

MIT (TA1): From Paper and Code to annotated Petri Nets

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0. Preprocessing

```
In [95]: import ast, json, requests, os
         from IPython import display

         API_ROOT = "http://100.26.10.46/"
         GPT_KEY = ""
```

Starting with the SIDARTHE [paper](#)

(https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7175834/pdf/41591_2020_Article_883.pdf) provided in Scenario 2, we can run COSMOS (thanks Enrique Noriega from UArizona!) to extract a JSON with entries like this:

```
In [99]: with open("documents_sidarthe--COSMOS-data.json", "r") as f:
         text = f.read()
         print(ast.literal_eval(text)[0])

{'pdf_name': '41591_2020_Article_883.pdf', 'dataset_id': 'documents_5Feb', 'page_num':
1, 'img_pth': '/mytmp/images/41591_2020_Article_883.pdf_1_pad', 'pdf_dims': [0.0, 0.0, 6
12.0, 792.0], 'bounding_box': [103.0, 51.0, 1341.0, 212.0], 'classes': ['Section Heade
r', 'Page Footer', 'Figure', 'Body Text', 'Other', 'Reference text', 'Equation', 'Page H
eader', 'Abstract', 'Table Caption', 'Figure Caption', 'Table', 'Table Note', 'Equation
label'], 'scores': [-5.5183234215, -7.2636179924, -7.3330821991, -8.6994543076, -8.96853
25623, -9.0146894455, -9.3787899017, -9.9470386505, -10.0574893951, -10.3444986343, -10.
5733766556, -11.2742881775, -11.5064592361, -12.4296512604], 'content': '', 'postprocess
_cls': 'Page Header', 'postprocess_score': 0.8623757958, 'detect_cls': 'Section Header',
'detect_score': -5.5183234215}
```

We can run a local script to consolidate the "content" fields to get just the text of the paper:

```
In [100]: with open("sidarthe.txt", "r") as f:
          text = f.read()
          print(text.replace('\n', ' ')[:500])
```

Modelling the COVID-19 epidemic and implementation of population-wide Modelling the COV
ID-19 epidemic and implementation of population-wide interventions in Italy Giulia Giord
ano 1 ✉, Franco Blanchini², Raffaele Bruno^{3,4}, Patrizio Colaneri^{5,6}, Alessandro Di Fili
ppo³, Angela Di Matteo³ and Marta Colaneri³ In Italy, 128,948 confirmed cases and 15,887
deaths of peo- discharged due to recovery and 15,887 had died⁷. In the early days of ple
who tested positive for SARS-CoV-2 were registered

From the COSMOS output, we can also keep metadata like the paper name and doi for later:

```
In [101]: with open("sidarthe_info.json", "r") as f:
           info = json.load(f)
           info_s = json.dumps(info)
           print(info_s)
```

```
{"pdf_name": "41591_2020_Article_883.pdf", "DOI": "https://doi.org/10.1038/s41591-020-0883-7"}
```

1. Extracting variables and annotating them

Using our API (powered by GPT-3), we can extract variables from the paper alongside a list of possible definitions, and ground each of these variables to the MIRA DKG (thanks Harvard team!). If you're interested, the JSON format of our intermediate output can be found [here](https://github.com/mikecafarella/mitaskem/blob/main/JSONformat.md) (<https://github.com/mikecafarella/mitaskem/blob/main/JSONformat.md>).

```
In [6]: with open("sidarthe_short.txt", "r") as f:
        text = f.read()
        dct = {"text":text, "gpt_key":GPT_KEY}
        r = requests.post(API_ROOT + "annotation/find_text_vars/", params=dct)
        print(r)
```

<Response [200]>

```
In [7]: json_str = r.text  
        ast.literal_eval(json_str)
```

```

Out[7]: [{'type': 'variable',
  'name': 'S',
  'id': 'v0',
  'text_annotations': ['Susceptible (uninfected)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ido:0000514', 'susceptible population']]],
{'type': 'variable',
  'name': 'I',
  'id': 'v1',
  'text_annotations': ['Infected (asymptomatic or pauci-symptomatic infected, undetecte
d)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'D',
  'id': 'v2',
  'text_annotations': ['Diagnosed (asymptomatic infected, detected)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'A',
  'id': 'v3',
  'text_annotations': ['Ailing (symptomatic infected, undetected)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'R',
  'id': 'v4',
  'text_annotations': ['Recognized (symptomatic infected, detected)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ncit:C28554', 'Dead']]],
{'type': 'variable',
  'name': 'T',
  'id': 'v5',
  'text_annotations': ['Threatened (infected with life-threatening symptoms, detecte
d)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'H',
  'id': 'v6',
  'text_annotations': ['Healed (recovered)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ncit:C28554', 'Dead']]],
{'type': 'variable',
  'name': 'E',
  'id': 'v7',
  'text_annotations': ['Extinct (dead)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'α',
  'id': 'v8',
  'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
  'dkg_annotations': []},
{'type': 'variable',
  'name': 'β',
  'id': 'v9',
  'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
  'dkg_annotations': [['doid:0080928', 'dialysis-related amyloidosis'],
    ['vo:0005114', 'β-propiolactone-inactivated SARS-CoV vaccine']]},

