Table 1: The descriptions of the tools that could solve entirely the first clinical question.

SCORE	**Tool Name**	**Tool URL**	**Tool Description**	**Input**	**Output**
4	cBio Cancer Genomics Data Server (CGDS) API	http://www.programmableweb.com/api/cbio-cancer-genomics-data-server-cgds	The service provides direct access by applications to genetic and genomic data stored by the Memorial Sloan-Kettering Cancer Center. Applications can retrieve information about cancer studies and their genetic findings, genetic profiles and indicators for specific cancer types and gene structures, and similar highly detailed data. Datasets document more than 5000 tumor samples from 20 research studies. API methods support retrieval of cancer research studies, with detailed filtering by specific topics and findings. Methods also allow retrieval of genetic profiles and case lists reported in cancer research, extended mutation data, protein and antibody information, and clinical data.	genetic data, genomic data, cancer, tumor	cancer, genetic finding, genetic profile, gene structure,mutation data, protein, antibody information, clinical data,Tab-delimited text

4	National Cancer Institute SEER API	http://www.programmableweb.com/api/national-cancer-institute-seer	The Surveillance, Epidemiology and End Results (SEER) Program, a service of the National Cancer Institute, is a cancer statistics resource. Collected data includes information on the incidence, prevalence and survival from specific geographic areas within the U.S., as well as cancer mortality for the entire country. The SEER API is a RESTful service supporting various program datasets and algorithms, and is available to developers who wish to incorporate SEER resources into their own systems. Exposed resources include Collaborative Staging, the Hematopoietic and Lymphoid Neoplasm Database, NAACCR documentation, the Antineoplastic Drugs Database, and incidence site recode variables. The API returns JSON formatted responses, communicates over HTTPS, and requires a free account and API key.	cancer, cancer mortality	antineoplastic drugs, hematopoietic, lymphoid neoplasm, JSON

4	**EUADR - Literature analysis**	http://www.myexperiment.org/workflows/2280.html	The aim of the "Literature Analysis" workflow is to automate the search of publications related to ADRs corresponding to a given drug/adverse event association. To do so, we defined an approach based on the MeSH thesaurus, using the subheadings «chemically induced» and «adverse effects» with the “Pharmacological Action” knowledge.	Toxicology Adverse effects (topic_2840), Drug identifier (data_0993)	Literature and reference (topic_3068)

Table 2: The free text tools that were exported automatically by the framework for the first research question.

Free Text Tools	
158	1. Correlation service 2. Drug Re-Purposing Workflow 3. EUADR – Literature analysis 4. Epidemic Marketplace API

	5. ADR-S 6. MiMI/Metabolomics API 7. Sierra Stanford HIV API 8. GSNAP 9. cBio Cancer Genomics Data Server (CGDS) API 10. tspair 11. iASeq 12. FastA protein similarity search API 13. DGIdb API 14. Predictionet 15. SciBite API 16. From cDNA Microarray Raw Data to Pathways and Published Abstracts 17. VirusSeq 18. National Cancer Institute SEER API 19. SLAP API 20. geneRecommender 21. bioNMF API 22. China Cancer Database API 23. Download pathways for external references list 24. FusionMap 25. Tracknburn FoodData API 26. BSMAP 27. ViralFusionSeq 28. ObTiMA 29. Oncosimulator 30. ChEMBL API 31. National Library of Medicine ChemSpell API 32. SomatiCA 33. Download pathways for external references list (Taverna 2) 34. INOH Pathway Database API

	35. Mirtarbase 36. BIOBASE API 37. National Drug File-Reference Terminology API 38. Drugle API 39. National Cancer Institue caDSR API 40. Get pathways by external reference 41. GBSeq test 42. MethylCoder 43. SSearch protein similarity search API 44. Snm 45. Copa 46. PcProf predict physico-chemical profiles of proteins API 47. DAVID Bioinformatics API 48. HIPAASpace API 49. DIAL 50. Vsn 51. Sizepower 52. Retrieve Pathways and Compound information from KEGG 53. MetMap 54. Perform a search through NCBI eUtils eSearch 55. Kegg pathway diagrams 56. BFAST 57. National Institute on Drug Abuse Drug Screening Tool API 58. Gviz 59. Protein search fetch align tree 60. BioCyc API 61. MuTect 62. Novocraft 63. MiRProf 64. CLCbio Genomics Workbench

