

This document outlines the API services for various medical image analysis and prediction tasks. Each service is exposed via a specific route and accepts defined inputs to produce corresponding outputs.

API Service Documentation

Here's a breakdown of each available service:

1. Cancer Subtype Classification

- **Endpoint:** `/cancer-subtype/`
- **HTTP Method:** `POST`
- **Description:** Classifies the subtype of cancer from an uploaded medical image.
- **Request:**
 - `file`: An image file (`UploadFile`). The image will be converted to RGB, resized to 224x224, and normalized before being fed to a `CustomSotaCNN` model.
- **Response (`PredictionResponse`):**
 - `predicted_class` (str): The predicted cancer subtype (e.g., 'adenocarcinoma', 'large.cell.carcinoma', 'normal', 'squamous.cell.carcinoma').
 - `confidence` (float): The confidence score of the prediction, rounded to 4 decimal places.
- **Details:**
 - The service uses a pre-trained `CustomSotaCNN` model with weights loaded from `"app/models/CancerClassification/best_custom_sota_model.pth"`.
 - Input images are transformed using ImageNet statistics (mean: `[0.485, 0.456, 0.406]`, std: `[0.229, 0.224, 0.225]`).

2. Patient Cancer Classification

- **Endpoint:** `/patient-cancer-classification/predict_patient_cancer_status`
- **HTTP Method:** `POST`
- **Description:** Predicts the cancer status for a patient based on a ZIP archive of their DICOM scan series.
- **Request:**
 - `scan_zip`: A ZIP file (`UploadFile`) containing the DICOM series for one patient.
 - `patient_id_form` (str, optional): An optional patient identifier. If not provided, it's derived from the ZIP filename.
- **Response (`PatientCancerPredictionResponse`):**
 - `patient_id` (str): Identifier for the patient.

- `message` (str): Status message of the prediction.
- `probability_cancer` (float, optional): The predicted probability of cancer.
- `predicted_class` (int, optional): The predicted class (1 for cancer, 0 for no cancer), based on a threshold of 0.5.
- `model_threshold_used` (float, optional): The probability threshold used for classification.
- `processed_scan_shape_zyx` (List[int], optional): The shape of the processed scan (Z, Y, X).
- `error_details` (str, optional): Details if an error occurred.
- **Details:**
 - The service uses a `Simp3DNet` model with weights from "app/models/PatientCancerClassification/simp3dnet_model_50_each_64cube_best.pth".
 - DICOM series are preprocessed: resampled to target spacing (1.5, 1.5, 1.5), segmented, normalized (HU range -1000 to 400), zero-centered (mean 0.25), and resized to the model's input shape (e.g., 64x64x64).
 - It automatically tries to find the main DICOM series folder within the extracted ZIP archive.

3. Nodule Candidate Detection

- **Endpoint:** `/nodule-detection/predict`
- **HTTP Method:** `POST`
- **Description:** Detects potential nodule candidates from a CT scan provided as MHD and RAW files.
- **Request:**
 - `mhd_file`: The MHD header file (`UploadFile`) for the CT scan.
 - `raw_file`: The RAW data file (`UploadFile`) for the CT scan, corresponding to the MHD file.
- **Response** (`NoduleDetectionResponse`):
 - `message` (str): Status message of the detection process.
 - `nodules` (List[`NodulePredictionItem`]): A list of detected nodule candidates. Each item includes:
 - `coordX`, `coordY`, `coordZ` (float): World coordinates of the nodule.
 - `voxelX_resampled`, `voxelY_resampled`, `voxelZ_resampled` (int): Voxel coordinates in the resampled image.
 - `probability` (float): The probability score of the nodule.
 - `estimated_radius_mm` (float): Estimated radius of the nodule in millimeters.

- `scan_shape_zyx_resampled` (List[int], optional): The shape (Z, Y, X) of the resampled scan volume used for detection.
- **Details:**
 - Uses a `UNet3D_MSA` model with weights from `"app/models/NoduleDetection/best_model_msa_unetinf.pth"`.
 - Preprocessing includes: resampling to target spacing (1.0, 1.0, 1.0), HU normalization (clipped between -1000 and 400 HU, then scaled to 0.0-1.0), and lung segmentation.
 - Inference is performed patch-wise (default patch size 96x96x96, stride 48x48x48) on the processed volume.
 - Heatmap peaks are identified, converted to world coordinates, and subjected to 3D Non-Maximum Suppression (NMS) to yield final candidates.

4. Nodule Classification

- **Endpoint:** `/nodule-classification/classify_candidates`
- **HTTP Method:** `POST`
- **Description:** Classifies provided nodule candidates from a CT scan (MHD/RAW) as nodule or non-nodule.
- **Request:**
 - `mhd_file`: The MHD header file (`UploadFile`) for the CT scan.
 - `raw_file`: The RAW data file (`UploadFile`) corresponding to the MHD file.
 - `candidates_json_str`: A JSON string (`str` passed as a Form field) representing a list of `CandidateCoordinateItem`. Each item should contain:
 - `id` (str or int): A unique identifier for the candidate.
 - `coordX`, `coordY`, `coordZ` (float): World coordinates (X, Y, Z) of the candidate.
- **Response** (`CandidateClassificationResponse`):
 - `message` (str): Status message of the classification.
 - `processed_scan_filename_base` (str): Base name of the processed scan file.
 - `predictions` (List[`CandidatePredictionItem`]): A list of classification results for each input candidate. Each item includes:
 - Original `id`, `coordX`, `coordY`, `coordZ`.
 - `probability_nodule` (float): The model's predicted probability of the candidate being a nodule.
 - `predicted_class` (int): The predicted class (1 if probability \geq threshold, else 0).

- `error_message` (str, optional): Any error message specific to processing this candidate.
 - `scan_resampled_shape_zyx` (List[int], optional): The shape (Z, Y, X) of the resampled scan.
 - `model_threshold_used` (float): The probability threshold used for classification (default 0.5).
- **Details:**
 - Utilizes a `Simple3DCNN` model with weights from `"app/models/NoduleClassification/candidate_detection_model_best.pth"`.
 - The input CT scan undergoes preprocessing: resampling to target spacing (1.0, 1.0, 1.0), lung segmentation, HU normalization (-1000 to 400 HU), and zero-centering (mean 0.25).
 - For each candidate, its world coordinates are converted to voxel coordinates in the resampled scan. A patch (default size from `PATCH_SIZE_CFG`) is extracted around this center and fed to the model for classification.

5. Lung Cancer Prediction

- **Endpoint:** `/cancer-prediction/predict_cancer_level`
- **HTTP Method:** `POST`
- **Description:** Predicts the risk level of lung cancer (Low, Medium, High) based on patient features.
- **Request** (`PatientFeatures`): A JSON object containing the following integer features:
 - `age` (0-120)
 - `gender` (0 or 1)
 - `air_pollution`
 - `alcohol_use`
 - `dust_allergy`
 - `occupational_hazards`
 - `genetic_risk`
 - `chronic_lung_disease`
 - `balanced_diet`
 - `obesity`
 - `smoking`
 - `passive_smoker`
 - `chest_pain`
 - `coughing_of_blood`

- fatigue
- weight_loss
- shortness_of_breath
- wheezing
- swallowing_difficulty
- clubbing_of_finger_nails
- frequent_cold
- dry_cough
- snoring
- **Response** (PredictionResponse):
 - predicted_class (str): The predicted cancer risk level ('Low', 'Medium', or 'High').
- **Details:**
 - The service loads a k-Nearest Neighbors (KNN) model from "app/models/LungCancerPrediction/lcp_model.joblib".
 - The input features are converted into a NumPy array for prediction by the KNN model.

6. Mortality Prediction

- **Endpoint:** /mortality-prediction/predict
- **HTTP Method:** POST
- **Description:** Predicts patient survival status based on a comprehensive set of features.
- **Request** (MortalityInput): A JSON object with the following fields:
 - age (float)
 - gender (int)
 - diagnosis_date (str, e.g., "2023-01-01")
 - cancer_stage (int)
 - beginning_of_treatment_date (str, e.g., "2023-01-15")
 - family_history (int)
 - bmi (float)
 - cholesterol_level (int)
 - hypertension (int)
 - asthma (int)
 - cirrhosis (int)
 - other_cancer (int)
 - end_treatment_date (str, e.g., "2023-06-01")
 - smoke_Current_Smoker (int)

- `smoke_Former_Smoker` (int)
- `smoke_Never_Smoked` (int)
- `smoke_Passive_Smoker` (int)
- `treatment_Chemotherapy` (int)
- `treatment_Combined` (int)
- `treatment_Radiation` (int)
- `treatment_Surgery` (int)
- **Response (JSON Object):**
 - `survived` (str): "Will Survive" or "Won't Survive".
 - `prediction` (int): The raw prediction from the model (e.g., 0 or 1).
 - `prediction_probability_class_0` (float): Probability for class 0.
 - `prediction_probability_class_1` (float): Probability for class 1.
 - `processed_input_features_ordered` (dict): A dictionary of the processed features used by the model, in the correct order.
- **Details:**
 - Loads a survival model from `"app/models/LungCancerMortalityPrediction/survival_model.joblib"`.
 - Input data undergoes preprocessing:
 - Renaming of smoking and treatment keys (e.g., `smoke_Current_Smoker` to `smoke_current_smoker`).
 - Date strings are converted to Unix timestamps.
 - `treatment_duration` is calculated in days from `beginning_of_treatment_date` and `end_treatment_date`.
 - Features are ordered according to `MODEL_FEATURE_ORDER` before being passed to the model.

7. Medical Image Enhancement

- **Endpoint:** `/image-enhancement/adjust_contrast/`
- **HTTP Method:** `POST`
- **Description:** Adjusts the contrast of an uploaded medical image.
- **Request:**
 - `file`: An image file (UploadFile).
 - `contrast_factor` (float, optional): The factor by which to adjust the contrast. Default is 2.0 (1.0 is original, >1.0 increases contrast).
- **Response:**
 - If successful: A `StreamingResponse` containing the enhanced image in PNG format (`media_type="image/png"`).

- If error (e.g., cannot open image): A `ContrastAdjustmentResponse` (JSON) with:
 - `message` (str): Error message.
 - **Details:**
 - Uses PIL (Pillow) `ImageEnhance.Contrast` to modify the image contrast.
 - The enhanced image is returned as a PNG.
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