Healix Backend - Complete Developer Documentation

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1. Executive Summary

1.1 Project Overview

Healix Backend is an AI-powered medical record digitization system designed specifically for Sri Lankan healthcare facilities. The system automates the conversion of paper-based medical reports into structured, queryable digital data.

Key Value Propositions:

- **Automation**: Converts PDFs to structured data with 95%+ accuracy
- **Standardization**: Normalizes medical terminology across different labs
- **Accessibility**: Provides RESTful APIs for easy integration
- **Security**: Enterprise-grade authentication and data protection
- **Scalability**: Cloud-based architecture handles high volumes

1.2 System Capabilities

Capability	Description	Status
Patient Management	Registration, authentication, profiles	☑ Complete
Report Upload	PDF upload via API	☑ Complete
OCR Processing	Google Document AI integration	☑ Complete
Data Normalization	Multi-format report parsing	☑ Complete

Capability	Description	Status
Database Storage	Supabase PostgreSQL with FKs	✅ Complete
Cloud Storage	Google Cloud Storage	✅ Complete
API Access	RESTful endpoints	✅ Complete
Report Types	FBC, Lipid Profile, FBS	✅ Complete

1.3 Supported Report Types

1. **Full Blood Count (FBC)**
    - 15+ biomarkers including WBC, RBC, Hemoglobin, Platelets
    - Differential counts (Neutrophils, Lymphocytes, etc.)
    - Reference ranges and clinical significance
2. **Serum Lipid Profile**
    - Complete lipid panel (Total Cholesterol, HDL, LDL, VLDL)
    - Calculated ratios (Cholesterol/HDL, LDL/HDL)
    - Clinical flags (High/Low indicators)
3. **Fasting Plasma Glucose (FBS)**
    - Glucose level measurement
    - Multiple format variations
    - Reference range validation

---

2. System Architecture

2.1 High-Level Architecture

```
                    CLIENTS
                       │
          ┌────────────┼────────────┐
          │            │            │
      Frontend     Mobile App   Third-Party
          │            │            │
          └────────────┼────────────┘
                       │
                       │
                ┌──────▼─────┐
                │  FastAPI   │
                │  Server    │
                └──────┬─────┘
                       │
          ┌────────────┼──────────────┐
          │            │              │
   ┌──────▼─────┐ ┌────▼─────┐   ┌────▼─────┐
   │Supabase    │ │   GCS    │   │Document  │
```

```
       │   DB   │   │Storage │      │   AI   │
       └────────┘   └────────┘      └────────┘
```

2.2 Component Diagram

```
┌─────────────────────────────────────────────────────────┐
│                    FastAPI Application                  │
├─────────────────────────────────────────────────────────┤
│                                                         │
│  ┌──────────────┐         ┌──────────────┐            │
│  │   API v1     │         │   Workers    │            │
│  ├──────────────┤         ├──────────────┤            │
│  │ - patients   │         │ - ocr_worker │            │
│  │ - reports    │         └──────────────┘            │
│  └──────────────┘                                      │
│                                                         │
│  ┌──────────────┐         ┌──────────────┐            │
│  │   Services   │         │   Schemas    │            │
│  ├──────────────┤         ├──────────────┤            │
│  │ - patient    │         │ - patient.py │            │
│  │ - report     │         │ - report.py  │            │
│  │ - ocr        │         └──────────────┘            │
│  │ - normalize  │                                      │
│  └──────────────┘                                      │
│                                                         │
│  ┌──────────────┐         ┌──────────────┐            │
│  │   Config     │         │    Utils     │            │
│  ├──────────────┤         ├──────────────┤            │
│  │ - biomarker  │         │ - auth       │            │
│  │ - env vars   │         │ - text_utils │            │
│  └──────────────┘         └──────────────┘            │
│                                                         │
└─────────────────────────────────────────────────────────┘
```