	65. GSVA 66. GeneCoDis2 API 67. ACME 68. EBI IntAct 69. JasparDB API 70. SOCS 71. VegaMC 72. VIOLIN API 73. SIMPA96 API 74. BioAID Discover proteins from text plus synonyms 75. H-InvDB API 76. Lexicomp API 77. Charm 78. maSigPro 79. FusionCatcher 80. Workflow for Protein Sequence Analysis 81. EpiGRAPH 82. RAWverna Image Evaluator - Evaluate relative 83. Bcbio-nextgen 84. Spiral Genetics 85. RxNorm Prescribable API 86. CIPF RENATO API 87. metaArray 88. get drugs by pathways 89. Biosemantics ACCCA API 90. coGPS 91. bgafun 92. MassArray 93. Genometa 94. arrayQualityMetrics

	95. biomvRCNS 96. FragGeneScan 97. Cufflinks 98. Aetna CarePass API 99. Translate Nucleotide sequence into Peptide sequence 100. new drug test 101. GeneTalk 102. Genefu 103. ZINBA 104. DeFuse 105. GOR protein secondary structure prediction API 106. Lumi 107. Bis-SNP 108. MiRDeep 109. GenomicTools 110. Get Pathway-Genes and gene description by Entrez gene id 111. DailyMed API 112. Rdiff 113. Dexus 114. ERNE 115. ShortFuse 116. STEPStools API 117. CleaveLand 118. Olego 119. Sherman 120. Kegg DrugID 121. Methpipe 122. RMAP 123. Protein alignment transmembrane 124. COILS predict protein coiled-coil regions API

	125. GeneCruiser API 126. SIM 127. OpenTox API 128. How are you API 129. HIV Drug Research Center API 130. FindPeaks 4.0 (Vancouver Short Read Package) 131. Image Mining with RapidMiner 132. SignalP/SignalP4 API 133. The Cancer Genome Atlas API 134. GenomeGraphs 135. NCBI Conserved Domain Database (CDD) API 136. myHealthAccount API 137. BioAID ProteinDiscovery filterOnHumanUniprot perDoc html 138. Pseudoviewer API 139. RxNorm API 140. Cigna Health API 141. biocGraph 142. Kissnp 143. ncRNA fRNAdb API 144. Biopieces 145. Bismark 146. miRNApath 147. Find pathways in which two genes co-occur (in WikiPathways) 148. Allen Brain Atlas API 149. AIDSinfo API 150. CNANorm 151. maDB 152. CancerMutationAnalysis 153. FastQ Screen 154. BRAT

	155. MetNet API 156. BS Seeker 157. Pillbox API 158. HUMAN Microarray CEL file to candidate pathways

Table 3: The descriptions of the tools that could solve entirely the second clinical question.

SCORE	**Tool Name**	**Tool URL**	**Tool Description**	**Input**	**Output**
3	miRNApath	http://www.bioconductor.org/packages/release/bioc/html/miR	miRNApath: Pathway Enrichment for miRNA Expression Data. This package provides pathway enrichment techniques for miRNA expression data. Specifically, the set of methods handles the many-to-many relationship between miRNAs and the multiple genes they are predicted to target (and thus affect.) It also handles the gene-to-pathway relationships separately. Both steps are designed to preserve the additive effects of miRNAs on genes, many miRNAs affecting one gene, one miRNA affecting multiple genes, or many miRNAs affecting many genes.		

