Learning to Answer Biomedical Factoid & List Questions: OAQA at BioASQ 3B

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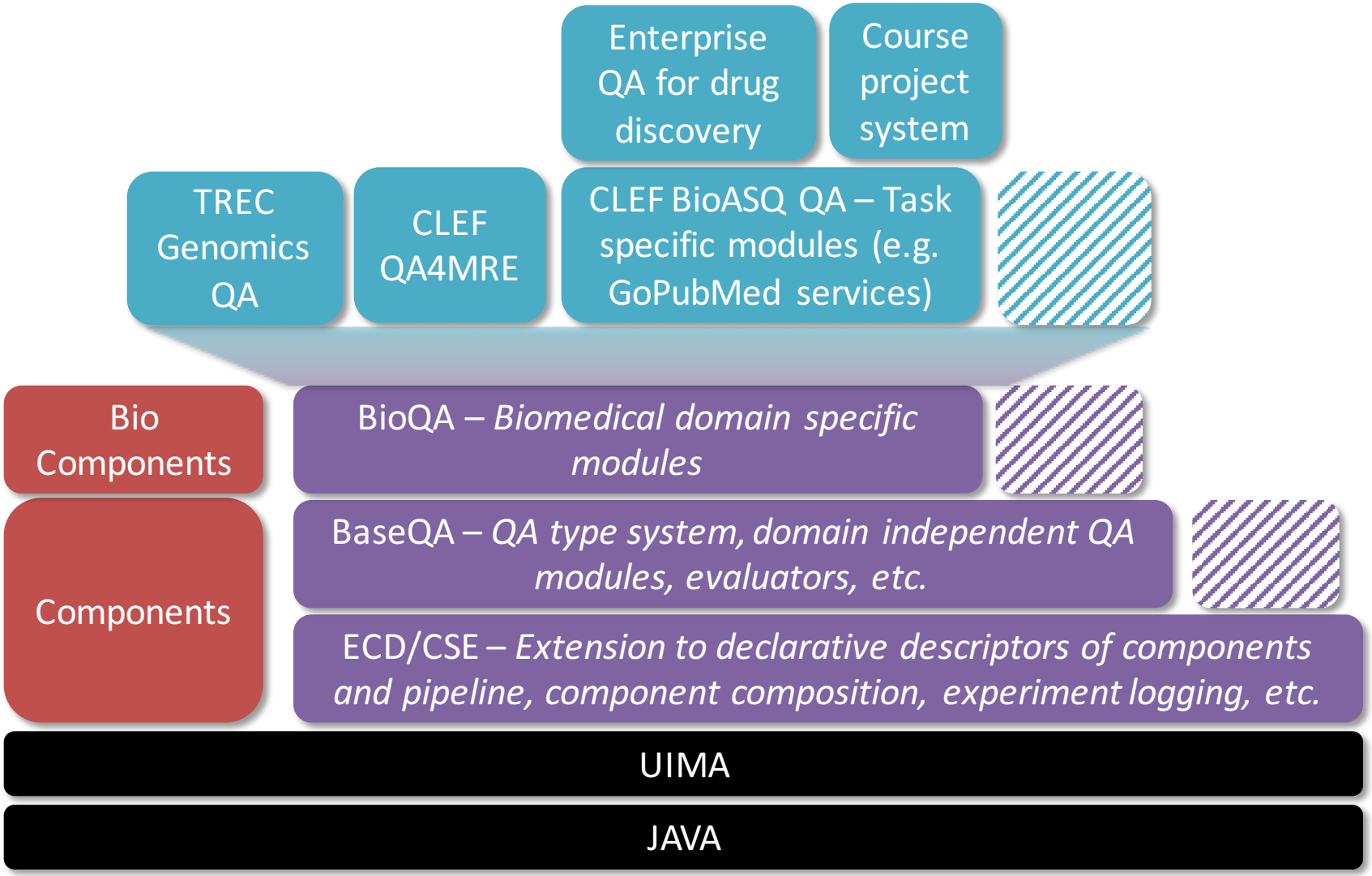
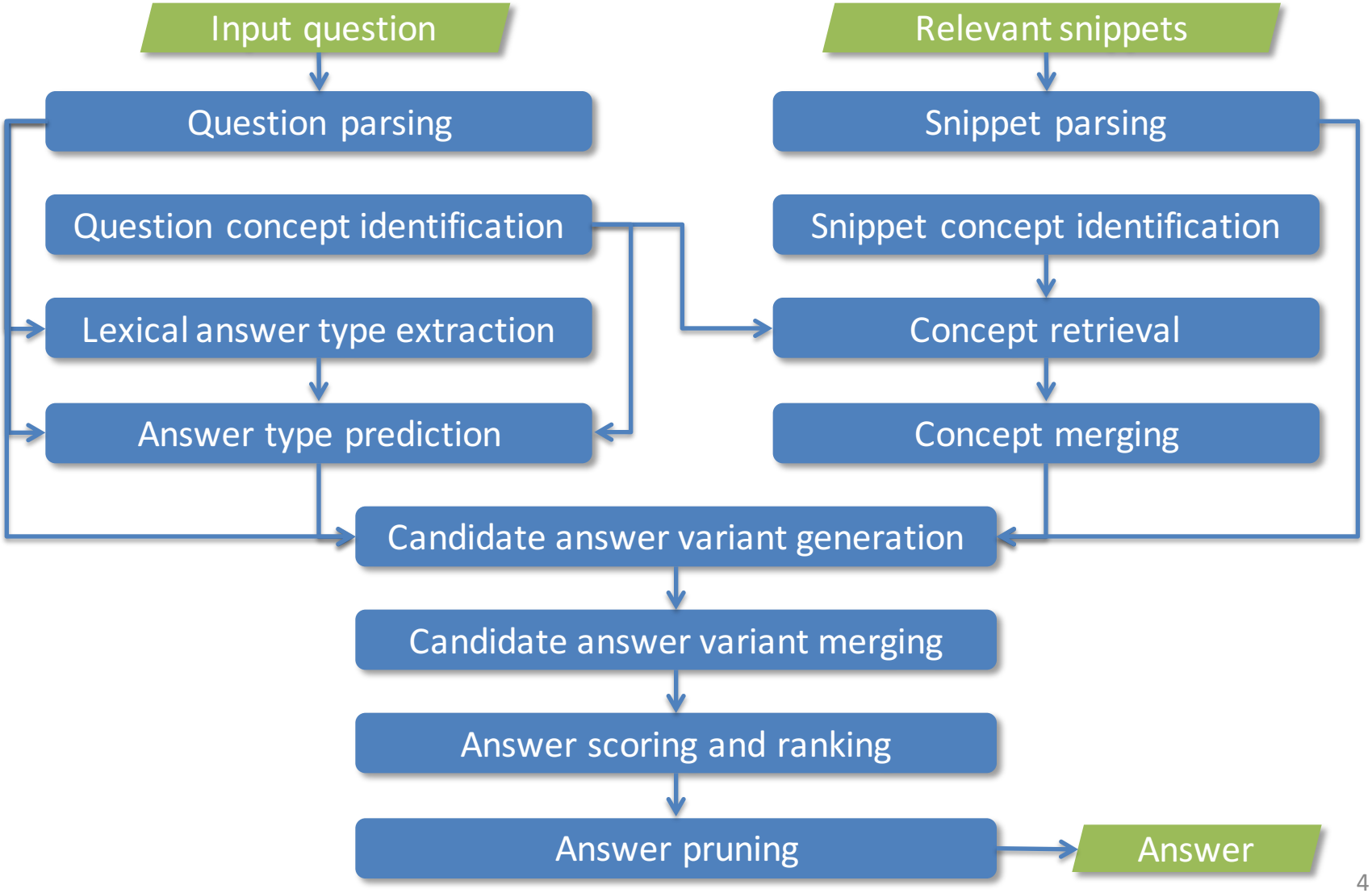
Overview

