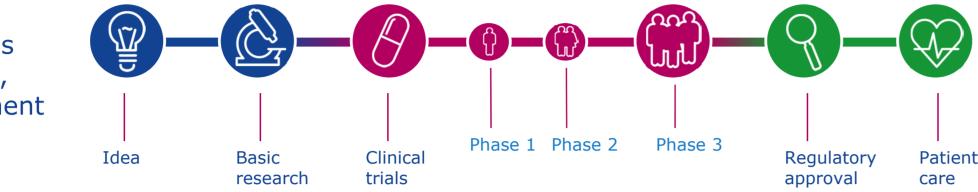
Bridging the gaps: NLP in translational research Jane Z Reed, Head of Life Science Strategy, Linguamatics



- For the past few years, artificial intelligence (AI) technologies such as ٠ natural language processing (NLP) have been hot topics in biomedicine, as researchers and healthcare providers consider ways to leverage innovative tools to transform bioscience research and clinical care, from bench to bedside.
- Accessing the right information is critical but much of the data is locked in textual format, such as scientific literature, clinical trial reports or electronic health records. NLP can effectively speed the extraction of critical information from unstructured scientific and clinical text.
- Use cases span discovery, development, and healthcare delivery such as utilization of text mining for genotype-phenotype annotation, selecting patients for clinical trials, and extracting key endpoints from pathology reports and EHRs for better patient care.

Accessing the right information is critical for translational research, across drug discovery, development



NLP enables deep linguistic analysis

- I2E uses deep linguistic analysis of text to deliver accurate and focused sets of results, which then reveal clearer insights. For example:
- **Identify subtleties of** language - I2E understands the difference between "history of cancer" and "family history of cancer".
- **Identify numerical** information in context - such as dosages of specific drugs or tumour size.
- Manage negation in medical **text** - by flagging concepts based on negative terms and the linguistic context. Thus, "No evidence of pneumonia" does not return a diagnosis of
- Identify, cluster and categorize by different concepts and classes – using plugged-in terminologies, thesauri or ontologies. For example: breast cancer and all its synonyms; or any type of cancer.

Linguamatics

- Use any terminologies such as ICD-9 & 10, RxNorm or SNOMED CT.
- **Connect and merge the I2E** results table with other structured data - whether from a relational database or from



NLP Text Mining in Biomedicine

- To make effective use of unstructured data in the biomedical domain, we need to distinguish concepts and their context within the text.
- It is essential to differentiate current diagnosis from family history of disease, when a disease term has been negated or ruled out and identify what drugs and dosages have been used
- NLP can do this. MLP allows more precise and efficient extraction of knowledge by capturing the different ways people express the same information.
- NLP: Find information however it is expressed, and understand relevant context

Different words, grammar, same meaning 5mg/kg of cyclosporine per day 5mg/kg per diem of ciclosporin Neoral 5mg per kg per day

> **Different expression**, same meaning Non-smoker Does not smoke Does not drink or smoke Denies tobacco use

> > Same word, different context Diagnosed with diabetes Family history of diabetes No family history of diabetes

"pneumonia"

other I2E results.

Normalisation of data

Finding concepts is not enough for rapid analysis and actionable information. Use of ontologies and pattern rules enables **normalisation** of concepts, for semantic tagging and data integration.