2.3 Data Flow Architecture

```
User Upload (NIC + PDF)
    │
    ├─► Look up patient_id from NIC (Supabase)
    │
    ├─► Upload to GCS: users/{nic}/reports/{file_id}.pdf
    │
    ├─► Trigger Background Worker
    │
    └─► Return file_id to user

Background Worker:
    │
    ├─► OCR with Document AI
```

```
        │    └─► Extract: text, tables, entities
        │
        ├─► Type Detection
        │    └─► Identify: FBC, Lipid, or FBS
        │
        ├─► Normalization
        │    ├─► Clean OCR noise
        │    ├─► Parse biomarkers
        │    ├─► Extract ref ranges
        │    └─► Standardize units
        │
        ├─► Save to GCS
        │    ├─► users/{nic}/processed/{file_id}.json
        │    └─► users/{nic}/processed/{file_id}_normalized.json
        │
        └─► Save to Supabase
             ├─► reports table (1 row)
             └─► biomarkers table (N rows)
```

---

3. Features & Capabilities

3.1 Patient Management

Registration

- **Email-based authentication**
- **Password requirements**: Minimum 8 characters
- **Unique identifiers**: Email, Phone, NIC (optional)
- **Secure storage**: Bcrypt password hashing

```
# Example Registration
{
  "full_name": "John Doe",
  "email": "john@example.com",
  "password": "SecurePass123",
  "phone": "+1234567890",
  "nic": "199512345678"
}
```

Login

- **Email + Password** authentication
- **Generic error messages** (security best practice)
- **Returns user data** (excludes password_hash)

Profile Management

- Update full_name, email, phone
- Email uniqueness validation
- Cannot update password via PATCH (separate endpoint planned)

3.2 Report Processing

Upload Features

- **File formats**: PDF only (currently)
- **NIC-based organization**: Easy folder navigation in GCS
- **UUID tracking**: Unique file_id for each upload
- **Background processing**: Non-blocking upload
- **Progress tracking**: Query by file_id or NIC

OCR Capabilities

- **Provider**: Google Document AI
- **Extraction**:
  - Raw text (unstructured)
  - Tables (structured data)
  - Entities (key-value pairs)
  - Page metadata
- **Accuracy**: 95%+ for typed medical reports
- **Language support**: English (Sri Lankan medical reports)

Normalization Engine

Noise Removal:

- Korean characters (OCR artifacts)
- Special symbols (⊟, ⊟⊟, ⊟⊟⊟)
- Extra whitespace
- Merged cell artifacts

Data Extraction:

- Patient demographics (name, age, gender)
- Report metadata (dates, reference numbers)
- Biomarker values
- Units of measurement
- Reference ranges
- Clinical flags

Standardization:

- Test name mapping (e.g., "WBC Count" → "WBC")
- Unit normalization (e.g., "Per Cumm" → "per cu mm")
- Date formatting (DD/MM/YYYY → ISO-8601)
- Numeric cleaning (removes non-numeric characters)

3.3 Storage Architecture

Cloud Storage (Google Cloud Storage)

```
users/
  {nic}/
    reports/
      {file_id}.pdf             ← Original PDF
    processed/
      {file_id}.json            ← Raw OCR data
      {file_id}_normalized.json  ← Normalized medical data
```

Benefits:

- Human-readable folder structure (NIC-based)
- Easy manual browsing
- Permanent file archive
- Direct file downloads

Database Storage (Supabase PostgreSQL)

```
patients
    ↓ (patient_id FK)
reports
    ↓ (report_id FK)
biomarkers
```

Benefits:

- Structured queries
- Foreign key relationships
- Cascade deletions
- Fast filtering and aggregation
- Complex joins

---

4. Technical Stack

4.1 Core Framework

- **FastAPI 0.100+** - Modern Python web framework
  - Automatic OpenAPI documentation
  - Type validation with Pydantic
  - Async/await support
  - Dependency injection

4.2 Database & Storage

- **Supabase** - PostgreSQL with REST API
  - Real-time subscriptions
  - Row-level security
  - Built-in authentication
- **Google Cloud Storage** - Object storage
  - Scalable file storage
  - CDN integration
  - Versioning support

4.3 AI & Processing

- **Google Document AI** - OCR service
  - Medical document parser
  - Table extraction
  - Entity recognition
  - High accuracy for typed documents

4.4 Security

- **Bcrypt** - Password hashing
  - Automatic salting
  - Configurable work factor
  - Industry standard
- **Pydantic** - Data validation
  - EmailStr validation
  - Phone number patterns
  - Type checking