```

```

    {'type': 'variable',
     'name': 'γ',
     'id': 'v10',
     'text_annotations': [' Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
     'dkg_annotations': [['askemo:0000013', 'recovery rate'],
      ['vo:0004915', 'vaccine specific interferon-γ immune response']]],
    {'type': 'variable',
     'name': 'δ',
     'id': 'v11',
     'text_annotations': [' Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)ε'],
     'dkg_annotations': [['askemo:0000011', 'progression rate'],
      ['vo:0005123', 'VSVΔG-MERS vaccine']]],
    {'type': 'variable',
     'name': 'θ',
     'id': 'v12',
     'text_annotations': [' probability rate of detection relative to symptomatic cases'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ζ',
     'id': 'v13',
     'text_annotations': [' probability rate at which an infected subject not aware of bein
g infected develops clinically relevant symptoms'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'η',
     'id': 'v14',
     'text_annotations': [' probability rate at which an infected subject aware of being in
fected develops clinically relevant symptomsμ'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ν',
     'id': 'v15',
     'text_annotations': [' Rate at which detected infected subjects develop life-threateni
ng symptoms'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'τ',
     'id': 'v16',
     'text_annotations': [' Mortality rate for infected subjects with life-threatening symp
toms'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'λ',
     'id': 'v17',
     'text_annotations': [' Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'κ',
     'id': 'v18',
     'text_annotations': [' Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ξ',
     'id': 'v19',
     'text_annotations': [' Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ρ',
     'id': 'v20',
     'text_annotations': [' Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',

```

```
'name': 'σ',
'id': 'v21',
'text_annotations': [' Rate of recovery for infected subjectsNone'],
'dkg_annotations': []}]
```

2. Extracting LaTeX from formula images

Here is a formula image from the SIDARTHE paper:

```
In [103]: display.Image("../resources/images/SIDARTHE/sidarthe_dAdt.png")
```

```
Out[103]:
```

$$\dot{A}(t) = \zeta I(t) - (\theta + \mu + \kappa)A(t)$$

As we demoed last week, we can extract LaTeX from such formula images (powered by `pix2tex`), also through a public API.

```
In [41]: directory = '../resources/images/SIDARTHE'
         latex_strs = []

         for filename in os.listdir(directory):
             f = os.path.join(directory, filename)
             latex_str = !python3 img_latex.py -p {f} # This is a local script that resizes the i
             mage and calls the public API.
             print(latex_str)
             latex_strs.append(latex_str[0])

         ['"\{\dot{A}\}(t)=\zeta I(t)-(\theta+\mu+\kappa)A(t)"]
         ['"\{\hat{D}\}(t)=\varepsilon I(t)-(\eta+\rho)D(t)"]
         ['"\{\dot{\bar{F}}\}(t)\longrightarrow\tau,T(t)"]
         ['"H(t)=i I(t)+\theta b(t)+\kappa d(t)+i R(t)+\sigma T(t)"]
         ['"\scriptstyle n=s q[a u_{1}+p u_{1}+s u_{1}+s u_{1})-(r+s+d v_{1})"]
         ['"R(t)=\eta D(t)+\theta A(t)-(\nu+\xi)R(t)"]
         ['"\delta(t)=-S(t)(a l(t)+\theta D(t)+r A(t)+\delta t(t)"]
         ['"\{\hat{T}\}(t)=\mu A(t)+\nu R(t)-(\sigma+\tau)\{\hat{T}\}(t)"]
```