		NApath.html			
2	**mirPath**	http://diana.imis.athena-innovation.gr/DianaTools/index.php?r=mirpath/index	DIANA-miRPath is a miRNA pathway analysis web-server, providing accurate statistics, while being able to accommodate advanced pipelines. miRPath can utilize predicted miRNA targets (in CDS or 3’-UTR regions) provided by the DIANA-microT-CDS algorithm or even experimentally validated miRNA interactions derived from DIANA-TarBase v6.0. These interactions (predicted and/or validated) can be subsequently combined with sophisticated merging and meta-analysis algorithms.miRPath v2.0 can perform advanced analysis pipelines, such as hierarchical clustering of miRNAs and pathways based on the levels of their interactions. Furthermore, users can easily create heat maps of miRNAs vs pathways interactions. Other supported features include the identification of pathological single nucleotide polymorphisms (SNPs) in miRNA binding sites, as well as the “Reverse Search	miRNA IDs (data_2642)	Pathway or network identifier (data_1082)

			module", where the user can identify all the predicted or experimentally validated miRNAs significantly targeting a selected pathway.		
3	mirtarbase	http://mirtarbase.mbc.nctu.edu.tw/	miRTarBase has accumulated more than fifty thousand miRNA-target interactions (MTIs), which are collected by manually surveying pertinent literature after data mining of the text systematically to filter research articles related to functional studies of miRNAs. Generally, the collected MTIs are validated experimentally by reporter assay, western blot, microarray and next-generation sequencing experiments. While containing the largest amount of validated MTIs, the miRTarBase provides the most updated collection by comparing with other similar, previously developed databases.	miRNA IDs (data_2642)	Gene ID (data_2295)

Table 4: The free text tools that were exported automatically by the framework for the second clinical sentence.

Free Text Tools	
231	1. Arabidopsis thaliana Microarray Analysis 2. KEGG pathways common to both QTL and microarray based investigations 3. MinePath 4. HUMAN Microarray CEL file to candidate pathways 5. From cDNA Microarray Raw Data to Pathways and Published Abstracts 6. miRNApath

	7. MitoMiner API 8. PathNet 9. ExpressionView 10. GSVA 11. Pathways and Gene annotations for QTL region 12. Macat 13. Betr 14. GPSeq 15. UnigeneID to KEGG Pathways 16. Dexus 17. adSplit 18. DEGseq 19. antiProfiles 20. NCBI Gi to Kegg Pathway Descriptions 21. Xps 22. BaySeq 23. Gene To Pathways (Vistrails) 24. GlobalAncova 25. maSigPro 26. Drug Re-Purposing Workflow 27. GeneProf API 28. microRNA to KEGG Pathways and Abstracts 29. Abarray 30. Identification of differential genes using the LIMMA Bioconductor package within R 31. Pipeline Pilot 32. Gage 33. Identification of differential genes using t-tests by R 34. Goseq 35. GenomeGraphs 36. MeV

	37. DEDS 38. phenoTest 39. ADR-S 40. Rmagpie 41. Bgmix 42. Allen Brain Atlas API 43. maDB 44. Calculating frequencies of gene expression levels using microarray data in MaxD 45. GENE-Counter 46. ArrayStar 47. Kegg pathway diagrams 48. clusterProfiler 49. ERGO Genome Analysis and Discovery System 50. Ocplus 51. diffGeneAnalysis 52. SeqGSEA 53. Ssize 54. Lymphoma type prediction based on microarray data 55. Mfuzz 56. Myrna 57. metaArray 58. Entrez Gene to KEGG Pathway 59. SNAGEE 60. BBSeq 61. LMGene 62. caArray data retrieving 63. WebScipio API 64. Genefu 65. Lumi 66. Kegg DrugID

