# Application of IBM Watson in the Medical Field

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# What is Watson?

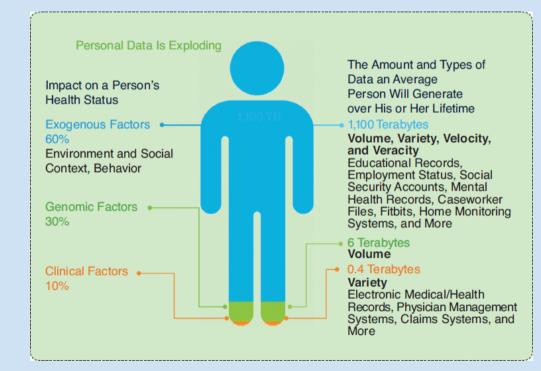


- Question Answering (QA) computing system
- Open domain datasets
  - Wikipedia
  - Twitter
  - Online Research Datasets

- The Problem
- Data in published medical research
- How Watson works
- Case Study
- Conclusions

# **The Problem**

- Drug Discovery [1]
  - Massive Investment
  - 80% fail to gain approval of FDA.
- Pressure on Researchers
- A lot more data
  - Limitation: Scalability

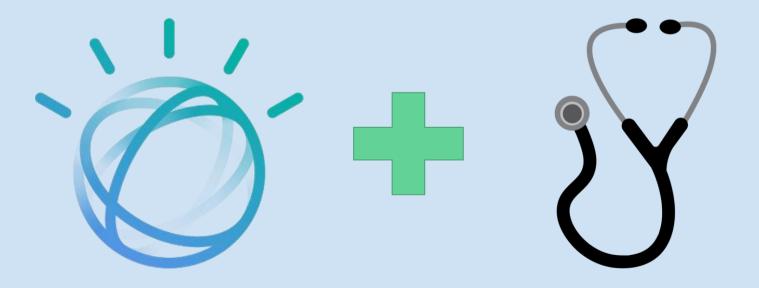


# Limitation: Scalability

- MEDLINE Corpus
  - U.S National Library of Medicine
  - 28 million+ abstracts
  - 5000+ journals
  - **1.8** million abstracts published annually
- Average Researcher
  - 250-300 articles in a given year
    - Time factors limit this

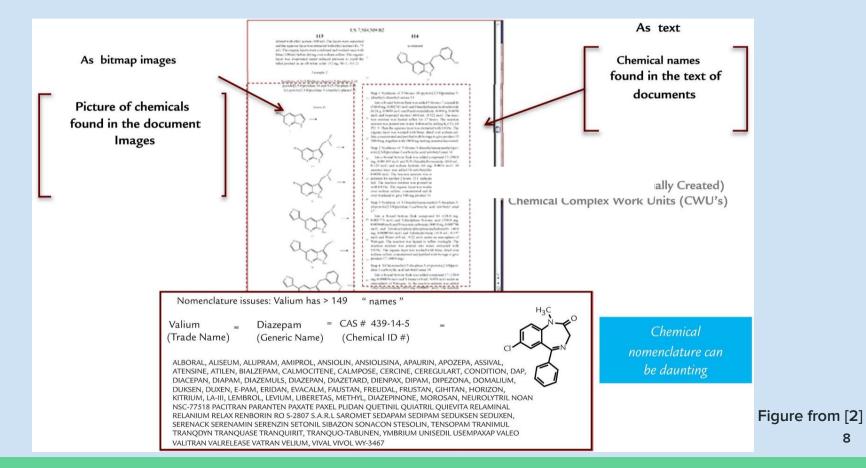
# The Need: Solution!!

#### Let Watson do (most of) the Work



- The Problem 🗸
- Data in published medical research
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#### **Understanding Data: Chemical Nomenclature**



## Understanding Data: MeSH

- Medical Subject Headings
- Manually curated series of vocabulary terms
  - National Library of Medicine

#### • Assigned to articles and books

- Index citations
- Facilitate Search health information

MeSH heading and definition: The definition describes how the term is used for indexing.