- Past history
  - First-time BioASQ participation
  - Built system for TREC Genomics QA & CLEF QA4MRE
- Hypothesis and preparation
  - Learning from past dryrun/1B/2B development set
  - Careful design of a flexible and extensible architecture, coupled with continuous, incremental experimentation and optimization over various combinations of existing state-of-the-art components
  - April 2 to Jun 10 (targeting for batches 3-5), 717 experiments have been recorded by the experiment database
    - Testing: 422, training: 167, caching: 80

Architecture



Factoid & List Question Answering for Phase B



Question and Answer Type Prediction

- Answer type definition
  - UMLS semantic types + QUANTITY + CHOICE
- "GS" answer type extraction
  - UTS maps GS answers to "GS" types
  - No types found for 82 out of 406 questions
- Learning
  - Lemma, begins with "do" or "be", contains "or", contains digits, semantic type (using MetaMap), dependency label
  - Multi-class classification via Logistic regression (10-fold cross prediction)

Candidate Answer Generation

- Concepts
  - MetaMap annotated, LingPipe NER identified, OpenNLP chunker annotated NP and NP-PP-NP
- QUANTITY
  - POS tag of CD as the key token
  - Expansion: 3.0 -> 3.0 mm
- CHOICE
  - Head token of the “or” token as the first option
  - All children of the first option that have a dep-label of conj as alternative options.
  - Expansion
- ~~CRF-based answer phrase~~