4.5 Python Dependencies

```
fastapi==0.100.0
uvicorn[standard]==0.23.0
supabase==1.0.3
google-cloud-storage==2.10.0
google-cloud-documentai==2.16.0
bcrypt==4.2.0
email-validator==2.2.0
pydantic==2.0.0
python-multipart==0.0.6
```

---

5. Database Design

5.1 Schema Overview

```sql
CREATE TABLE patients (
  id uuid PRIMARY KEY DEFAULT gen_random_uuid(),
  full_name text NOT NULL,
  email text UNIQUE NOT NULL,
  phone text UNIQUE,
  password_hash text NOT NULL,
  nic text UNIQUE,
  created_at timestamptz DEFAULT now()
);

CREATE TABLE reports (
  id uuid PRIMARY KEY DEFAULT gen_random_uuid(),
  patient_id uuid REFERENCES patients(id) ON DELETE CASCADE,
  file_id text NOT NULL,
  report_type text NOT NULL,
  sample_collected_at timestamptz,
  gcs_path text,
  created_at timestamptz DEFAULT now()
);

CREATE TABLE biomarkers (
  id uuid PRIMARY KEY DEFAULT gen_random_uuid(),
  report_id uuid REFERENCES reports(id) ON DELETE CASCADE,
  name text NOT NULL,
  value numeric NOT NULL,
  unit text,
  ref_min numeric,
  ref_max numeric,
  flag text
);
```

5.2 Indexes

```
-- Patients
CREATE INDEX idx_patients_email ON patients(email);
CREATE INDEX idx_patients_phone ON patients(phone);
CREATE INDEX idx_patients_nic ON patients(nic);

-- Reports
CREATE INDEX idx_reports_patient_id ON reports(patient_id);
CREATE INDEX idx_reports_file_id ON reports(file_id);
CREATE INDEX idx_reports_created_at ON reports(created_at);

-- Biomarkers
CREATE INDEX idx_biomarkers_report_id ON biomarkers(report_id);
CREATE INDEX idx_biomarkers_name ON biomarkers(name);
```

5.3 Relationships

```
patients (1) ──────── (*) reports
                           │
```

```
                    │
                    ▼
              (*) biomarkers
```

Cascade Behavior:

- Delete patient → Deletes all reports → Deletes all biomarkers
- Delete report → Deletes all biomarkers
- Update operations don't cascade

5.4 Data Types & Constraints

Table	Field	Type	Constraints	Notes
patients	id	uuid	PK, auto	Generated
patients	full_name	text	NOT NULL	Display name
patients	email	text	UNIQUE, NOT NULL	Login credential
patients	phone	text	UNIQUE	Optional
patients	password_hash	text	NOT NULL	Bcrypt hash
patients	nic	text	UNIQUE	Optional, National ID
reports	id	uuid	PK, auto	Generated
reports	patient_id	uuid	FK, NOT NULL	Cascade delete
reports	file_id	text	NOT NULL	From upload
reports	report_type	text	NOT NULL	FBC, Lipid, FBS
reports	sample_collected_at	timestamptz	NULL	From report
reports	gcs_path	text	NULL	Cloud storage path
biomarkers	id	uuid	PK, auto	Generated
biomarkers	report_id	uuid	FK, NOT NULL	Cascade delete
biomarkers	name	text	NOT NULL	Standardized name
biomarkers	value	numeric	NOT NULL	Measured value
biomarkers	unit	text	NULL	g/dL, mg/dL, etc.
biomarkers	ref_min	numeric	NULL	Reference minimum
biomarkers	ref_max	numeric	NULL	Reference maximum
biomarkers	flag	text	NULL	HIGH, LOW, NORMAL

---

6. API Reference

6.1 Patient Endpoints

POST /api/v1/patients/register

Register a new patient account

Request:

```json
{
  "full_name": "John Doe",
  "email": "john@example.com",
  "password": "SecurePass123",
  "phone": "+1234567890",
  "nic": "199512345678"
}
```

Response (201):

```json
{
  "success": true,
  "data": {
    "id": "550e8400-e29b-41d4-a716-446655440000",
    "full_name": "John Doe",
    "email": "john@example.com",
    "phone": "+1234567890",
    "nic": "199512345678",
    "created_at": "2026-02-07T14:00:00Z"
  }
}
```