	67. MiMI/Metabolomics API 68. BiologicalNetworks API 69. Import and convert gene list 70. Mouse Microarray Analysis 71. Ffpe 72. CancerMutationAnalysis 73. ReactomePA 74. PADOG 75. GeneCoDis2 API 76. Pathview 77. coGPS 78. AffyRNADegradation 79. BioDB Hyperlink Management System API 80. MiRProf 81. geneRecommender 82. Import and convert gene list 83. Find pathways in which two genes co-occur (in WikiPathways) 84. EnrichNet API 85. Retrieve Pathways and Compound information from KEGG 86. BioCyc API 87. Get Pathway-Genes and gene description by Entrez gene id 88. FusionHunter 89. Copa 90. mirPath 91. CIPF RENATO API 92. MmPalateMiRNA 93. DeconRNASeq 94. H-InvDB API 95. DSGseq 96. cBio Cancer Genomics Data Server (CGDS) API

	97. GeneCruiser API 98. Biosemantics ACCCA API 99. DESeq 100. metabolic pathway.xml 101. SplicingGraphs 102. MMSEQ 103. EdgeR 104. Annmap 105. ALTER Reflective API 106. Match concept profiles with predefined set 107. ABBA 108. Genefilter 109. Mgsa 110. NOISeq 111. SeqSite 112. Puma 113. DGIdb API 114. Limma 115. GMOD API 116. goTools 117. piano 118. EDASeq 119. FragGeneScan 120. DAVID Bioinformatics API 121. Perform a search through NCBI eUtils eSearch 122. National Institute on Drug Abuse Drug Screening Tool API 123. Correlation service 124. G-Mo.R-Seq 125. test workbench demo '14 126. Get Gene Ids for Human

	127. Gowinda 128. VegaMC 129. Associated Region to Gene List 130. SIMPA96 API 131. Liliopsida Protein Alignment 132. FusionCatcher 133. tRNAscan 134. SomatiCA 135. gene ontology diagram.xml 136. oneChannelGUI 137. AgiMicroRna 138. DeFuse 139. ALEXA-Seq 140. topGO 141. ASC 142. SiLoCo 143. MiRanalyzer 144. gene subset extract 145. Mapping OligoNucleotides to an assembly 146. Gene to Pubmed 147. Epigenome 148. bioNMF API 149. tspair 150. TopHat-Fusion 151. Kegg API 152. JasparDB API 153. MiRCat 154. Oncosimulator 155. Pathway Commons API 156. pathRender

	157. How are you API 158. sigPathway 159. FastQ Screen 160. Promedas API 161. SLAP API 162. Ingenuity Variant Analysis 163. Retrieve a protein from the GPCRDB 164. Download pathways for external references list 165. get elements by pathway 166. Extract unique proteins from blast results 167. BSMAP 168. MapDamage 169. BIOBASE API 170. Drugle API 171. RmiR 172. VisANT API 173. Mapping microarray data onto metabolic pathways 174. Workflow for Protein Sequence Analysis 175. MiRDeep 176. GraphPAC 177. SSearch protein similarity search API 178. Breakpointer 179. E-miR 180. RxNorm Prescribable API 181. PALMA 182. FusionSeq 183. ObTiMA 184. PcProf predict physico-chemical profiles of proteins API 185. myHealthAccount API 186. ZINBA

	187. AIDSinfo API 188. MirTools 189. STEPStools API 190. get drugs by pathways 191. ZORRO 192. SeqBuster 193. DIAL 194. Predictionet 195. maCorrPlot 196. ChimeraScan 197. Write pathway to disk 198. Chipster 199. Triplex 200. Batman 201. Methpipe 202. Bgafun 203. Get pathways by external reference 204. INOH Pathway Database API 205. Retrieve Protein Sequence 206. Bililite API 207. GenomicTools 208. Les 209. segmentSeq 210. cPath API 211. iPAC 212. HIPAASpace API 213. Mirtarbase 214. NPS 215. Simplify a BLAST text file 216. LVSmiRNA

	217. Pillbox API 218. lifeIMAGE API 219. MANOR 220. NucleR 221. Download pathways for external references list (Taverna 2) 222. Qseq 223. Fetch PDB flatfile from RCSB server 224. SequenceVariantAnalyzer 225. mBPCR 226. test30 227. MetNet API 228. EBI CENSOR 229. methyAnalysis 230. ChEMBL API 231. ExiMiR