Year introduced: The term is searchable back to the earliest date shown.

Subheadings: Lists subheadings that have been used with this heading. Select subheadings for searching using the checkboxes.

#### Ventilation-Perfusion Ratio

The ratio of alveolar ventilation to simultaneous alveolar capillary blood flow in any part of the lung. (Stedman, 25th ed Year introduced: 1970(1968)

PubMed search builder options

Subheadings:

drug effects
 etiology
 immunology

Restrict to MeSH Major Topic.

instrumentation
 methods
 physiology

radiation effects
 veterinary

9

- The Need 🗸
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#### How Watson works

#### How Watson Humans reason

- Observation
  - reading, listening, watching and other sensory inputs.

• <u>Pre-existing</u> <u>knowledge</u>

#### How Watson Humans reason

#### • Observation

• reading, listening, watching and other sensory inputs.

• <u>Pre-existing</u> <u>knowledge</u>

#### How Watson Humans reason

- Observation
  - reading, listening, watching and other sensory inputs.

• <u>Pre-existing</u> <u>knowledge</u>

#### **Foundational Knowledge**

- \*Establish a unique corpus
  - Dictionaries of domain-specific knowledge
- Key Concepts in the medical field
  - Genes
  - Drugs
  - Diseases
  - Symptoms
  - Chemicals

• Entity Types and Entity

#### Examples

- List of proteins associated with each gene.
- Approval status of drugs.
- Synonyms

- The Need  $\checkmark$
- Data in published medical research  $\checkmark$
- How Watson works
  - Foundational Knowledge
  - Named Entity Recognition
  - Named Entity Resolution
  - Semantic Relationship Extraction
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## **Named Entity Recognition**

- 1,3,7-trimethyl-purine-2,6-dione
- CHEMBL113
- "Caffeine is the world's most widely consumed psychoactive drug.....the oral administration of

CHEMBL113 was observed to. . . "

#### Dictionaries

- $\circ \quad \text{compound names} \quad$
- o synonyms
- Rule-based approach



#### **Rule based-approach**

#### Context Rules

- Prevent subterms to be extracted
  - "Carbon" in context of "Carbon Dioxide"
- Acronyms
  - Numerous
  - Lack of consistency
  - Temporary definition

- The Need  $\checkmark$
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## **Named entity Resolution**

- General Normalization
  - Case normalization
    - Carbon, carbon, CARBON → carbon
  - Accent normalization
    - é → e
- Canonical form
- Normalization based on entity types
  - Chemicals, Compounds, Genes

#### **Gene Normalization**

- "We show that PINK1 and Parkin promote Drp1dependent mitochondrial fission by mechanism that are least in part independent"
- Context terms
- MeSH terms
- Frequency of normalization