Candidate Answer Scoring

- Extend the approach used by Weissenborn et al. to 11 groups of features
  - Type coercion
  - CAO (candidate answer occurrence) count
  - Name count
  - Avg. covered token count
  - Stopword count
  - Token/concept overlap count
  - Token/concept proximity
  - LAT count
  - Parse proximity
- Use Logistic regression to learn the scoring function

Answer Pruning (for List Questions)

- Batch 4: an absolute threshold
- Batch 5: a relative threshold
- ~~Collective reranking of candidates~~

Results (Phase B) - *Tentative*

- Exact answers

Batch	Factoid			List		
	Strict Accuracy	Lenient Accuracy	MRR	Precision	Recall	F-measure
3	.1154 (1)	.2308 (1)	.1615 (1)	.0539 (8)	.6933 (1)	.0969 (7)
4	.4483 (1)	.6207 (1)	.5155 (1)	.3836 (1)	.3480 (1)	.3168 (1)
5	.2273 (1)	.3182 (1)	.2727 (1)	.1704 (1)	.2573 (5)	.1875 (1)

Error Analysis (Phase B)

- Concept type identification/answer type prediction (25)
- Concept identification (10)
  - *Neurostimulation of which nucleus is used for treatment of dystonia?*
    - Bilateral globus pallidus internus (Gpi)
- Complex answer (9)
  - "Effect", "role", "function", etc.
  - *What is the function of capspases?*
    - Executors/mediators of apoptosis
- Mistakenly use question phrase as answer (7)
  - What is the effect of enamel matrix derivative on pulp regeneration?
    - ~~EMD~~

Error Analysis (Phase B, cont'd)

- Tokenization (6)
  - t(11;22)(q24:q12)
- Definition question (3)
  - *What is Piebaldism?*
  - *How are ultraconserved elements called when they form clusters?*
- Question type (2)
  - *Alpha-spectrin and beta-spectrin subunits form parallel or antiparallel heterodimers?*
  - *What is the risk of developing acute myelogenous leukemia in Fanconi?*
- Snippets that have no information (2)
  - What is the main role of Ctf4 in dna replication?
    - ~~Ctf4 remains a central player in DNA replication~~

Conclusion

- We present a three-layered architecture and the describe the components.
- The official evaluation results show the effectiveness of the proposed approach in factoid and list QA.
- We have been adopting BioASQ task and the benchmark in a number of CMU courses since 2014
  - 11-791 Design & Engineering of Intelligent Information Systems (final project): 30–70 students / year
  - 11-796/7 Question Answering (an option*)
  - 11-632 Data Science Analytics Capstone (an option*)

    * Other options include Entrance Exam World History task.

Conclusion (cont'd)

- Collaboration with Roche Pharmaceuticals
  - Funding for open source software development in biomedical question answering via Apache license
  - Internal use / development based on the open source release, but adapted to specific scenarios / proprietary resources
- In the stage of code refactoring for the purposes of
  - Open source release as the agreement requires
  - 2015 fall students in 11-791 for their final project

Thank you!

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Retrieval Approaches (Phase A)

- Document retrieval
  - Lucene index (10K documents)
  - Negative Query Generation model (100 documents)
  - LETOR with random forest (10 documents)
- Snippet retrieval
  - Sentences as candidate snippets
  - Lucene, logistic regression for reranking
- Concept retrieval
  - MetaMap, LingPipe (GeneTag)
  - GoPubMed service
- Triple retrieval
  - Append [obj] and [sub] to each keyword
  - Enumerate all letter case possibilities
  - GoPubMed service

Results (Phase A)

- Document retrieval

Batch	Precision	Recall	F-measure	MAP	GMAP
3	.2310 (15)	.3242 (15)	.2311 (15)	.1654 (15)	.0136 (15)
4	.2144 (15)	.3320 (15)	.2263 (15)	.1524 (15)	.0081 (14)
5	.2130 (15)	.4474 (15)	.2605 (15)	.1569 (15)	.0267 (8)

- Snippet retrieval

Batch	Precision	Recall	F-measure	MAP	GMAP
3	.1133 (3)	.1044 (5)	.0891 (3)	.0892 (1)	.0013 (5)
4	.1418 (5)	.1264 (10)	.1153 (8)	.0957 (5)	.0027 (6)
5	.1472 (9)	.1756 (9)	.1391 (9)	.1027 (9)	.0040 (5)