3. Linking variables from the LaTeX formulas to variables from the text

We just extracted all these equations in LaTeX, which include variables. Let's link these variables to the variables we found from the text in part 1. Again, the output (internal)JSON format can be found [here](https://github.com/mikecafarella/mitaskem/blob/main/JSONformat.md) (<https://github.com/mikecafarella/mitaskem/blob/main/JSONformat.md>).

```
In [42]: full_json_str = json_str
latex_strs = latex_strs
for latex_str in latex_strs:
    print(latex_str)
    dct2 = {"json_str":full_json_str, "formula": latex_str, "gpt_key":GPT_KEY}

    r2 = requests.post(API_ROOT + "annotation/link_latex_to_vars/", params=dct2)
    print(r2)
    full_json_str = r2.text
```

```
"{\dot{A}}(t)=\zeta I(t)-(\theta+\mu+\kappa)A(t)"
<Response [200]>
"{\hat{D}}(t)=\varepsilon I(t)-(\eta+\rho)D(t)"
<Response [200]>
"\dot{\bar{F}}(t)\,,\,\longrightarrow\,,\,\tau\,,T(t)"
<Response [200]>
"H(t)=i I(t)+\theta b(t)+\kappa d(t)+i R(t)+\sigma T(t)"
<Response [200]>
"\scriptstyle n=s\,q|a\,u_{1}+p\,u_{1}+s\,u_{1}+s\,u_{1})-(r+s+d\,v_{1})"
<Response [200]>
"R(t)=\eta D(t)+\theta A(t)-(\nu+\xi)R(t)"
<Response [200]>
"\delta(t)=-S(t)(a\,l(t)+\theta D(t)+r\,A(t)+\delta\,t(t)"
<Response [200]>
"{\hat{T}}(t)=\mu A(t)+\nu R(t)-(\sigma+\tau){\hat{T}}(t)"
<Response [200]>
```

```
In [43]: ast.literal_eval(full_json_str)
```



```

Out[43]: [{'type': 'variable',
  'name': 'S',
  'id': 'v0',
  'text_annotations': ['Susceptible (uninfected)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ido:0000514', 'susceptible population']]],
{'type': 'variable',
  'name': 'I',
  'id': 'v1',
  'text_annotations': ['Infected (asymptomatic or pauci-symptomatic infected, undetecte
d)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'D',
  'id': 'v2',
  'text_annotations': ['Diagnosed (asymptomatic infected, detected)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'A',
  'id': 'v3',
  'text_annotations': ['Ailing (symptomatic infected, undetected)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'R',
  'id': 'v4',
  'text_annotations': ['Recognized (symptomatic infected, detected)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ncit:C28554', 'Dead']]],
{'type': 'variable',
  'name': 'T',
  'id': 'v5',
  'text_annotations': ['Threatened (infected with life-threatening symptoms, detecte
d)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'H',
  'id': 'v6',
  'text_annotations': ['Healed (recovered)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ncit:C28554', 'Dead']]],
{'type': 'variable',
  'name': 'E',
  'id': 'v7',
  'text_annotations': ['Extinct (dead)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']]],
{'type': 'variable',
  'name': 'α',
  'id': 'v8',
  'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
  'dkg_annotations': []},
{'type': 'variable',
  'name': 'β',
  'id': 'v9',
  'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
  'dkg_annotations': [['doid:0080928', 'dialysis-related amyloidosis'],
    ['vo:0005114', 'β-propiolactone-inactivated SARS-CoV vaccine']]},

```

```

    {'type': 'variable',
     'name': 'γ',
     'id': 'v10',
     'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
     'dkg_annotations': [['askemo:0000013', 'recovery rate'],
      ['vo:0004915', 'vaccine specific interferon-γ immune response']]},
    {'type': 'variable',
     'name': 'δ',
     'id': 'v11',
     'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)ε'],
     'dkg_annotations': [['askemo:0000011', 'progression rate'],
      ['vo:0005123', 'VSVΔG-MERS vaccine']]},
    {'type': 'variable',
     'name': 'θ',
     'id': 'v12',
     'text_annotations': ['probability rate of detection relative to symptomatic cases'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ζ',
     'id': 'v13',
     'text_annotations': ['probability rate at which an infected subject not aware of bein
g infected develops clinically relevant symptoms'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'η',
     'id': 'v14',
     'text_annotations': ['probability rate at which an infected subject aware of being in
fected develops clinically relevant symptomsμ'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ν',
     'id': 'v15',
     'text_annotations': ['Rate at which detected infected subjects develop life-threateni
ng symptoms'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'τ',
     'id': 'v16',
     'text_annotations': ['Mortality rate for infected subjects with life-threatening symp
toms'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'λ',
     'id': 'v17',
     'text_annotations': ['Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'κ',
     'id': 'v18',
     'text_annotations': ['Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ξ',
     'id': 'v19',
     'text_annotations': ['Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',
     'name': 'ρ',
     'id': 'v20',
     'text_annotations': ['Rate of recovery for infected subjects'],
     'dkg_annotations': []},
    {'type': 'variable',

