Integrating Syntactic and Semantic Annotation of Biomedical Text

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Goal

#Information Extraction from the biomedical literature, particularly Medline Enzyme Inhibition Relations Expression of CYP3A11 and PXR was suppressed by inactivation of HNF4alpha customer: GlaxoSmithKline Mutation/Malignancy Relations Ki-ras mutations were detected in 17.2% of the adenomas. customer: eGenome

#Annotate 1-10K abstracts for each domain

Approach to Information Extraction

₩Phase 1:

Develop definitions and ontologies

Annotate data according to definitions

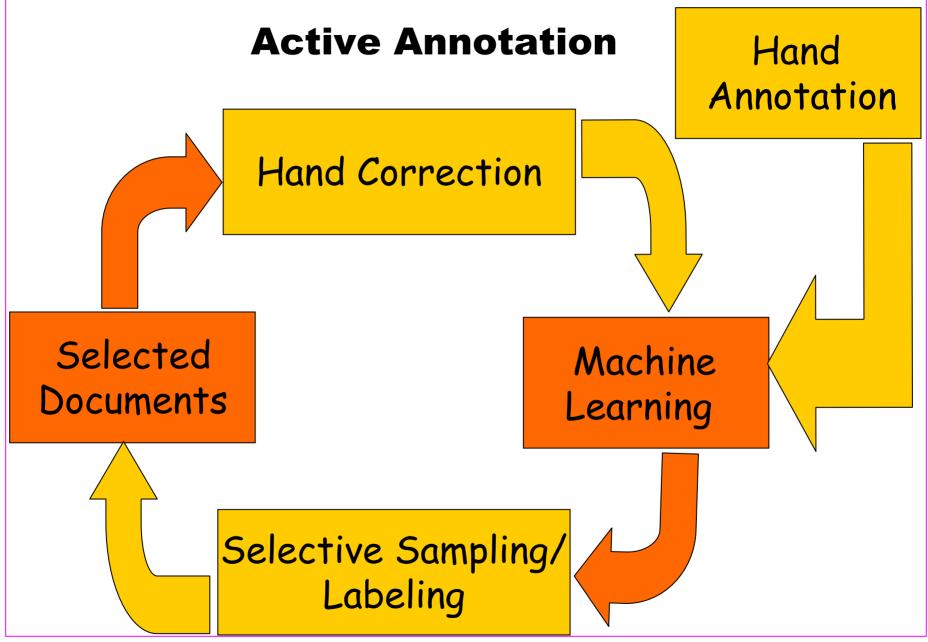
Phase 2: Train corpus-based algorithms exploiting various annotation:

■Parsing

≥Predicate-argument analysis

☑ Reference resolution

% Phase 3: "Active Annotation"



Challenge: Diversity in Expression

- 1. "Activation of the C-Ki-ras genes by point mutations in codons 12 or 13..."
- "Point mutations in codons 12 and 13 activated C-Ki-ras"
- 3. "Point mutations in codons 12 and 13 were activators of C-Ki-ras gene"