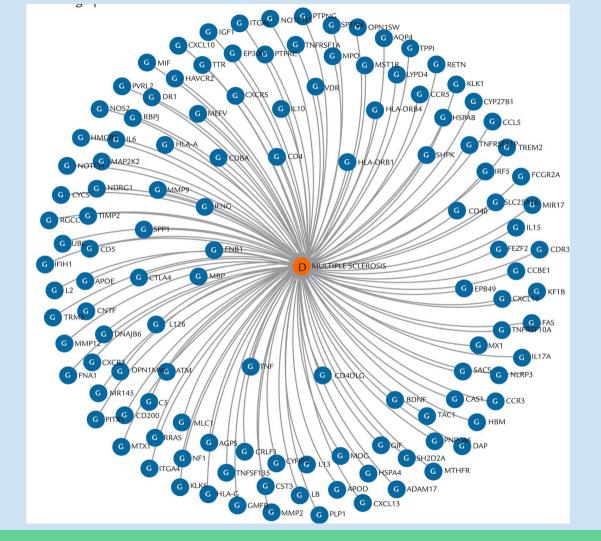
| Candidate gene canonical name        | DNM1L    | DAPK2    | DENR     | CRMP1    | UTRN     |
|--------------------------------------|----------|----------|----------|----------|----------|
| PINK1                                | 0.192771 | 0.036145 | 0        | 0        | 0        |
| Parkin                               | 0.037671 | 0        | 0        | 0        | 0        |
| promote                              | 0.000680 | 0        | 0.00068  | 0.001134 | 0        |
| Drp1-dependent                       | 0.222222 | 0        | 0        | 0        | 0        |
| mitochondrial                        | 0.017527 | 0.008238 | 0.002665 | 0.000162 | 0        |
| fission                              | 0.089744 | 0.028340 | 0.016869 | 0        | 0        |
| Animals                              | 0.000432 | 0.000235 | 0.000135 | 0.000435 | 0.000466 |
| COS cells                            | 0.002001 | 0.000858 | 0.000250 | 0.000465 | 0.000071 |
| Cercopithecus aethiops               | 0.002371 | 0.000677 | 0.000452 | 0.000339 | 0.000113 |
| Dynamins/metabolism                  | 0.106719 | 0.079051 | 0.015810 | 0        | 0        |
| Humans                               | 0.000222 | 0.000249 | 0.000174 | 0.000297 | 0.000202 |
| Mitochondria/metabolism              | 0.015716 | 0.004208 | 0.001460 | 0        | 0        |
| Mitochondrial Degradation            | 0        | 0.020202 | 0        | 0        | 0        |
| Mitochondrial Dynamics               | 0        | 0.017341 | 0.005780 | 0        | 0        |
| Mitochondrial Proteins/metabolism    | 0.027596 | 0.002581 | 0.003971 | 0        | 0        |
| Mutation/genetics                    | 0.000771 | 0.000514 | 0.000043 | 0        | 0.000043 |
| Parkinson Disease/genetics           | 0.010508 | 0        | 0.000876 | 0        | 0        |
| Phosphorylation                      | 0.000298 | 0.000613 | 0.000033 | 0.001043 | 0.000215 |
| Protein Binding                      | 0.000386 | 0.000303 | 0.000052 | 0.000564 | 0.000230 |
| Protein Kinases/metabolism           | 0.000942 | 0        | 0        | 0        | 0        |
| Signal Transduction                  | 0.000127 | 0.000174 | 0.000032 | 0.000681 | 0.000317 |
| Ubiquitin-Protein Ligases/metabolism | 0.001651 | 0.000381 | 0        | 0        | 0        |
| TOTAL                                | 0.730355 | 0.200110 | 0.049282 | 0.005120 | 0.001662 |

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## **Semantic Relationship Extraction**

#### Relationship

- Two distinct entities
  - Agent
  - Target
- Domain-relevant verb or Trigger word
- Example
  - "The results show that ERK2 phosphorylated p53".
- Normalization
  - • "phosphorylated" → "phosphorylate"
  - "bring" or "overlap" → "association"



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## **Case Study**

- Artificial intelligence in neurodegenerative disease research:use of IBM Watson to identify additional RNA-binding proteins altered in amyotrophic lateral sclerosis
  - 2017 study
  - Identifying proteins altered in ALS
- What is ALS?
  - Disease
    - loss of muscle control
  - No effective treatment
  - Linked to RNA binding proteins(RBPs) in patients

## Background

#### • RBPs

- 1542 RBPs-encoding genes in human genome
- 11 genes have shown mutations related to ALS
- 6 other RBPs with alterations related to ALS
  - Gene hasn't been linked to a mutation
- Less than 1% of RBPs have yet to be linked to ALS
- Hypothesis:
  - Additional RBPs contribute to ALS
- Predict potential candidates
- Limitation
  - Only **1,478 RBPs** were mentioned at least once in published abstracts