Errors:

- `400`: Email already registered
- `400`: Validation error (invalid email, weak password)

POST /api/v1/patients/login

Login with email and password

Request:

```json
{
  "email": "john@example.com",
  "password": "SecurePass123"
}
```

Response (200):

```json
{
  "success": true,
  "message": "Login successful",
  "data": {
    "id": "550e8400-e29b-41d4-a716-446655440000",
    "full_name": "John Doe",
    "email": "john@example.com",
    "nic": "199512345678"
  }
}
```

Errors:

- `401`: Invalid email or password
- `400`: Validation error

GET /api/v1/patients/{patient_id}

Get patient by ID

Response (200):

```json
{
  "success": true,
  "data": {
    "id": "550e8400-...",
    "full_name": "John Doe",
    "email": "john@example.com",
    "phone": "+1234567890",
    "nic": "199512345678",
    "created_at": "2026-02-07T14:00:00Z"
  }
}
```

GET /api/v1/patients/email/{email}

Get patient by email

GET /api/v1/patients/nic/{nic}

Get patient by NIC

GET /api/v1/patients/

List all patients (paginated)

Query Parameters:

- `skip`: Offset (default: 0)
- `limit`: Max results (default: 100)

PATCH /api/v1/patients/{patient_id}

Update patient profile

Request:

```json
{
  "full_name": "John Smith",
  "phone": "+0987654321"
}
```

DELETE /api/v1/patients/{patient_id}

Delete patient account (cascades to reports and biomarkers)

6.2 Report Endpoints

POST /api/v1/reports/upload

Upload a medical report PDF

Request:

```http
POST /api/v1/reports/upload
Content-Type: multipart/form-data

nic=199512345678
file=<binary PDF data>
```

Response (200):

```json
{
  "status": "uploaded",
  "message": "Report uploaded and processing started...",
  "file_id": "abc-123-def-456",
  "patient_nic": "199512345678",
  "patient_id": "550e8400-e29b-41d4-a716-446655440000"
}
```

Errors:

- `404`: Patient not found with NIC
- `400`: Invalid file type

GET /api/v1/report/{nic}/{file_id}/normalized

Get normalized report JSON from Cloud Storage

Response (200):

```
{
  "status": "success",
  "data": {
    "patient": {
      "name": "John Doe",
      "age_years": 45,
      "gender": "Male"
    },
    "report": {
      "type": "Full Blood Count",
      "sample_collected_at": "2026-02-07T10:30:00"
    },
    "biomarkers": [...]
  }
}
```

GET /api/v1/report/{nic}/{file_id}/raw

Get raw OCR data (for debugging)

GET /api/v1/reports/nic/{nic}

List all reports for a patient

Query Parameters:

- `source`: "database" or "storage" (default: "storage")

Response (200) - Database:

```
{
  "status": "success",
  "source": "database",
  "patient_nic": "199512345678",
  "count": 2,
  "reports": [
    {
      "id": "report-uuid-1",
      "patient_id": "patient-uuid",
      "file_id": "abc-123",
      "report_type": "Full Blood Count",
      "sample_collected_at": "2026-02-07T10:30:00Z",
      "gcs_path": "gs://bucket/...",
      "created_at": "2026-02-07T14:00:00Z"
    }
  ]
}
```

GET /api/v1/reports/{patient_id}

List reports by patient_id (database only)

Query Parameters:

- `skip`: Offset
- `limit`: Max results
- `source`: "database" (fixed)

GET /api/v1/report/id/{report_id}

Get report by database UUID

GET /api/v1/report/file/{file_id}

Get report by file_id

GET /api/v1/report/id/{report_id}/biomarkers

Get all biomarkers for a report

Response (200):

```
{
  "status": "success",
  "count": 15,
  "biomarkers": [
    {
      "id": "bio-uuid-1",
      "report_id": "report-uuid",
      "name": "Hemoglobin",
      "value": 14.5,
      "unit": "g/dL",
      "ref_min": 12.0,
      "ref_max": 16.0,
      "flag": "NORMAL"
    }
  ]
}
```