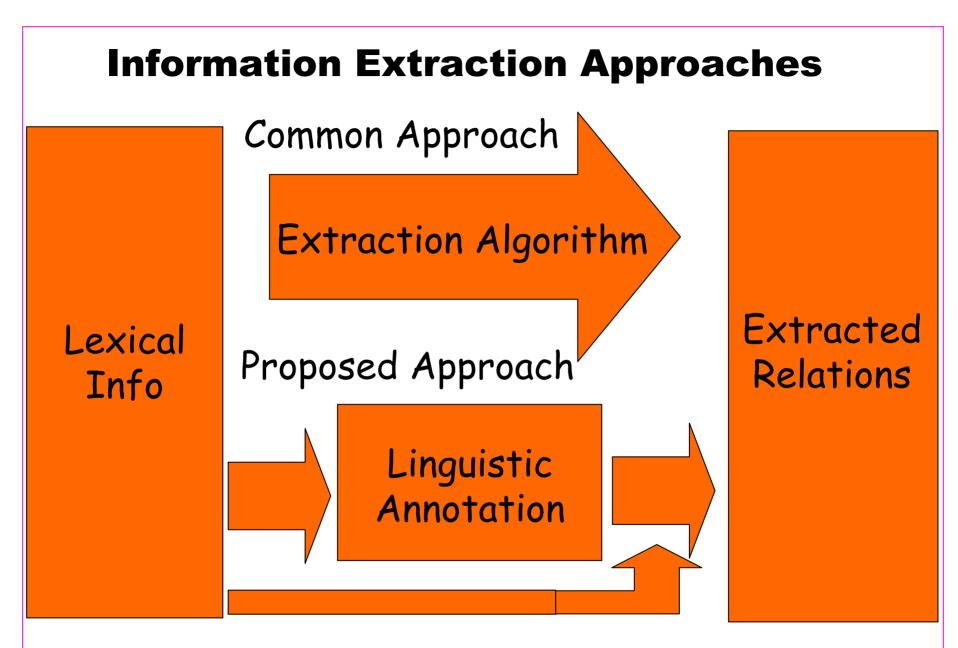
Want to populate a factbank with: activation(C-Ki-ras, point mutation in codon 12) activation(C-Ki-ras, point mutation in codon 13)

Approaches to Handling Diversity

Current Approach is to either: Hand build extraction patterns to cover all variant expressions

or

Annotate lots of data to get examples of variant expressions (for machine learning)
 Proposed Approach:
 Linguistic analysis of the sentences

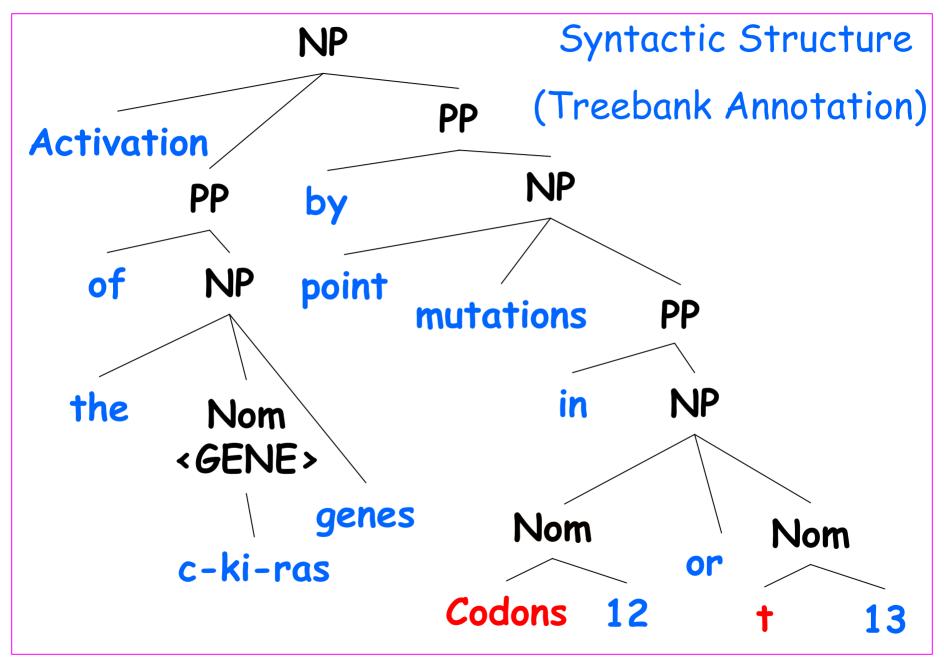


Our Annotation Effort

Together for the first time...

Annotations include:

Treebank (Syntax)
 Probank (predicate-argument structure)
 Entities (genes, malignancies)
 Reference and Coreference
 Factbanking (end goal)



More Examples of Coordination

"the ortho and meta positions"

(= the ortho positions and meta positions)

- # "PLC and cytochrome P450 arachidonate epoxygenase activity"
 - [
 [= PLC arachidonate epoxygenase activity
 and cytochrome P450 arachidonate...)