Table 5: The specific semantic categories of named entities

Abbreviation	**URI**	**Semantic Category**
aggp	http://linkedlifedata.com/resource/umls-semnetwork/T100	AGE
amas	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
bacs	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE

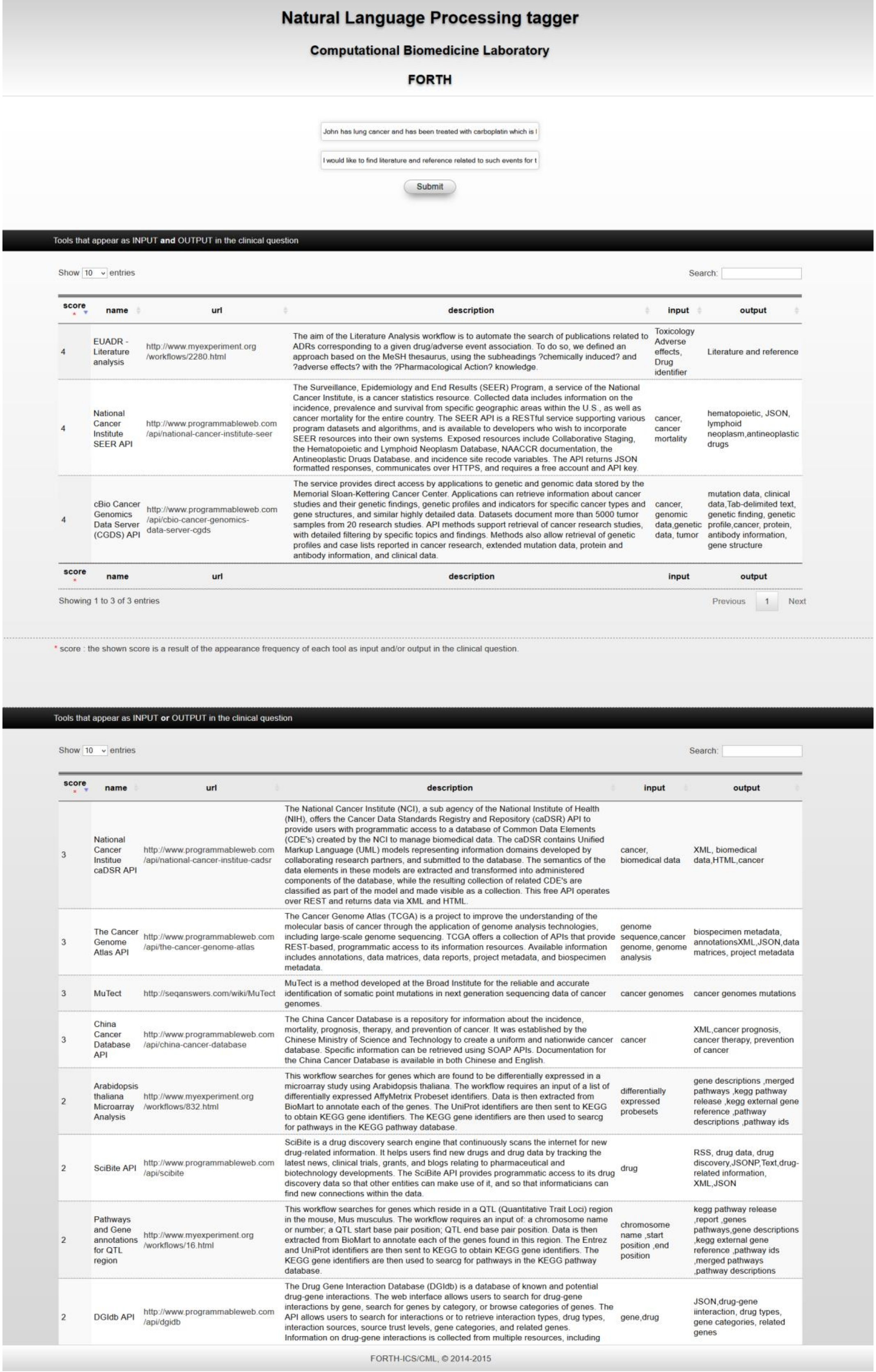
bact	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
biof	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
enzy	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
genf	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
mbrt	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
moft	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
mosq	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
bmod	http://linkedlifedata.com/resource/umls-semnetwork/T091	BIOMEDICAL
bodm	http://linkedlifedata.com/resource/umls-semnetwork/T091	BIOMEDICAL
anab	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART
anst	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART
bdsu	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART
bdsy	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART
blor	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART
bpoc	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART

bsoj	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART
ortf	http://linkedlifedata.com/resource/calbc-group/ANAT	BODY_PART
celc	http://linkedlifedata.com/resource/umls-semnetwork/T025	CELL
celf	http://linkedlifedata.com/resource/umls-semnetwork/T025	CELL
cell	http://linkedlifedata.com/resource/umls-semnetwork/T025	CELL
comd	http://linkedlifedata.com/resource/umls-semnetwork/T025	CELL
clna	http://linkedlifedata.com/resource/umls-semnetwork/T201	CLINICAL_ATTRIBUTE
medd	http://linkedlifedata.com/resource/umls-semnetwork/T074	DEVICE
diap	http://linkedlifedata.com/resource/umls-semnetwork/T060	DIAGNOSIS
dsyn	http://linkedlifedata.com/resource/umls-semnetwork/T047	DISEASE
clnd	http://linkedlifedata.com/resource/umls-semnetwork/T200	DRUG
antb	http://linkedlifedata.com/resource/umls-semnetwork/T200	DRUG
food	http://linkedlifedata.com/resource/umls-semnetwork/T168	FOOD
gngm	http://linkedlifedata.com/resource/umls-semnetwork/T028	GENE
inpo	http://linkedlifedata.com/resource/umls-semnetwork/T037	INJURY_or_POISONING

lbpr	http://linkedlifedata.com/resource/umls-semnetwork/T034	LABORATORY
lbtr	http://linkedlifedata.com/resource/umls-semnetwork/T034	LABORATORY
podg	http://linkedlifedata.com/resource/umls-semnetwork/T101	PATIENT
nnon	http://linkedlifedata.com/resource/calbc-group/CHEM	DRUG
nusq	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
aapp	http://linkedlifedata.com/resource/calbc-group/CHEM	DRUG
carb	http://linkedlifedata.com/resource/calbc-group/CHEM	DRUG
crbs	http://linkedlifedata.com/resource/calbc-group/GENE	MOLECULAR_SEQUENCE
sosy	http://linkedlifedata.com/resource/umls-semnetwork/T184	SYMPTOM
virs	http://linkedlifedata.com/resource/umls-semnetwork/T005	VIRUS
vita	http://linkedlifedata.com/resource/umls-semnetwork/T127	VITAMIN
neop	http://linkedlifedata.com/resource/umls-semnetwork/T047	DISEASE
nsba	http://linkedlifedata.com/resource/calbc-group/CHEM	DRUG
orch	http://linkedlifedata.com/resource/calbc-group/CHEM	DRUG
orga	http://linkedlifedata.com/resource/calbc-group/CHEM	DRUG