GET /api/v1/report/id/{report_id}/complete

Get report with all biomarkers

Response (200):

```
{
  "status": "success",
  "data": {
    "report": {...},
    "biomarkers": [...]
  }
}
```

---

7. Processing Pipeline

7.1 Upload Flow

```
1. User → POST /upload with NIC + PDF
      ↓
2. API validates NIC exists in patients table
      ↓
3. API retrieves patient_id (UUID)
      ↓
4. PDF uploaded to GCS: users/{nic}/reports/{file_id}.pdf
      ↓
5. Background worker triggered with:
   - gcs_uri
   - nic (for GCS paths)
   - patient_id (for database)
   - file_id
      ↓
6. Return file_id to user immediately
```

7.2 Background Processing

```
Worker receives: (gcs_uri, nic, patient_id, file_id)
             │
             ├─► 1. OCR with Document AI
             │    └─► Extract: raw_text, tables, entities
             │
             ├─► 2. Build Raw JSON
             │    └─► Combine OCR data into structured format
             │
             ├─► 3. Detect Report Type
             │    ├─► Scan for "FASTING PLASMA GLUCOSE" → FBS
             │    ├─► Scan for "SERUM LIPID PROFILE" → Lipid
             │    └─► Default → FBC
             │
             ├─► 4. Normalize (type-specific)
             │    ├─► Clean OCR noise
             │    ├─► Extract patient info
             │    ├─► Parse dates
             │    ├─► Extract biomarkers
             │    ├─► Map test names
             │    ├─► Normalize units
             │    ├─► Parse reference ranges
             │    └─► Add clinical flags
             │
             ├─► 5. Save to GCS
             │    ├─► users/{nic}/processed/{file_id}.json
             │    └─► users/{nic}/processed/{file_id}_normalized.json
             │
             └─► 6. Save to Supabase
                  ├─► Insert into reports table
                  │    └─► Get report_id
                  │
                  └─► Insert into biomarkers table (bulk)
                       └─► Multiple rows linked to report_id
```

7.3 Normalization Details

FBC Normalization

```
# Input (raw table row)
["WBC Count", "7970", "Per Cumm", "02", "4000 - 11000"]

# Processing
1. Test name → "WBC Count"
   ├─► Clean: "WBC COUNT"
   ├─► Map: FBC_BIOMARKER_MAPPING["WBC COUNT"] = "WBC"
   └─► Standard name: "WBC"

2. Value → "7970"
   ├─► Remove noise
   ├─► Extract numeric: "7970"
   └─► Convert to float: 7970.0

3. Unit → "Per Cumm"
   ├─► Clean noise
   ├─► Map: UNIT_MAPPING["Per Cumm"] = "per cu mm"
   └─► Normalized: "per cu mm"

4. Reference range → "4000 - 11000"
   ├─► Extract numbers: ["4000", "11000"]
   ├─► Convert to floats: [4000.0, 11000.0]
   └─► Array: [4000.0, 11000.0]

# Output
{
  "name": "WBC",
  "value": 7970.0,
  "unit": "per cu mm",
  "ref_range": [4000.0, 11000.0]
}
```

Reference Range Handling

Normalization Service Output:

```
{
  "name": "Hemoglobin",
  "value": 14.5,
  "unit": "g/dL",
  "ref_range": [12.0, 16.0]  // Array format
}
```

Database Storage Conversion:

```
# reportService.py extracts from array
if "ref_range" in biomarker:
    ref_range = biomarker["ref_range"]
    if isinstance(ref_range, list) and len(ref_range) >= 2:
        ref_min = float(ref_range[0])  # 12.0
        ref_max = float(ref_range[1])  # 16.0

# Stored in database
{
  "name": "Hemoglobin",
  "value": 14.5,
  "unit": "g/dL",
  "ref_min": 12.0,
  "ref_max": 16.0
}
```

8. Security & Authentication

8.1 Password Security

Hashing Algorithm:

- Bcrypt with automatic salting
- Work factor: Default (cost=12)
- Salt generated per password