"enhanced CYP2C9 expression and 11,12 EET production"

(= enhanced CYP2C9 expression and enhanced 11,12 EET production)

Predicate-Argument Annotation: Propbank

- % "Point mutations in codons 12 and 13 were activators of C-K-ras genes"
- ***** "Activation of the C-K-ras genes by point mutations in Codons 12 or 13..."
- %Predicate-Argument Structure (Propbank):
 - REL: activation
 - activatee: c-ki-ras genes
 - activator: point mutations in codons 12 or 13

REL: mutations

type: point
position(s): Codons 12 or 13

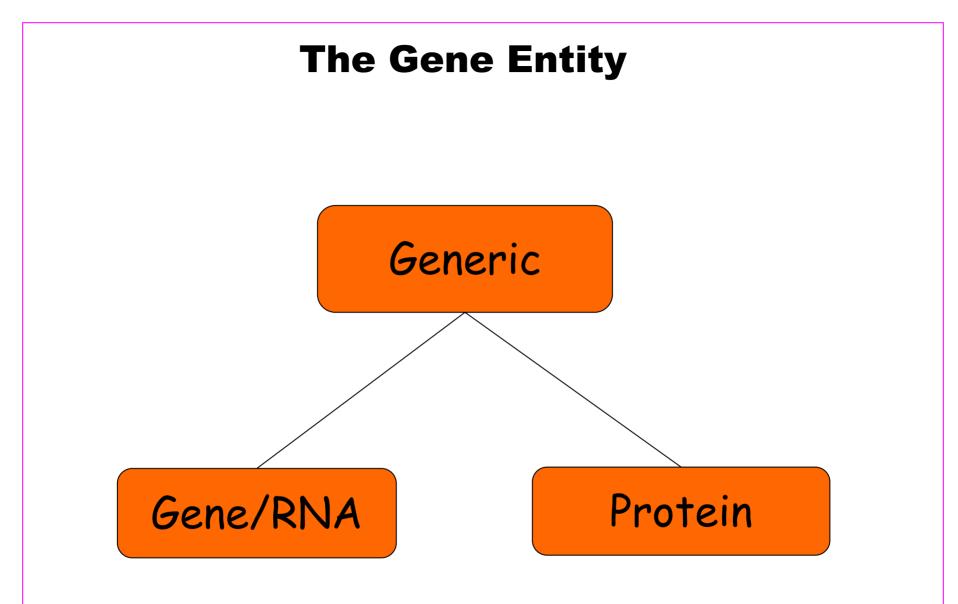
Why Combine Treebank and Propbank?

#Treebank indicates constituents Subject, verb, direct object, etc.
 #Propbank indicates roles of constituents △ "agent," "theme," "quantification", etc. inhibitor, inhibitee, inhibition rate #Prior work combines Treebank/Propbank for financial text IE: (Surdeneau et al., 2003, Gildea and Palmer,

2002)

Entity Annotation

🗯 Entities we annotate include: "gene", "protein", "substance", "malignancy" **#**Metonymy Issues: ○ We use subtypes, following ACE conference convention Gene is broken in to three categories: "Generic," "Gene/RNA" and "Protein"



