The **NCBI C++ Toolkit**

17: Access to NCBI data

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Overview

The overview for this chapter consists of the following topics:

- Introduction
- Chapter Outline

Introduction

This chapter describes access to the NCBI data using the NCBI C++ Toolkit.

Chapter Outline

- Object Manager: Generic API for retrieving and manipulating biological sequence data
- E-Utils: Access to Entrez Data

Object Manager: Generic API for retrieving and manipulating biological sequence data

The information about Object Manager library is here.

E-Utils: Access to Entrez Data

EUtils requests

The base class for all requests is CEUtils_Request. Derived request classes provide *Get/Set* methods to specify arguments for each request. The returned data can be read in several ways:

- *Read()* - reads the data returned by the server into a string.
- *GetStream()* - allows to read plain data returned by the server.
- *GetObjectIStream()* - returns serial stream for reading data (in most cases it's an XML stream).

Connection context

CEUtils_ConnContext allows transferring EUtils context from one request to another. It includes user-provided information (tool, email) and history data (WebEnv, query_key). If no context is provided for a request (the *ctx* argument is *NULL*), a temporary context will be created while executing the request.

EUtils objects

Most requests return specific data types described in EUtils DTDs. The C++ classes generated from the DTDs can be found in include/objtools/eutils/*<util-name>*.

Sample application

An example of using EUtils API can be found in sample/app/eutils/eutils_sample.cpp.