PyPharma NLP Tutorial 2019: Learning by doing NLP

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Agenda

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PyPharma Conference 2019 (1/2)

- Aimed at python users in the pharmaceutical industry and academia, all aspects of the pharmaceutical lifecycle and data modalities.
- Attendance is estimated at around 100 people (still growing).
- Attendants and speakers from Roche, Novartis, GSK, AstraZeneca, UNIBAS, UNIL, IBM, ETHZ, UZH, SIB, and various other companies and universities.

PyPharma Conference 2019 (2/2)

- Two days, single track, invite only, free to attend.
- Hosts: Roche, Novartis, and the University of Basel.
- Day 1: November 21st at the University of Basel, Day 2: November 22nd at the Roche Viaduktstrasse amphitheater.

Natural Language Processing (1/2)

- Automate the processing of data in natural language form.
- Look at text as a database that we want to be able to query in various ways.
- Combines elements of linguistics, computer science, statistics, artificial intelligence, etc.
- One natural way to do this is to use machine learning to perform tasks such as text classification, named entity extraction, relation extraction, etc.

Natural Language Processing (2/2)

- In recent years, deep learning based methods have shown great promise in terms of performance.
- But also the ability to transfer knowledge across datasets as well as across tasks.
- Examples include models such as
 - word2vec
 - GloVe
 - ELMO
 - BERT
 - etc

Natural Language Processing (3/2)

- The usual transfer learning procedure is
 - Step 1: train a base model to perform generic tasks on very large datasets (websites, books, wikipedia, social media, etc).
 - Step 2: fine tune the model to perform a specific task on a smaller dataset.
- Extensions to these methods to biomedical applications often follow (e.g. Pyysalo embeddings for word2vec, BioBERT for BERT, etc).

PyPharma NLP 2019

- A tutorial on Pharma and Biomedical NLP that will take place on Day 1 of PyPharma (November 21st at the University of Basel).
- The goal is for intermediate pharmaceutical and biomedical python users to learn how to do state of the art NLP by doing it.
- Since doing it is usually hard, we provide tools for them to make the process easier.
- We provide notebooks with examples of various tasks and datasets.

Notebooks: Format (1/2)

- They will be hosted in Google Colab as well as Azure Notebooks.
- No need to install anything in your computer, or buy a new one, to do state of the art, deep learning based NLP (yay!).
- Prior to using the notebooks, an introduction to deep learning based NLP will be done.

Notebooks: Format (2/2)

- The common structure will be:
 - Downloading the training datasets.
 - Exploring the training data and how it is seen by the model (inputs and outputs).
 - Training the model and **storing** the results in a **checkpoint**.
 - Re-loading the checkpoint and performing predictions on new data, as well as exploring the results interactively.

Examples: Masked Language Modelling

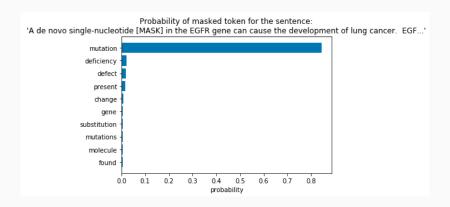


Figure 1:

Examples: Detecting Adverse Events

Sentence Lab
Jointones Edit
INTRODUCTION: Neuropsychiatric symptoms are a well-described side effect of systemic corticosteroid therapy and can range from mild to severe.
CASE PRESENTATION: We describe a case of substance-induced psychosis following epidural injection of 10 mg dexamethasone.
Three days after the procedure, the patient developed symptoms including anger, hostility, insomnia, paranoia, and delusions.
Symptoms resolved between 7 and 17 days.
DISCUSSION: In the past 50 years, there have been several case reports of severe neuropsychiatric effects following intraarticular or other interventional pain injections with various corticosteroids.
More recent reviews have identified possible risk factors, including corticosteroid dose, patient age, sex, and history of neuropsychiatric disorder, among others, although these conclusions are not duplicated across all studies.
CONCLUSION: Recommendations for practice include patient and family education on possible adverse effects of corticosteroid administration, utilization of minimum effective doses for interventional procedures, and the consideration of close follow-up and multidisciplinary coordination, especially in high-risk patients.