WordFreak Annotation Tool

Morton, Lacivita, Pancoast: <u>www.annotation</u>.org

🏀 WordFreak		🕵 Chooser 🛛 🗙			
File Edit Viewer Annotation Tagger Project Font Window Help		<	>	+	_
		«	>>>) 	
Untitled Project Text		Named Entity	·		
11: J Pathol 1998 Sep;186(1):41-50		Type Features gene			
Pancreatic endocrine tumours: evidence for a tumour suppressor pathogenesis and		Gene/Rna			
for a tumour suppressor gene on chromosome 17p.		Protien			
eghelli S, Pelosi G, Zamboni G, Falconi M, Iacono C, Bordi C, Scarpa A.		Generic			
Istituto di Anatomia Patologica Universita di Verona, Italy.		variation			
Two molecular pathways leading to cancer are known. Common-type cancers arise		Location			
from the 'tumour' suppressor' pathway, characterized by gross chromosomal changes and allelic losses (LOH) in an average of 25 per cent or more of randomly chosen		State			
chromosomal loci. The 'mutator pathway' has been recognized in a subset of		Туре			
cancers, characterized by widespread microsatellite DNA instability and rarity		Malignancy			
of chromosomal losses. The present study has investigated 20 pancreatic endocrine tumours (PETs) for loss of heterozygosity (LOH) at seven chromosomal		Head: tumour			
loci (3p14, 7q31-32, 11q13, 13q14, 18q21, 17p13, and 17q21); microsatellite		Co-Reference			
instability; and Ki-ras, N-ras, and p53 gene mutations. LOH was found in an average of 24 per cent of the chromosomal loci analysed. No tumour showed		New	Clear	Merge	Re-Number
microsatellite instability. Ki-ras and p53 mutations were each found in one					
case. The frequency of losses was higher in malignant (40 per cent) than in benign (17 per cent) tumours (p = 0.009), and the specific chromosome 17p13 LOH					r; cancer; cancers 📥
was associated with extrapancreatic extension of disease (p = 0.007), high		Imalignancy#2 (pancreatic endocrine tumours; P			
proliferative activity ($p = 0.001$), and absence of progesterone receptors ($p = 0.001$).		🛛 🗢 🔲 🛨 gene#3 (tumour suppressor; tumour suppresso			
0.01). A common deleted region on chromosome 17p13 and the rarity of p53 gene mutations suggest the existence of a novel tumour suppressor gene involved in		• 🔽 🛨 variation#4 (p53 gene mutations; p53 mutations			
the pathogenesis of PETs in this chromosomal area.		🗢 🔲 🔸 variation#8 (loss of heterozygosity (LOH) at seve			
PMID: 9875139 [PubMed - indexed for MEDLINE]		👁 🔲 🔸 gene#7 (Ki-ras; Ki-ras)			
		🗢 🗌 🔸 ge	ne#6 (p53; p	53)	
	-		ristion#5 (alle	lic Insees I O	
👌 📏 yang jin (malignancy#1) 9399 🔲 1 37.35	i 💶 🔤	comment:			

Reference and Co-reference Annotation

% Co-reference is an equivalence relation
% subtypes prevent nonsense in a co-ref graph
Example of reference types:

"K-Ras is a member of the Ras family of Oncogenes. The protein form is actively expressed in..."

class-membership(K-Ras, Ras family)
anaphor(K-Ras_protein, protein form)

Current Activities

#In Progress:

 Entity Annotation of "Gene," "Chemical," "Malignancy," "genetic variation," etc.
 POS annotation

△Training Treebank Syntactic Annotators
Starting Up:

Start coreference annotation

△Build our first entity tagging models

Some Projected Milestone Dates

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∺January 2004 -
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Entity tagging and coreference on oncology domain complete. We publish:

annotation guidelines

data

baseline statistical taggers

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₩May 2004 -
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First draft syntactic analysis of oncology domain

(1-10K Medline abstracts)

Some Annotation Projects and Related Research

#GENIA Project and U Tokyo Work: http://www-tsujii.is.s.u-tokyo.ac.jp/GENIA **#**Pasta system and Sheffield Work: http://nlp.shef.ac.uk/research/areas/bio.html **#**GENIES system and Columbia/CUNY Work **#**Modeling Linguistic Phenomenon: Ray/Craven, IJCAI-2001 Pustejovsky et al. 2003

The End.

Some Examples Follow

Reference and Co-reference

Our reference subtypes are:

- Acronyms (definitions and linkages)
- Anaphor (such as pronouns)
- Classes versus their members
- ∠"Is-a" relation,
- i.e. "{CYP450}, {an enzyme} found in..." Standardized database reference

Complex Coordination Example

Inhibition of CB -52 and -101 metabolism

Note coordination of "CB" and also "metabolism"!

The sentence above can be represented as:

Inhibition of CB-52 metabolism and CB-101 metabolism)