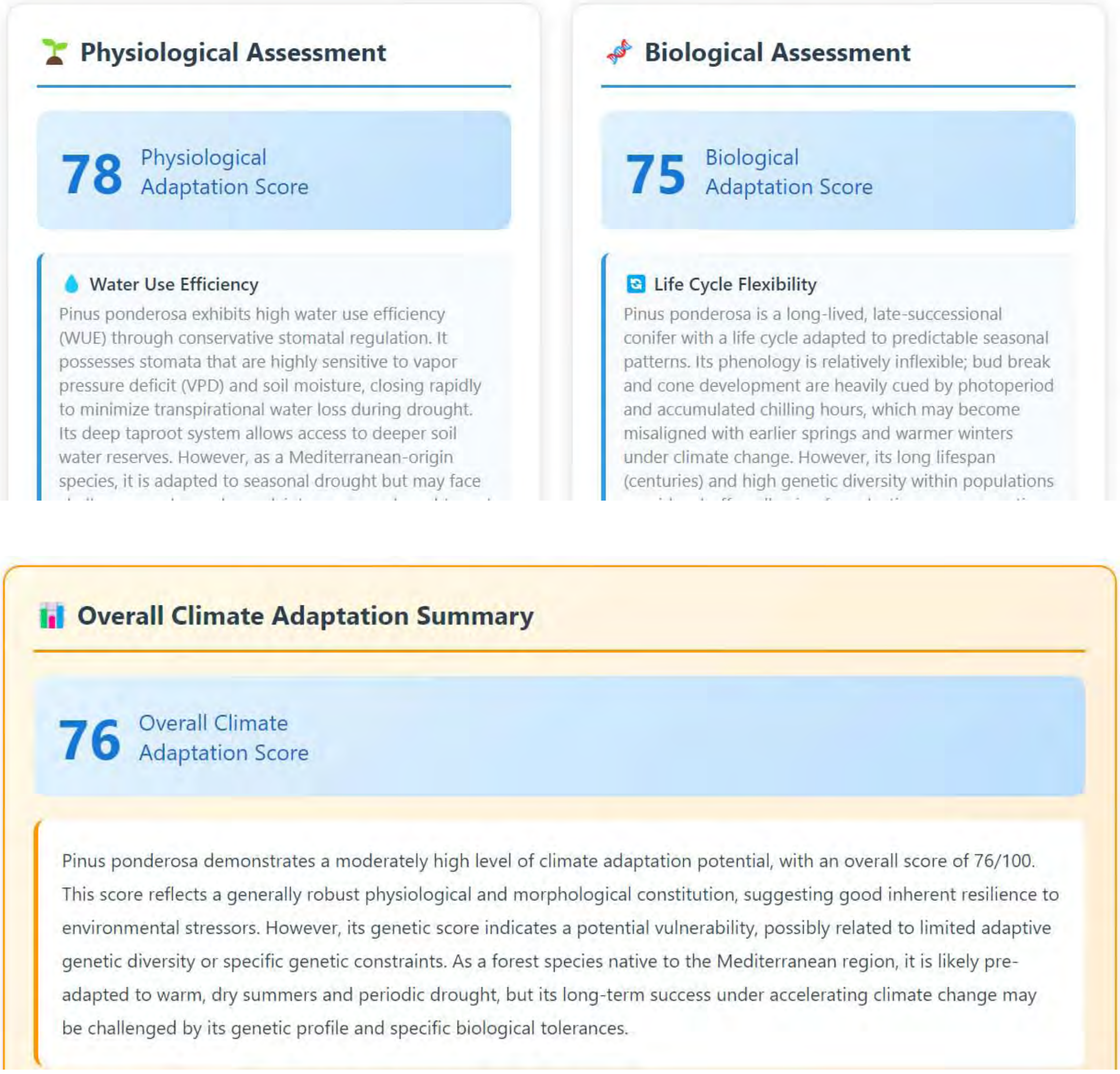

Fig. 2 Results.

References

Farooq M, Anjum W, Khan KR, et al. 2019. Pioneer community level syntaxonomy of forests of lesser Himalayan belt of upper Tanawal Mansehra, Pakistan. Proceedings of the International Academy of Ecology and Environmental Sciences, 9(4): 127-136

Podong C, Poolsiri R. 2013. Forest structure and species diversity of secondary forest after cultivation in relation to various sources at lower northern Thailand. Proceedings of the International Academy of Ecology and Environmental Sciences, 3(3): 208-218

Shobairi SOR, Roudbari SH, Ayombekov Q, et al. 2024. Tracking the impact of climate factors on vegetation dynamics across the Alashan Plateau semi desert ecoregion. Computational Ecology and Software, 14(2): 77-101

Singh D, Verma S, Jayakumar S. 2016. Tree inventory along the altitudinal gradients in Singara Range, Western Ghats, India. Proceedings of the International Academy of Ecology and Environmental Sciences, 6(4): 97-109

Sundar S, Mishra AK, Naresh R, Shukla JB. 2020. Modeling the dynamics of methane emission from rice paddies and livestock populations and its effects on global warming: A comparison of model with data. Computational Ecology and Software, 10(1): 1-14

Zhang WJ. 2014. Interspecific associations and community structure: A local survey and analysis in a grass community. Selforganizology, 1(2): 89-129. http://www.iaees.org/publications/journals/Selforganizology/articles/2014-1(2)/interspecific-associations-and-community-structure-local-survey.pdf

Zhang WJ. 2025. A web-based data generator for Mendelian Randomization (MR) analysis. Network Pharmacology, 10(3-4): 14-65. http://www.iaees.org/publications/journals/np/articles/2025-10(3-4)/1-Zhang-Abstract.asp

Zhang WJ. 2026a. A GWAS data fetcher with AI for Mendelian Randomization analysis. Network Pharmacology, 11(3-4): 62-89. http://www.iaees.org/publications/journals/np/articles/2026-11(3-4)/1-Zhang-Abstract.asp

Zhang WJ. 2026b. AI-driven assessment of animal adaptation to climate change: The web tool based on physiological, morphological, behavioral, and genetic indicators of animal species. Computational Ecology and Software, 16(1): 58-98. http://www.iaees.org/publications/journals/ces/articles/2026-16(1)/3-Zhang-Abstract.asp

Zhang WJ, Liu CH. 2012. Some thoughts on global climate change: will it get warmer and warmer? Environmental Skeptics and Critics, 1(1): 1-7. http://www.iaees.org/publications/journals/environsc/articles/2012-1(1)/some-thoughts-on-global-climate - change.pdf

Zhang WJ, Qi YH. 2026. Fetching GWAS (Genome-Wide Association Study) data via AI: A web tool to synthesize genotype, phenotype, and summary statistics. Ornamental and Medicinal Plants, 9(1-4): 1-21. http://www.iaees.org/publications/journals/omp/articles/2026-9(1-4)/1-Zhang-Abstract.asp

Zhang WJ, Wang R, Zhang DL, et al. 2014. Interspecific associations of weed species around rice fields in Pearl River Delta, China: A regional survey. Selforganizology, 1(3-4): 143-205. http://www.iaees.org/publications/journals/selforganizology/articles/2014-1(3-4)/interspecific-associations-of-weed-species.pdf