orgf	http://linkedlifedata.com/resource/calbc-group/PHYS	ORGANISM_FUNCTION
patf	http://linkedlifedata.com/resource/calbc-group/DISO	ORGANISM_FUNCTION
phsf	http://linkedlifedata.com/resource/calbc-group/PHYS	ORGANISM_FUNCTION
phsu	http://linkedlifedata.com/resource/umls-semnetwork/T200	DRUG
tisu	http://linkedlifedata.com/resource/umls-semnetwork/T024	DRUG
tmco	http://linkedlifedata.com/resource/umls-semnetwork/T079	TEMPORAL_CONCEPT
topp	http://linkedlifedata.com/resource/umls-semnetwork/T061	MEDICAL_PROCEDURE
antb	http://linkedlifedata.com/resource/umls-semnetwork/T200	DRUG
diap	http://linkedlifedata.com/resource/umls-semnetwork/T061	MEDICAL_PROCEDURE
fndg	http://linkedlifedata.com/resource/umls-semnetwork/T033	FINDING
EDAM_data	http://edamontology.org/data	EDAM_DATA
EDAM_format	http://edamontology.org/format	EDAM_DATA
EDAM_operation	http://edamontology.org/operation	EDAM_OPERATION
EDAM_topic	http://edamontology.org/topic	EDAM_TOPIC
EDAM_identifier	http://edamontology.org/identifier	EDAM_ID

Figure 1: The results of the NLP framework for the first clinical question as shown in the web application



Natural Language Processing tagger

Computational Biomedicine Laboratory

FORTH

John has lung cancer and has been treated with carboplatin which is l

I would like to find literature and reference related to such events for t

Tools that appear as INPUT **and** OUTPUT in the clinical question

score	name	url	description	input	output
4	EUADR - Literature analysis	http://www.myexperiment.org/workflows/2280.html	The aim of the Literature Analysis workflow is to automate the search of publications related to ADRs corresponding to a given drug/adverse event association. To do so, we defined an approach based on the MeSH thesaurus, using the subheadings ?chemically induced? and ?adverse effects? with the ?Pharmacological Action? knowledge.	Toxicology Adverse effects, Drug identifier	Literature and reference
4	National Cancer Institute SEER API	http://www.programmableweb.com/api/national-cancer-institute-seer	The Surveillance, Epidemiology and End Results (SEER) Program, a service of the National Cancer Institute, is a cancer statistics resource. Collected data includes information on the incidence, prevalence and survival from specific geographic areas within the U.S., as well as cancer mortality for the entire country. The SEER API is a RESTful service supporting various program datasets and algorithms, and is available to developers who wish to incorporate SEER resources into their own systems. Exposed resources include Collaborative Staging, the Hematopoietic and Lymphoid Neoplasm Database, NAACCR documentation, the Antineoplastic Drugs Database, and incidence site recode variables. The API returns JSON formatted responses, communicates over HTTPS, and requires a free account and API key.	cancer, cancer mortality	hematopoietic, JSON, lymphoid neoplasm,antineoplastic drugs
4	cBio Cancer Genomics Data Server (CGDS) API	http://www.programmableweb.com/api/cbio-cancer-genomics-data-server-cgds	The service provides direct access by applications to genetic and genomic data stored by the Memorial Sloan-Kettering Cancer Center. Applications can retrieve information about cancer studies and their genetic findings, genetic profiles and indicators for specific cancer types and gene structures, and similar highly detailed data. Datasets document more than 5000 tumor samples from 20 research studies. API methods support retrieval of cancer research studies, with detailed filtering by specific topics and findings. Methods also allow retrieval of genetic profiles and case lists reported in cancer research, extended mutation data, protein and antibody information, and clinical data.	cancer, genomic data,genetic data, tumor	mutation data, clinical data,Tab-delimited text, genetic finding, genetic profile,cancer, protein, antibody information, gene structure
score *	name	url	description	input	output

Showing 1 to 3 of 3 entries

* score : the shown score is a result of the appearance frequency of each tool as input and/or output in the clinical question.