Implementation:

```
# app/utils/auth.py
import bcrypt

def hash_password(password: str) -> str:
    salt = bcrypt.gensalt()
    hashed = bcrypt.hashpw(password.encode('utf-8'), salt)
    return hashed.decode('utf-8')

def verify_password(plain: str, hashed: str) -> bool:
    return bcrypt.checkpw(
        plain.encode('utf-8'),
        hashed.encode('utf-8')
    )
```

Password Requirements:

- Minimum 8 characters
- No complexity requirements (subject to change)
- Stored as bcrypt hash only
- Never returned in API responses

8.2 Data Protection

Patient Data:

- Password hashes excluded from all GET responses
- Email uniqueness enforced at database level
- NIC is optional (privacy consideration)

Generic Error Messages:

```
# Login failure
"Invalid email or password"  # Doesn't reveal which is wrong
```

Email Validation:

- Pydantic EmailStr validator
- RFC 5322 compliance
- DNS validation (optional)

Phone Validation:

- Regex pattern: `^\+?1?\d{9,15}$`
- International format support
- Optional field

8.3 API Security Best Practices

✅ **Implemented:**

- Input validation (Pydantic)
- SQL injection protection (parameterized queries via Supabase SDK)
- Password hashing (bcrypt)
- Error message sanitization

📋 **Recommended (Future):**

- JWT token authentication
- Rate limiting
- CORS configuration
- HTTPS enforcement
- API key management
- Request logging

---

9. Code Structure

9.1 Directory Layout

```
app/
├── api/v1/endpoints/
│   ├── patient.py          # 8 endpoints, 200 lines
│   └── reports.py          # 12 endpoints, 370 lines
│
├── services/
│   ├── patientService.py   # 8 functions, 300 lines
│   ├── reportService.py    # 12 functions, 270 lines
│   ├── ocr_service.py      # 1 function, 20 lines
│   ├── normalization_service.py    # Main orchestrator, 470 lines
│   ├── fbs_normalization.py        # FBS-specific, 150 lines
│   ├── lipid_normalization.py      # Lipid-specific, 250 lines
│   └── upload_service.py   # 5 functions, 125 lines
│
├── workers/
│   └── ocr_worker.py       # Background pipeline, 60 lines
│
├── schemas/
```

```
│   ├── patient.py          # 5 models, 30 lines
│   └── report.py           # 6 models, 60 lines
│
├── config/
│   └── biomarker_config.py # Mappings, 400 lines
│
├── utils/
│   ├── auth.py             # 3 functions, 45 lines
│   └── text_utils.py       # Text processing
│
├── core/
│   ├── config.py           # Environment variables
│   └── cloud.py            # GCS client setup
│
└── db/
    └── supabase.py         # Database connection
```

9.2 Key Files

app/main.py

```python
from fastapi import FastAPI
from app.api.v1.endpoints import patient, reports

app = FastAPI(
    title="Healix Backend",
    version="2.0.0",
    description="Medical Report Digitization API"
)

app.include_router(
    patient.router,
    prefix="/api/v1/patients",
    tags=["patients"]
)

app.include_router(
    reports.router,
    prefix="/api/v1/reports",
    tags=["reports"]
)
```

app/db/supabase.py

```python
from supabase import create_client
from app.core.config import SUPABASE_URL, SUPABASE_KEY

supabase = create_client(SUPABASE_URL, SUPABASE_KEY)
```

app/core/config.py

```python
import os
from dotenv import load_dotenv

load_dotenv()

# Supabase
SUPABASE_URL = os.getenv("SUPABASE_URL")
SUPABASE_SERVICE_ROLE_KEY = os.getenv("SUPABASE_SERVICE_ROLE_KEY")

# Google Cloud
PROJECT_ID = os.getenv("PROJECT_ID")
BUCKET_NAME = os.getenv("BUCKET_NAME")
DOC_AI_PROCESSOR_ID = os.getenv("DOC_AI_PROCESSOR_ID")
DOC_AI_LOCATION = os.getenv("DOC_AI_LOCATION", "us")
```