```

```

'name': 'σ',
'id': 'v21',
'text_annotations': [' Rate of recovery for infected subjectsNone'],
'dkg_annotations': []},
{'type': 'equation',
'latex': '{\dot{A}}(t)=\zeta I(t)-(\theta+\mu+\kappa)A(t)',
'id': 'e6723424166643005760',
'matches': {'A': ['v0', 'v3'],
't': ['v16', 'v12'],
'ζ': ['v13', 'v16'],
'I': ['v1', 'v16'],
'θ': ['v12', 'v16'],
'μ': ['v14', 'v15'],
'κ': ['v18', 'v19']}},
{'type': 'equation',
'latex': '{\hat{D}}(t)=\varepsilon I(t)-(\eta+\rho)D(t)',
'id': 'e10710427853041289346',
'matches': {'{\hat{D}}': ['v11', 'v16'],
't': ['v16', 'v12'],
'\x0barepsilon': ['v11', 'v12'],
'I': ['v1', 'v16'],
'\eta': ['v14', 'v15'],
'\rho': ['v19', 'v20'],
'D': ['v0', 'v2']}},
{'type': 'equation',
'latex': '{\dot{\bar{F}}}(t)\,,\,\,\,\longrightarrow\,,\,\,\tau\,,\,T(t)',
'id': 'e8173302260107437895',
'matches': {'\dot{\bar{F}}(t)': ['v15', 'v16'],
'\tau': ['v15', 'v16'],
'T(t)': ['v16', 'v5']}},
{'type': 'equation',
'latex': 'H(t)=i I(t)+\theta b(t)+\kappa d(t)+i R(t)+\sigma T(t)',
'id': 'e1717826786438107513',
'matches': {'H(t)': ['v6'],
'I(t)': ['v1'],
'b(t)': ['v9', 'v16'],
'd(t)': ['v16', 'v11'],
'R(t)': ['v4', 'v16'],
'T(t)': ['v16', 'v5'],
'i': ['v1', 'v8'],
'θ': ['v12', 'v16'],
'κ': ['v18', 'v19'],
'σ': ['v21', 'v19']}},
{'type': 'equation',
'latex': '\scriptstyle n=s q|a u_{1}+p u_{1}+s u_{1}+s u_{1})-(r+s+d v_{1})',
'id': 'e16597563706615027249',
'matches': {'n': ['v15', 'v16'],
'sq': ['v21', 'v19'],
'au_1': ['v8', 'v9'],
'pu_1': ['v20', 'v19'],
'su_1': ['v21', 'v15'],
'ru_1': ['v20', 'v16'],
'r': ['v4', 'v20'],
's': ['v0', 'v21'],
'dv_1': ['v8', 'v9']}},
{'type': 'equation',
'latex': 'R(t)=\eta D(t)+\theta A(t)-(\nu+\xi)R(t)',
'id': 'e10907236396390968726',
'matches': {'R(t)': ['v4', 'v16'],
'D(t)': ['v2'],
'A(t)': ['v8', 'v16'],
'η': ['v14', 'v16'],
'θ': ['v12', 'v16'],
'ν': ['v15', 'v16'],

```

```

    'ξ': ['v19', 'v16']]],
    {'type': 'equation',
     'latex': '\\\\delta(t)=-S(t)(a l(t)+\\theta D(t)+r A(t)+\\delta t(t)',
     'id': 'e16603981726015827811',
     'matches': {'δ': ['v11', 'v16'],
                  'S': ['v0', 'v1'],
                  'a': ['v8', 'v9'],
                  'l': ['v17', 'v18'],
                  'θ': ['v12', 'v16'],
                  'D': ['v0', 'v2'],
                  'r': ['v4', 'v20'],
                  'A': ['v0', 'v3'],
                  't': ['v16', 'v12']]],
    {'type': 'equation',
     'latex': '\\\\hat{T}(t)=\\mu A(t)+\\nu R(t)-(\\sigma+\\tau){\\hat{T}}(t)',
     'id': 'e11475613384250171865',
     'matches': {'T': ['v16', 'v12'],
                  'μ': ['v14', 'v15'],
                  'A': ['v0', 'v3'],
                  'ν': ['v15', 'v16'],
                  'R': ['v0', 'v1'],
                  'σ': ['v21', 'v19'],
                  'τ': ['v16', 'v12']}]

