



# **Food-diseases relations extraction using spaCy**

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# Agenda

1. **Rule-based** food and diseases **entities extraction**
2. **Rule-based** food-diseases **relations extraction**
3. **Snowball algorithm** for food-diseases **relations extraction**
4. **Tools, performance and architecture**
5. **Hands-on presentation**

# Rule-based **entities extraction** - diseases

1. Distinctive “base” words

... **cancer** -> (**lung | kidney | ...**) **cancer**

2. Distinctive latin suffixes (with exceptions - stop words)

...**is** -> (**Acute Flaccid**) **Myelitis**

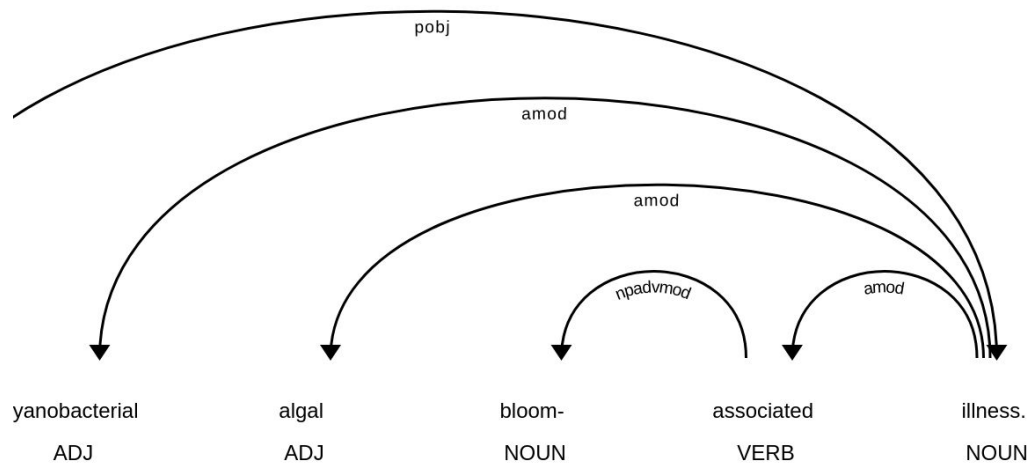
...**is** -> **this**

3. Initialisms (using a scraped list)

**ADHD, COVID-19, ...**

# Rule-based **entities extraction** - diseases

4. Grammar dependencies and their multiple combinations for bigger recall



# Rule-based **entities extraction** - food

## 1. Distinctive words

**diet** -> **Western diet**

**meal** -> **home cooked meal**

## 2. Distinctive phrases

**consumption of ...** -> **consumption of fruit and vegetables**

**... intake** -> **fish intake**

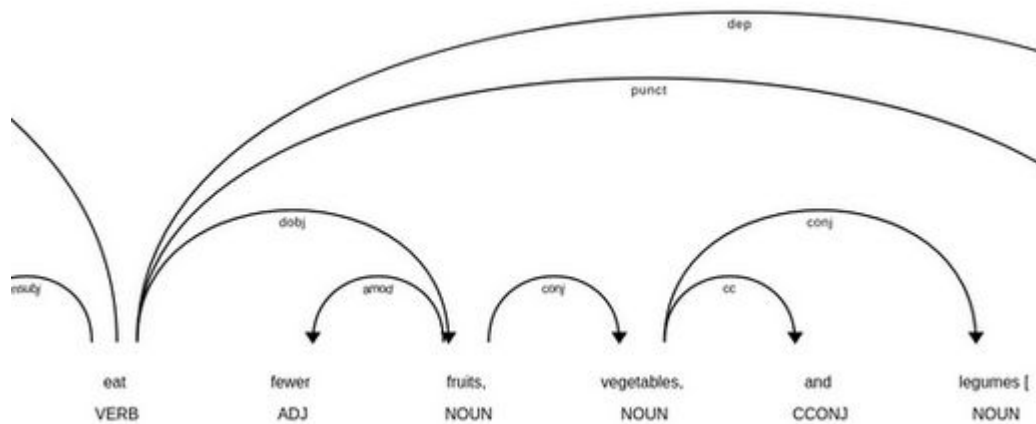
**eat ...** -> **consume processed meals**

## 3. Initialisms (using a scraped list)

**MDS, DASH, NFI**

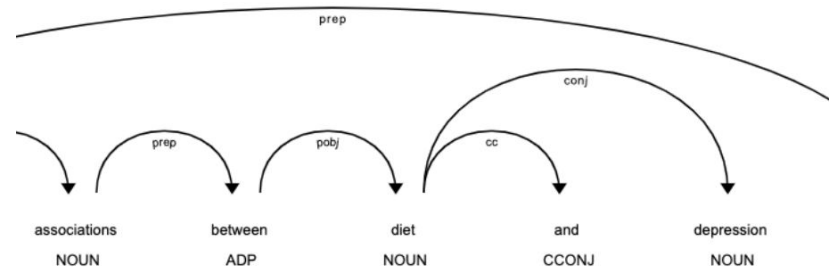
# Rule-based **entities extraction** - food

4. Grammar dependencies and their multiple combinations for bigger recall

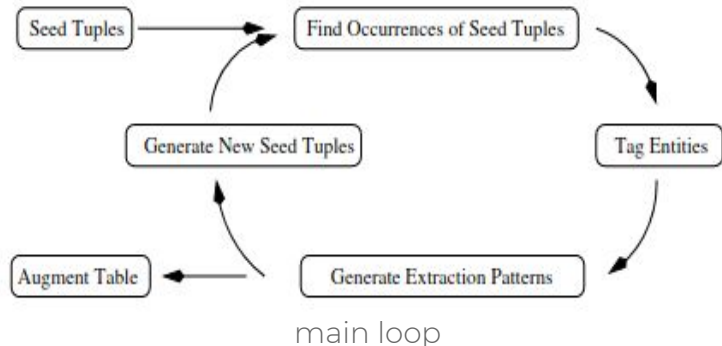


# Rule-based **relations extraction**

1. Uses food and diseases extractors
2. Uses distinctive words indicating relations  
**association -> associations between <FOOD> and <DIS>**  
**cause -> <FOOD> consumption causes <DIS>**
3. Looks for food and diseases entities being children of the same distinctive node within the same sentence



# Snowball algorithm



```
articles = load_articles(datapath)

sents = []
for art in articles:
    doc = extract_entities(art)
    sents += leave_food_dis_sents_only(doc)

seed_tuples = get_seed_tuples()
for i in range(n_iter):
    occur = find_occurrences(seed_tuples)
    patterns = pattern_from_occurrences(occur, w_size)
    patterns = single_pass_clustering(patterns, tau_cl)
    patterns = drop_insufficient(patterns, tau_supp)
    seed_tuples += get_new_tuples(patterns, tau_sim)
```

pseudocode

(CLI parameters in bold)

example of seed tuple occurrence with context ( $w\_size = 3$ )

the effect of **diet FOOD** on the risk of **IBD DIS** have been retrospective



# Tools & performance

**Python** 3.8.10

**spaCy** 3.0.6

**aws**

**NumPy** 1.20.2

tau_cl	tau_supp	tau_sim	iteration 1	iteration 2	iteration 3
3	3	3	42.4	-	-
3	3	3	45s	492.5s	2028.6s
3.5	4	3.5	46.2s	36.2s	-
3.25	3	3.25	50.7s	64.2s	83.7s

*\*testing setup: Intel Core i5-5200U CPU @ 2.20GHz, 8GB RAM*