## Validating Watson

- Leave-one-out cross validation (LOOCV)
  - Applied an algorithm 11 times
  - A different RBP from known gene mutation is moved into the candidate set alongside the other 1,478 RBPs
- 90% of the known proteins ranked are in top 7 %

|   | Protein  | Rank |
|---|----------|------|
| ĺ | TARDBP   | 1    |
|   | FUS      | 5    |
|   | SETX     | 11   |
| ĺ | MATR3    | 12   |
|   | TAF15    | 13   |
| ĺ | ATXN2    | 21   |
|   | HRNPA2B1 | 60   |
| ĺ | ARHGEF28 | 61   |
|   | HNRNPA1  | 106  |
|   | GLE1     | 107  |
|   | ANG      | 713  |

## **Retrospective Study**

#### • Literature published up to 2012

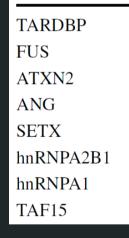
- 8 known RBPs linked to mutations
- **1,439 out 1,487 RBPs**

#### • Goal:

- How would Watson rank the other three ?
  - MATR3, ARGHEF28 and GLE1
  - Found 2013 2017

| Protein  | Rank |
|----------|------|
| TARDBP   | 1    |
| FUS      | 5    |
| SETX     | 11   |
| MATR3    | 12   |
| TAF15    | 13   |
| ATXN2    | 21   |
| HRNPA2B1 | 60   |
| ARHGEF28 | 61   |
| HNRNPA1  | 106  |
| GLE1     | 107  |
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Known Gene set



29

#### **Retrospective Study Results**

#### • Blue Box

- Proteins with known gene mutations
- Red Box:
  - Altered proteins without known gene mutation
- Ranked in top 165 (11%) of candidate gene set
- What if Watson was used in 2012 ?
  - MATR3 → May 2014

| Candidate Gene set | Score (GD) | Rank |
|--------------------|------------|------|
| MATR3              | 0.00204078 | 1    |
| NUPL2              | 0.00181635 | 2    |
| SRSF2              | 0.0017781  | 3    |
| SYNCRIP            | 0.00175763 | 4    |
| hnRNPU             | 0.00174455 | 5    |
| RBM6               | 0.00161879 | 6    |
| IGHMBP2            | 0.00154716 | 7    |
| hnRNPA3            | 0.00154361 | 8    |
| hnRNPC             | 0.00153549 | 9    |
| hnRNPM             | 0.00151568 | 10   |
| _                  |            |      |
| RBM45              | 7.79E-04   | 43   |
| TIA1               | 7.76E-04   | 50   |
| ARHGEF28           | 3.95E-04   | 89   |
| GLE1               | 3.85E-04   | 165  |

#### **Prospective Study**

#### • 1478 RBPs and 11 known genes

| Candidate Gene set | Score (GD) | Rank |
|--------------------|------------|------|
| hnRNPU             | 0.002914   | 1    |
| SYNCRIP            | 0.002747   | 2    |
| RBM45              | 0.00268    | 3    |
| RBMS3              | 0.002494   | 4    |
| SRSF2              | 0.002459   | 5    |
| hnRNPH2            | 0.002255   | 6    |
| NUPL2              | 0.002152   | 7    |
| CAPRIN1            | 0.002109   | 8    |
| RBM6               | 0.001915   | 9    |
| MTHFSD             | 0.00191    | 10   |
| _                  |            |      |
| hnRNPA3            | 0.001534   | 18   |
| _                  |            |      |
| SMN2               | 7.72E-04   | 63   |
| EWSR1              | 7.71E-04   | 66   |

Altered proteins without known gene mutation

## **Validation and Results**

#### • Validation

- Positive control: 8 of the top 10 candidates
- Negative control: Bottom 3 candidates (rank 1476-1478)
- 4 different biological methods
  - Show significant difference in at least two methods
- Results
  - 5/8 RBPs showed significant alterations.
  - No alternations in bottom RBPs

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# Conclusion

- Powerful tool
  - Analyzing published literature at a scale
  - Better selection of candidates for further examination
- Widespread Adoption ?

# Acknowledgements

# Thanks to Nic Mcphee and Elena Machkasova for their advice.

#### Questions

#### References

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