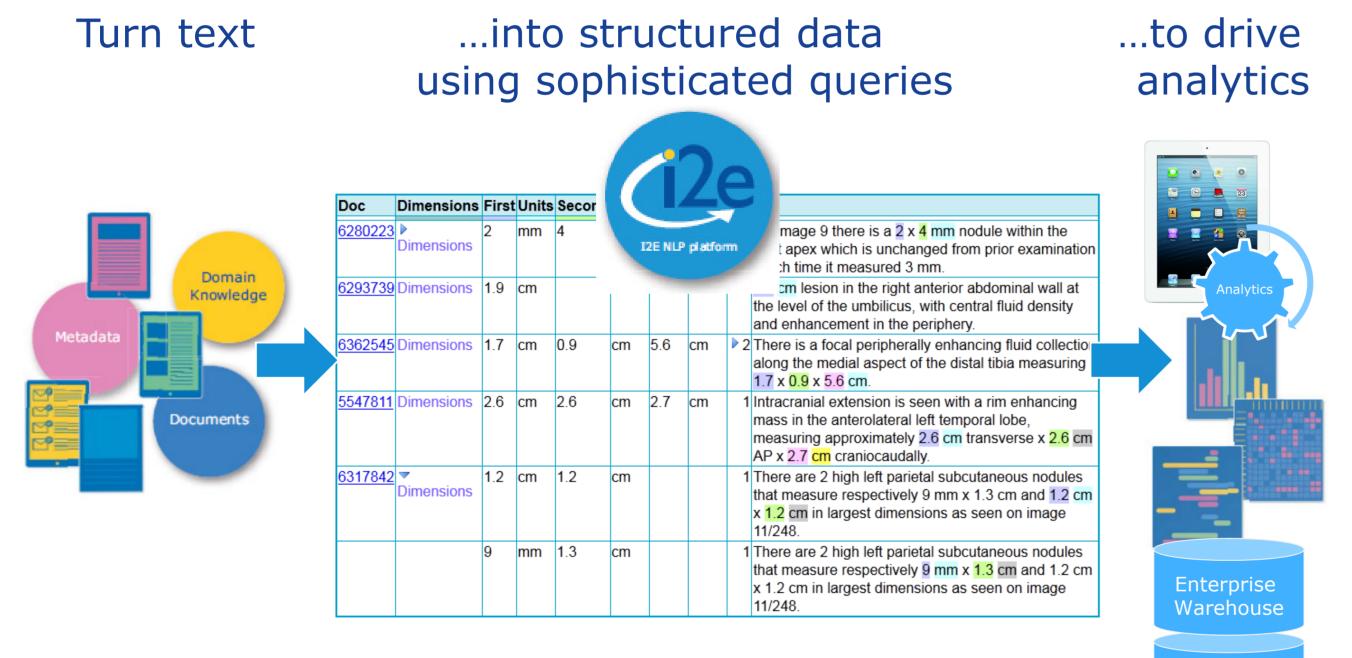
Concept	Text	Normalized Value		
Diseases	breast cancer	Breast Neoplasm		
	carcinoma of the breast			
Genes	Raf-1	RAF1		
	Raf I			
Dates	27 th Feb 2014	20140227		
	2014/02/27			
Measurements	0.2g	200 mg		
	Two hundred milligrams			
Mutations	Val 158 Met	V158M		
	Val by Met at codon 158			

"Nimesulide, a selective COX2 inhibitor ..."



TNM Staging from Pathology Reports

I2E Transforms Text into Actionable Insights



Linguamatics NLP-based text mining solution, I2E, takes unstructured text documents, indexes these with ontologies and other metadata, and enables queries to extract key facts in a structured form, that can then power analytics workflows e.g. in clinical risk models.

Genotype-Phenotype in Rare disease

Shire Pharmaceutical's innovative implant device can

Cancer

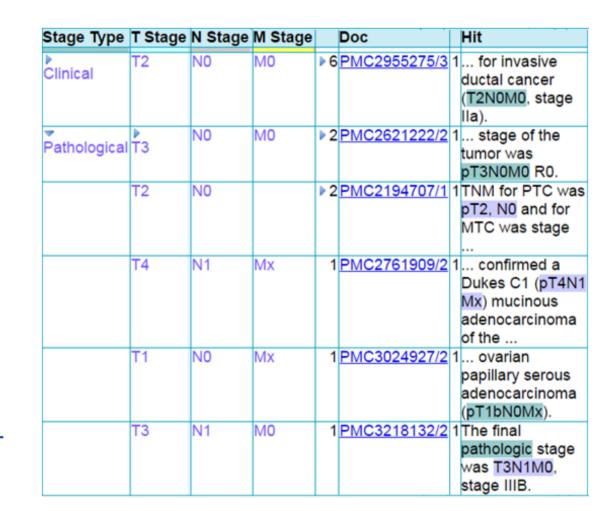
registry

Cancer information is one of the most common areas for NLP to be applied to in healthcare, providing key insights into disease progression and long term outcomes. Valuable research insights hidden in **pathology** documents can be extracted, such as tumour size, type and stage; and lab results showing bone marrow and blood measurements, providing much richer data for diagnostics and risk prediction.

I2E is used in healthcare organisations to mine cancer pathology reports systematically, extracting and structuring relevant data e.g. tumour, node and metastasis (TNM) staging.

TNM Stage		Doc		Hit
T2 N0 M0	▶5	PMC2955275/3	1	for invasive ductal cancer (T2N0M0, stage IIa).
pT3 N0 M0	▶2	PMC2621222/2	1	stage of the tumor was pT3N0M0 R0.
T3 N0 M0	▶2	PMC3337737/3	1	study reported an adenocarcinoma, T3N0M0.
pT1b N0	1	PMC3024927/2	1	ovarian papillary serous adenocarcinoma (pT1bN0Mx).
Mx				
pT2 N0	1	PMC3016302/3	1	International Cancer Control classification was pT2, pN0
				(0/12)
pT3 N1 M0	1	PMC2621222/1	1	a rectal adenocarcinoma, staged pT3 N1 M0 R0 with
				complete mesorectal excision
pT3 N2 M0	1	PMC2843670/2	1	lymph node metastasis (Stage pT3N2M0).
T1 N3 M0	1	PMC3010544/4	1	diagnosed as hypopharyngeal cancer (T1N3M0) underwent
				5-weeks of radiation
T1b N0 M0	1	PMC3010544/3	1	diagnosed as glottic cancer (T1b-N0M0) underwent 8-weeks
				of radiation
T4 N1 M0	1	PMC3276824/1	1	carcinoma supraglottic larynx (stage T4N1M0).