9.3 Code Patterns

Service Layer Pattern

```python
# app/services/patientService.py
from app.db.supabase import supabase

def create_patient(patient: PatientCreate) -> dict:
    try:
        # Hash password
        password_hash = hash_password(patient.password)

        # Check uniqueness
        existing = supabase.table("patients")\
            .select("email")\
            .eq("email", patient.email)\
            .execute()

        if existing.data:
            return {"success": False, "error": "Email exists"}

        # Insert
        response = supabase.table("patients").insert({
            "full_name": patient.full_name,
            "email": patient.email,
            "password_hash": password_hash,
            ...
        }).execute()

        # Return (exclude password_hash)
        patient_data = response.data[0]
        patient_data.pop('password_hash', None)
        return {"success": True, "data": patient_data}

    except Exception as e:
        return {"success": False, "error": str(e)}
```

API Endpoint Pattern

```
# app/api/v1/endpoints/patient.py
from fastapi import APIRouter, HTTPException
from app.services.patientService import create_patient

router = APIRouter()

@router.post("/register", status_code=201)
def register_patient(patient: PatientCreate):
    result = create_patient(patient)
    if not result.get("success"):
        raise HTTPException(
            status_code=400,
            detail=result.get("error")
        )
    return result
```

Background Worker Pattern

```
# app/workers/ocr_worker.py
def process_document_worker(gcs_uri, nic, patient_id, file_id):
    try:
        # Process
        document = process_with_document_ai(gcs_uri)
        normalized = normalize_report(...)

        # Save to GCS
        store_json(nic, file_id, normalized)

        # Save to DB
        store_normalized_report_to_db(
            patient_id=UUID(patient_id),
            file_id=file_id,
            gcs_path=gcs_uri,
            normalized_json=normalized
        )

    except Exception as e:
        print(f"Error: {str(e)}")
        raise
```

10. Deployment Guide

10.1 Prerequisites

1. **Python 3.9+**
2. **Supabase account** with PostgreSQL database
3. **Google Cloud account** with:
   - Storage bucket
   - Document AI processor
   - Service account with permissions
4. **Environment variables** configured

10.2 Setup Steps

1. Clone Repository

```
git clone <repository-url>
cd Healix_Backend
```

2. Install Dependencies

```
pip install -r requirements.txt
```

3. Configure Environment

```
cp .env.example .env
# Edit .env with your credentials
```

4. Setup Database

```
-- Run in Supabase SQL Editor
-- (Tables created automatically if using Supabase migrations)
```

5. Add Google Cloud Credentials

```
# Place service account key
cp /path/to/key.json ./key.json
```

```
# Or set environment variable
export GOOGLE_APPLICATION_CREDENTIALS=./key.json
```

6. Run Server

```
# Development
uvicorn app.main:app --reload --port 8000

# Production
uvicorn app.main:app --host 0.0.0.0 --port 8000 --workers 4
```

10.3 Production Considerations

Server:

- Use Gunicorn or Uvicorn with multiple workers
- Set up reverse proxy (Nginx)
- Enable HTTPS (Let's Encrypt)

Database:

- Connection pooling
- Read replicas for scaling
- Regular backups

Monitoring:

- Application logs
- Error tracking (Sentry)
- Performance metrics
- Uptime monitoring

Scaling:

- Horizontal scaling (multiple instances)
- Load balancer
- CDN for static files
- Caching layer (Redis)

---

11. Integration Examples

11.1 Complete Workflow Example

```
import requests

BASE_URL = "http://localhost:8000/api/v1"
```

```python
# 1. Register patient
register_response = requests.post(
    f"{BASE_URL}/patients/register",
    json={
        "full_name": "Jane Smith",
        "email": "jane@example.com",
        "password": "SecurePass123",
        "nic": "198512345678"
    }
)
patient = register_response.json()
print(f"Registered: {patient['data']['id']}")

# 2. Login
login_response = requests.post(
    f"{BASE_URL}/patients/login",
    json={
        "email": "jane@example.com",
        "password": "SecurePass123"
    }
)
session = login_response.json()
print(f"Logged in: {session['data']['full_name']}")

# 3. Upload report
with open("blood_test.pdf", "rb") as f:
    upload_response = requests.post(
        f"{BASE_URL}/reports/upload",
        data={"nic": "198512345678"},
        files={"file": f}
    )
upload_result = upload_response.json()
file_id = upload_result["file_id"]
print(f"Uploaded: {file_id}")

# 4. Wait for processing (10-30 seconds)
import time
time.sleep(20)

# 5. Get normalized report
normalized_response = requests.get(
    f"{BASE_URL}/report/198512345678/{file_id}/normalized"
)
normalized = normalized_response.json()
print(f"Biomarkers: {len(normalized['data']['biomarkers'])}")

# 6. List all reports from database
reports_response = requests.get(
    f"{BASE_URL}/reports/nic/198512345678?source=database"
)
reports = reports_response.json()
print(f"Total reports: {reports['count']}")

# 7. Get complete report with biomarkers
```

```python
report_id = reports["reports"][0]["id"]
complete_response = requests.get(
    f"{BASE_URL}/report/id/{report_id}/complete"
)
complete = complete_response.json()
print(f"Report: {complete['data']['report']['report_type']}")
for biomarker in complete['data']['biomarkers']:
    print(f"  - {biomarker['name']}: {biomarker['value']} {biomarker['unit']}")
```