Tools that appear as INPUT **or** OUTPUT in the clinical question

score	name	url	description	input	output
3	National Cancer Institue caDSR API	http://www.programmableweb.com/api/national-cancer-institue-cadsr	The National Cancer Institute (NCI), a sub agency of the National Institute of Health (NIH), offers the Cancer Data Standards Registry and Repository (caDSR) API to provide users with programmatic access to a database of Common Data Elements (CDE's) created by the NCI to manage biomedical data. The caDSR contains Unified Markup Language (UML) models representing information domains developed by collaborating research partners, and submitted to the database. The semantics of the data elements in these models are extracted and transformed into administered components of the database, while the resulting collection of related CDE's are classified as part of the model and made visible as a collection. This free API operates over REST and returns data via XML and HTML.	cancer, biomedical data	XML, biomedical data,HTML,cancer
3	The Cancer Genome Atlas API	http://www.programmableweb.com/api/the-cancer-genome-atlas	The Cancer Genome Atlas (TCGA) is a project to improve the understanding of the molecular basis of cancer through the application of genome analysis technologies, including large-scale genome sequencing. TCGA offers a collection of APIs that provide REST-based, programmatic access to its information resources. Available information includes annotations, data matrices, data reports, project metadata, and biospecimen metadata.	genome sequence,cancer genome, genome analysis	biospecimen metadata, annotationsXML,JSON,data matrices, project metadata
3	MuTect	http://seqanswers.com/wiki/MuTect	MuTect is a method developed at the Broad Institute for the reliable and accurate identification of somatic point mutations in next generation sequencing data of cancer genomes.	cancer genomes	cancer genomes mutations
3	China Cancer Database API	http://www.programmableweb.com/api/china-cancer-database	The China Cancer Database is a repository for information about the incidence, mortality, prognosis, therapy, and prevention of cancer. It was established by the Chinese Ministry of Science and Technology to create a uniform and nationwide cancer database. Specific information can be retrieved using SOAP APIs. Documentation for the China Cancer Database is available in both Chinese and English.	cancer	XML,cancer prognosis, cancer therapy, prevention of cancer
2	Arabidopsis thaliana Microarray Analysis	http://www.myexperiment.org/workflows/832.html	This workflow searches for genes which are found to be differentially expressed in a microarray study using Arabidopsis thaliana. The workflow requires an input of a list of differentially expressed AffyMetrix Probeset identifiers. Data is then extracted from BioMart to annotate each of the genes. The UniProt identifiers are then sent to KEGG to obtain KEGG gene identifiers. The KEGG gene identifiers are then used to searcg for pathways in the KEGG pathway database.	differentially expressed probesets	gene descriptions ,merged pathways ,kegg pathway release ,kegg external gene reference ,pathway descriptions ,pathway ids
2	SciBite API	http://www.programmableweb.com/api/scibite	SciBite is a drug discovery search engine that continuously scans the internet for new drug-related information. It helps users find new drugs and drug data by tracking the latest news, clinical trials, grants, and blogs relating to pharmaceutical and biotechnology developments. The SciBite API provides programmatic access to its drug discovery data so that other entities can make use of it, and so that informaticians can find new connections within the data.	drug	RSS, drug data, drug discovery,JSONP,Text,drug-related information, XML,JSON
2	Pathways and Gene annotations for QTL region	http://www.myexperiment.org/workflows/16.html	This workflow searches for genes which reside in a QTL (Quantitative Trait Loci) region in the mouse, Mus musculus. The workflow requires an input of: a chromosome name or number; a QTL start base pair position; QTL end base pair position. Data is then extracted from BioMart to annotate each of the genes found in this region. The Entrez and UniProt identifiers are then sent to KEGG to obtain KEGG gene identifiers. The KEGG gene identifiers are then used to searcg for pathways in the KEGG pathway database.	chromosome name ,start position ,end position	kegg pathway release ,report ,genes pathways,gene descriptions ,kegg external gene reference ,pathway ids ,merged pathways ,pathway descriptions
2	DGIdb API	http://www.programmableweb.com/api/dgidb	The Drug Gene Interaction Database (DGIdb) is a database of known and potential drug-gene interactions. The web interface allows users to search for drug-gene interactions by gene, search for genes by category, or browse categories of genes. The API allows users to search for interactions or to retrieve interaction types, drug types, interaction sources, source trust levels, gene categories, and related genes. Information on drug-gene interactions is collected from multiple resources, including	gene,drug	JSON,drug-gene iinteraction, drug types, gene categories, related genes

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