Structured tabular results from I2E NLP queries to extract tumour staging information from full text pathology reports. I2E's flexibility enables outputs to be formatted to accommodate the needs of the user or organisation.



NLP for Pneumonia prediction

Kaiser Permanente used I2E to develop a system that categorizes potential

- deliver enzyme replacement therapy to the CNS of Hunter Syndrome patients. The procedure is invasive and unpleasant, so ideally would be provided to those infants likely to have more **severe phenotypes**.
- Shire used I2E to identify all the iduronate-2-sulfatase (IDS) gene mutations recorded in Hunter patients (and patients with Hunter-like symptoms) and link them to phenotypes, enabling a clear picture of which genotypes were associated with the more **severe cognitive** impairment phenotypes. **Shire**
- Increased understanding of IDS mutational spectrum for provider diagnostics
- Enabled **better clinical** decision-making and a focused precision medicine approach for patient care

PMID	Source	Mutation Genes/Prote	Severity		Doc		Hit
8111411	▶ PDF	Q531X	mild	▶2	Hopwood gene 8111411		1 and R48P, L196S, Q531X (mild phenotype).
15614569	▶ PDF	H138R	severe	▶2	Chang Ex II 15614569	1	Patients with R88C and H138R mutations displayed a severe phenotype.
17391447	▶ PDF	E177X	attenuated	▶2	Froissar ppl 17391447		1 In contrast, the attenuated phenotype reported in the patient carrying the E177X mutation (26) is
9660053	▶ PDF	nonsense mutation	very mild	▶2	Froissar enet 9660053	1	 This nonsense mutation is associated with a very mild phenotype (patient 56, aged
24125893	▶ PDF	c.1122C>T	attenuated	1	Mucopoly nts 24125893	1	1 mutations present correlation with the attenuated form (c.1122C>T), while a greater
24780617	Abstract	p.lle360Tyrfs*31	severe	1	24780617	Þ:	 mutations whereas the p.Ser142Phe and p.Ile360Tyrfs*31 mutations caused the severe disease manifestation.
9712538	PDF	A deletion involving exons 2-4 in the iduronate-2-sulfatase gene	intermediate	1	Bonuccel enet 9712538	•	2A deletion involving exons 2-4 in the iduronate-2- sulfatase gene of a patient with intermediate Hunter syndrome
1284597	Abstract	R468W	mild	1	1284597		Mutation R468W of the iduronate-2-sulfatase gene in mild Hunter syndrome (mucopolysaccharidosis type II)
7887413	▶ PDF	P469H	mild	1	Jonsson enet 7887413		1 mutations in exon 9 had mild disease (P469H; Y523C; R468W,
7981716	PDF	R468W	mild	▶2	Mutation S II 7981716	1	1 C (1992) Mutation R468W of the iduronate-2- sulfatase gene in mild Hunter syndrome (mucopolysaccaridosis type II)
8566953	Abstract	A346D	mild	1	8566953	1	1 The A346D mutation was associated with the mild phenotype, all others with the
9501270	▶ PDF	Q389X	severe	1	<u>Isogai 1 bDis 9501270</u>		 nonsense mutations (Q80X; Q389X) in patients with severe Hunter syndrome (mucopolysaccharidosis type II)



Many **subtleties of language** are used by radiologists when writing their notes and the diagnosis is generally inferred from a set of individual observations. In the past, this inference was performed manually, making it difficult to use radiology reports at any scale in retrospective analyses.

Now, however, physician-developed criteria are used by I2E to categorize the reports automatically into the following categories:

- 1. The patient **has** pneumonia
- 2. The patient **possibly has** pneumonia



3. The patient **doesn't have** pneumonia

The system was assessed against a 300 patient gold standard and achieved selectivity and specificity scores of over 90%. It has since been run with over 200,000 patient reports.

Liu et al. BMC Med Inform Decis Mak. 2013 Aug 15;13:90 PMID: 23947340



Linguamatics is the world leader in deploying innovative, health-science-focused NLP solutions for high-value knowledge discovery, information extraction and decision support. Linguamatics I2E is used by leading healthcare organisations (providers, medical centres, payors), the US FDA, and 18 of the top 20 global pharmaceutical companies. They use I2E to take unstructured and semi-structured 'Big Data' and deliver improved patient care and insights. For more information, visit <u>www.linguamatics.com</u> or contact <u>info@linguamatics.com</u>