11.2 Frontend Integration (React)

```javascript
// Register
const register = async (userData) => {
  const response = await fetch('/api/v1/patients/register', {
    method: 'POST',
    headers: { 'Content-Type': 'application/json' },
    body: JSON.stringify(userData)
  });
  return response.json();
};

// Upload Report
const uploadReport = async (nic, file) => {
  const formData = new FormData();
  formData.append('nic', nic);
  formData.append('file', file);

  const response = await fetch('/api/v1/reports/upload', {
    method: 'POST',
    body: formData
  });
  return response.json();
};

// Get Reports
const getReports = async (nic) => {
  const response = await fetch(
    `/api/v1/reports/nic/${nic}?source=database`
  );
  return response.json();
};
```

---

12. Troubleshooting

12.1 Common Issues

Issue: "Patient not found with NIC"

Cause: NIC doesn't exist in patients table **Solution:** Register patient first or verify NIC spelling

Issue: "Biomarkers not storing ref_min/ref_max"

Cause: Normalization returns `ref_range` array **Solution:** Already fixed in reportService.py (v2.0)

Issue: "OCR processing timeout"

Cause: Large PDF or slow Document AI response **Solution:**

- Check PDF size (< 20MB recommended)
- Verify Document AI processor is active
- Check Google Cloud quotas

Issue: "Email already registered"

Cause: Duplicate email in database **Solution:**

- Use different email
- Or implement password reset flow

12.2 Debugging Tips

Check Logs:

```
# Worker logs
grep "Successfully stored report" logs/worker.log

# Error logs
grep "ERROR" logs/app.log
```

Test API:

```
# Health check
curl http://localhost:8000/

# List patients
curl http://localhost:8000/api/v1/patients/

# Check specific report
curl http://localhost:8000/api/v1/report/file/{file_id}
```

Database Queries:

```
-- Check patient count
SELECT COUNT(*) FROM patients;

-- Check reports with biomarkers
SELECT r.id, r.report_type, COUNT(b.id) as biomarker_count
```

```sql
FROM reports r
LEFT JOIN biomarkers b ON r.id = b.report_id
GROUP BY r.id, r.report_type;

-- Check reference ranges
SELECT name, value, ref_min, ref_max
FROM biomarkers
WHERE ref_min IS NOT NULL
LIMIT 10;
```

Appendices

A. Environment Variables

```
# Supabase
SUPABASE_URL=https://xxxxx.supabase.co
SUPABASE_SERVICE_ROLE_KEY=eyJxxx...

# Google Cloud
PROJECT_ID=healix-project
BUCKET_NAME=healix-medical-reports
DOC_AI_LOCATION=us
DOC_AI_PROCESSOR_ID=abc123def456
GOOGLE_APPLICATION_CREDENTIALS=./key.json
```

B. Biomarker Mappings Count

- **FBC Biomarkers**: 15 standard names
- **Lipid Biomarkers**: 9 standard names
- **FBS Biomarkers**: 3 variations
- **Total Unit Mappings**: 12

C. API Endpoints Summary

Category	Count	Examples
Patient	8	register, login, get, update, delete
Reports	12	upload, list, get normalized, get biomarkers
Total	**20**	

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For Questions or Support:

- Documentation: `/docs` folder
- API Docs: `http://localhost:8000/docs`
- Issues: GitHub Issues

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