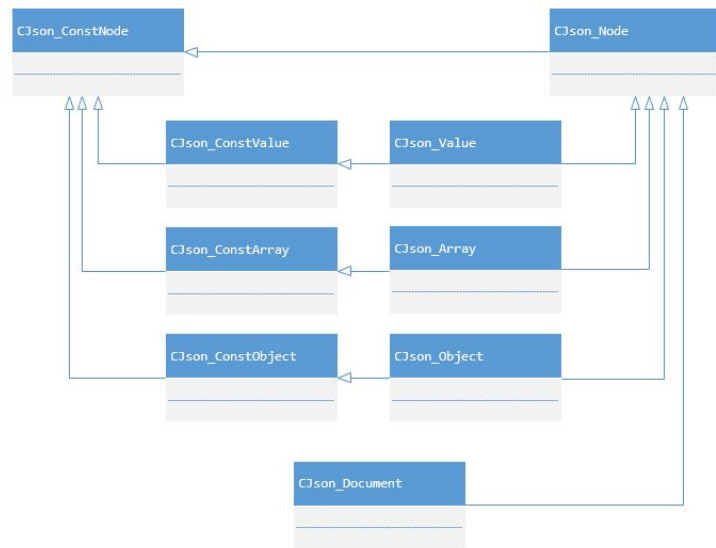


Making an xml/asn.1 to FHIR compliant JSON converter for genomic data

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Motivation

- Existing tools to convert from XML to JSON
 - C++ Toolkit (JSONWRAPP)
 - Eutils
 - Not made for Bioinformaticians
 - Not user-friendly
 - Issues with being FHIR compliant
- Make output FHIR compliant JSON
- Use case examples
 - Find all gene positions for Candida albicans
 - Find all Clean variants and their positions



JsonWrapp library class relationship
diagram.

Source NCBI C++ Toolkit

Motivation

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Table 1

– Entrez Unique Identifiers (UIDs) for selected databases

Entrez Database	UID common name	E-utility Database Name
BioProject	BioProject ID	bioproject
BioSample	BioSample ID	biosample
Biosystems	BSID	biosystems
Books	Book ID	books
Conserved Domains	PSSM-ID	cdd
dbGaP	dbGaP ID	gap
dbVar	dbVar ID	dbvar
Epigenomics	Epigenomics ID	epigenomics
EST	GI number	nucest
Gene	Gene ID	gene

(Entrez Programming Utilities)

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Candida albicans

Pipeline