Examples: Extracting Disease Mentions

Sentence ID	Token	True Label	Predicted Label
13	None	0	0
13	of	0	0
13	the	0	0
13	patients	0	0
13	had	0	0
13	decompensated	0	0
13	liver	В	В
13	disease	- 1	1
13		0	0

Examples: Extracting Gene-Disease Associations

Our data shows no association between @DISEASE\$ and the Leu432Val polymorphism of the @GENE\$ gene or the tetranucleotide repeats of the CYP19 gene.	1	1
Our study showed that gene polymorphisms of @GENE\$ and SULT1A1 induce an individual susceptibility to @DISEASE\$ among current smokers.	1	1
We conclude that the @GENE\$* 3 allele appears to be a factor for susceptibility to @DISEASE\$ in Turkish women especially those with a BMI greater than 24 kg/m(2).	1	1
Our results suggested that the Val @GENE\$ allele increases the susceptibility to @DISEASE\$ in women exposed to waste incinerator or agricultural pollutants.	1	1
These results do not support a favoring role of @GENE\$*3 in @DISEASE\$ development in our population.	1	1
We found no evidence for an overall association between @GENE\$ genotype and @DISEASE\$ risk, nor was there any clear indication of gene-environment interaction.	1	1
These results suggest that HLA class I antigens and @GENE\$ A-308G are not associated with susceptibility or resistance to the development of TDI-induced @DISEASE\$.	0	1
These results suggest that the C1772T polymorphism in @GENE\$ is not involved in @DISEASE\$ or metastasis of colorectal carcinoma.	0	0
These results provide substantial evidence that genetic variation within or extremely close to @GENE\$ impacts both @DISEASE\$ risk and traits related to the severity of AD.	0	0
This study provides the first evidence that @GENE\$ may be a candidate susceptibility loci that affects the @DISEASE\$ of atherosclerosis in Japanese subjects.	0	0
Since only eight out @GENES ion-overloaded HbH patients carry a @DISEASES in the TFR2 or HFE gene in the heterozygote state and their iron loading status was comparable to the matched controls without such delects, it would appear that the accumulation of excess iron in HbH disease is more likely a result of increase dietary absorption secondary to ineffective erythropolesis.	0	0
The H63D @DISEASES of the @GENES gene has a moderate but significant influence on sTIR concentration in the general opulation, the presence of one or two mutated alleles being associated with an average of 0.27 mg/L less STIR than nommutated homozygotes.	0	0

Figure 4:

Examples: Question Answering (1/2)

Importance: Osimertinib mesylate is used globally to treat EGFR-mutant non-small cell lung cancer (NSCLC) with tyrosine kinase inhibitor resistance mediated by the EGFR T790M mutation. Acquired resistance to osimertinib is a growing clinical challenge that is poorly understood. Objective: To understand the molecular mechanisms of acquired resistance to osimertinib and their clinical behavior, Design, Setting, and Participants; Patients with advanced NSCLC who received osimertinib for T790M-positive acquired resistance to prior EGFR tyrosine kinase inhibitor were identified from a multi-institutional cohort (n = 143) and a confirmatory trial cohort (NCTO1802632) (n = 110), Next-generation sequencing of tumor biopsies after osimertinib resistance was performed. Genotyping of plasma cell-free DNA was studied as an orthogonal approach, including serial plasma samples when available. The study and analysis were finalized on November 9, 2017. Main Outcomes and Measures: Mechanisms of resistance and their association with time to treatment discontinuation on osimertinib. Results: Of the 143 patients evaluated, 41 (28 [68%] women) had tumor next-generation sequencing after acquired resistance to osimertinib. Among 13 patients (32%) with maintained T790M at the time of resistance, EGFR C797S was seen in 9 patients (22%). Among 28 individuals (68%) with loss of T790M, a range of competing resistance mechanisms was detected, including novel mechanisms such as acquired KRAS mutations and targetable gene fusions. Time to treatment discontinuation was shorter in patients with T790M loss (6.1 vs 15.2 months), suggesting emergence of pre-existing resistant clones; this finding was confirmed in a validation cohort of 110 patients with plasma cell-free DNA genotyping performed after osimertinib resistance. In studies of serial plasma levels of mutant EGFR, loss of T790M at resistance was associated with a smaller decrease in levels of the EGFR driver mutation after 1 to 3 weeks of therapy (100% vs 83% decrease; P = .01). Conclusions and Relevance: Acquired resistance to osimertinib mediated by loss of the T790M mutation is associated with early resistance and a range of competing resistance mechanisms. These data provide clinical evidence of the heterogeneity of resistance in advanced NSCLC and a need for clinical trial strategies that can overcome multiple concomitant resistance mechanisms or strategies for preventing such resistance.

Examples: Question Answering (2/2)

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QUESTION:
What mediates TKI resistance? EGFR T790M mutation.
ANSWER: tyrosine kinase inhibitor resistance mediated by the EGFR T790M mutation
What are the main outcomes of this study?
ANSWER: Mechanisms of resistance and their association with time to treatment discontinuation on osimertinib
How many patients participated in this study?
ANSWER: 143
What are some competing resistance mechanisms to T790M?
ANSWER: acquired KRAS mutations and targetable gene fusions
What is the objective of the study?
ANSWER: To understand the molecular mechanisms of acquired resistance to osimertinib
When was the study finalized?
ANSWER: November 9, 2017
How many of the patients in this study were women?
ANSWER: 28 [68%
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Figure 6: