# Project Documentation: ChemoTrace

Version: 1.0

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## 1. Project Overview

ChemoTrace is a command-line simulation tool written in C++ that models the treatment of Hodgkin's Lymphoma with chemotherapy. Its primary purpose is to serve as an educational and illustrative tool, demonstrating how oncologists make complex decisions based on patient characteristics, treatment response, and toxicities.

The simulation guides a user through the process of creating a patient profile, selecting an appropriate risk-adapted initial therapy, and dynamically adjusting the treatment plan over multiple cycles based on clinical feedback.

## 2. Key Features

* **Detailed Patient Profile:** The simulation begins by creating a comprehensive patient profile, including demographics, disease stage, and key health metrics.
* **BSA-Based Dosing:** Chemotherapy dosages are not fixed; they are calculated based on the patient's Body Surface Area (BSA), which is the standard of care in oncology.
* **Risk-Adapted Therapy:** The initial chemotherapy regimen is chosen based on the patient's risk profile, distinguishing between favorable early-stage and advanced-stage disease.
* **Graded Toxicity System:** The model uses a 0-4 graded system for clinical feedback on toxicities like neutropenia and neuropathy, mirroring the real-world CTCAE standard.
* **Dynamic Dose Adjustments:** The simulation adjusts drug dosages based on specific toxicities. For example, neuropathy can trigger a reduction in the Vinblastine dose.
* **Response-Based Treatment Escalation:** If a patient shows an inadequate response to initial therapy on an interim PET-CT scan, the simulation can automatically escalate the treatment to a more intensive regimen.
* **Cycle Delays:** The program correctly simulates the delay of a treatment cycle in response to severe toxicities like Grade 3+ neutropenia.
* **Cumulative Dose Tracking:** The simulation tracks the cumulative dose of cardiotoxic drugs like Doxorubicin, a critical factor in long-term patient safety.

## 3. Software Architecture & Design

The project is constructed using object-oriented principles with a clear separation of concerns among different classes.

* **main.cpp**: Serves as the main driver of the application. It handles all user interaction (input/output) and manages the main simulation loop.
* **Patient (Patient.h, Patient.cpp)**: A data class that holds all information related to the patient, including their demographics, disease characteristics, and baseline health metrics.
* **ChemotherapyRegimen (ChemotherapyRegimen.h, ChemotherapyRegimen.cpp)**: An abstract base class that defines the interface for any chemotherapy regimen.
  + **Derived Classes (ABVD, BEACOPP)**: Concrete implementations of specific chemotherapy protocols. They contain the logic for their drug compositions, cycle counts, and rules for dose adjustments.
* **TreatmentPlan (TreatmentPlan.h, TreatmentPlan.cpp)**: The core engine of the simulation. It owns the Patient and ChemotherapyRegimen objects and contains the high-level clinical logic for choosing, running, and adjusting the treatment course, including regimen escalation.
* **ClinicalConcepts.h**: A header file containing key data structures used throughout the simulation, such as BodyMetrics for BSA calculations and the ToxicityGrade enum.
* **Constants.h**: A centralized header for all global constants, such as clinical thresholds, toxicity grades for action, and dose caps. This makes the simulation's logic easy to view and modify.

## 4. Core Clinical Concepts Modeled

* **Body Surface Area (BSA) Dosing**: Dosages are calculated using the Du Bois formula, a standard method in oncology. The BSA value can be capped to prevent toxicity in larger patients.
* **Graded Toxicity**: The ToxicityGrade enum allows the simulation to respond with appropriate actions based on severity.
  + A cycle is delayed for Grade 3 or higher neutropenia or thrombocytopenia.
  + A dose reduction is triggered for Grade 2 or higher neuropathy.
* **Treatment Pathways**:
  + The initial regimen is selected based on whether the patient meets the criteria for "favorable early-stage" disease.
  + The interim PET-CT scan after cycle 2 of ABVD is a critical decision point.
    - An excellent response (Deauville score ≤ 2) triggers de-escalation by removing Bleomycin.
    - An inadequate response (Deauville score ≥ 4) triggers escalation to BEACOPP.

## 5. File Structure

All project files should be organized in a single directory.

ChemoTrace/  
├── main.cpp  
├── Constants.h  
├── ClinicalConcepts.h  
├── Patient.h  
├── Patient.cpp  
├── ChemotherapyRegimen.h  
├── ChemotherapyRegimen.cpp  
├── TreatmentPlan.h  
└── TreatmentPlan.cpp

## 6. Setup and Usage

### Prerequisites

A modern C++ compiler that supports the C++17 standard (e.g., g++, Clang, MSVC).

### Compilation

1. Navigate to the project directory (ChemoTrace/) in your terminal.
2. Run the following command to compile all source files into a single executable named chemotrace:  
   Bash  
   g++ main.cpp Patient.cpp ChemotherapyRegimen.cpp TreatmentPlan.cpp -o chemotrace -std=c++17

### Execution

1. After a successful compilation, run the program from the terminal:
   * On Linux or macOS: ./chemotrace
   * On Windows: chemotrace.exe
2. The program will start and prompt you to enter patient data to begin the simulation.

## 7. Example Walkthrough

This example demonstrates the treatment escalation pathway.

1. **Patient Input**: A user enters data for a patient with favorable early-stage Hodgkin's Lymphoma.
2. **Initial Regimen**: The system correctly selects ABVD as the starting regimen.
3. **Cycle 1-2**: The simulation proceeds. After Cycle 2, the user inputs clinical feedback indicating a poor response.
   * **Input**: Neuropathy Grade: 2, Deauville Score: 5.
4. **System Response**: The simulation detects the Grade 2 neuropathy and reduces the Vinblastine dose. More importantly, it detects the inadequate PET response (Deauville > 4) and triggers a treatment escalation.
5. **Regimen Change**: The TreatmentPlan discards the ABVD regimen and creates a new BEACOPP regimen. The cycle count is reset.
6. **Continuation**: The simulation continues with the more intensive BEACOPP regimen until the user chooses to stop or all cycles are complete.
7. **Final Summary**: The program outputs a summary detailing the initial plan, the reason for escalation, and the final status of the patient.