```

4. Getting a Petri net (as a pyascet) from code

Let's now turn our attention to code. We have a python function that describes the SIDARTHE dynamics:

```

In [66]: with open("../resources/jan_evaluation/scenario_2_sidarthe/sidarthe_code.py", "r") as
f:
    code = f.read()
    print(code)

# define SIDARTHE_model
def SIDARTHE_model(y, t, alpha, beta, gamma, delta, epsilon, mu, zeta, lamda, eta, rho,
theta, kappa, nu, xi, sigma, tau):
    S, I, D, A, R, T, H, E = y
    dSdt = -S*(alpha(t)*I + beta(t)*D + gamma(t)*A + delta(t)*R)
    dIdt = S*(alpha(t)*I + beta(t)*D + gamma(t)*A + delta(t)*R) - (epsilon(t) + zeta(t)
+ lamda(t))*I
    dDdt = epsilon(t)*I - (eta(t) + rho(t))*D
    dAdt = zeta(t)*I - (theta(t) + mu(t) + kappa(t))*A
    dRdt = eta(t)*D + theta(t)*A - (nu(t) + xi(t))*R
    dTdt = mu(t)*A + nu(t)*R - (sigma(t) + tau(t))*T
    dHdt = lamda(t)*I + rho(t)*D + kappa(t)*A + xi(t)*R + sigma(t)*T
    dEdt = tau(t)*T

    return dSdt, dIdt, dDdt, dAdt, dRdt, dTdt, dHdt, dEdt

```

Using calls to the public MIT API, we can get Petri net components (places, transitions, hypothesized arcs) from this piece of code.

```
In [67]: dict_petri = {"code": code, "gpt_key": GPT_KEY}
places = requests.post(API_ROOT + "petri/get_places", params=dict_petri).text
print(places)

["S"," I"," D"," A"," R"," T"," H"," E"]
```

```
In [68]: transitions = requests.post(API_ROOT + "petri/get_transitions", params=dict_petri).text
print(transitions)

["alpha"," beta"," gamma"," delta"," epsilon"," mu"," zeta"," lamda"," eta"," rho"," the
ta"," kappa"," nu"," xi"," sigma"," tau"]
```

```
In [69]: arcs = requests.post(API_ROOT + "petri/get_arcs", params=dict_petri).text
print(arcs)

[["S"," I"],["I"," D"],["I"," A"],["I"," R"],["D"," E"],["A"," R"],["A"," T"],["R","
H"],["T"," H"],["I"," H"],["D"," H"],["A"," H"],["R"," H"],["T"," E"]]
```

We can then convert these outputs into a py-acset (thanks to Justin Lieffers from Arizona for some of the conversion code and to Owen Lynch for the py-acset code!)

```
In [91]: dict_acset = {"places_str": places, "transitions_str": transitions, "arcs_str": arcs}

acset = requests.post(API_ROOT + "petri/get_pyacset", params=dict_acset).text

pyacset_s = acset
print(acset)

{"S":[{"sname":"S","uid":1}, {"sname":"I","uid":2}, {"sname":"D","uid":3}, {"sname":"A","uid":4}, {"sname":"R","uid":5}, {"sname":"T","uid":6}, {"sname":"H","uid":7}, {"sname":"E","uid":8}], "T":[{"tname":"alpha","uid":10}, {"tname":" beta","uid":11}, {"tname":" gamma","uid":12}, {"tname":" delta","uid":13}, {"tname":" epsilon","uid":14}, {"tname":" mu","uid":15}, {"tname":" zeta","uid":16}, {"tname":" lamda","uid":17}, {"tname":" eta","uid":18}, {"tname":" rho","uid":19}, {"tname":" theta","uid":20}, {"tname":" kappa","uid":21}, {"tname":" nu","uid":22}, {"tname":" xi","uid":23}, {"tname":" sigma","uid":24}, {"tname":" tau","uid":25}], "I":[{"it":1,"is":1}, {"it":2,"is":2}, {"it":3,"is":2}, {"it":4,"is":2}, {"it":5,"is":3}, {"it":6,"is":4}, {"it":7,"is":4}, {"it":8,"is":5}, {"it":9,"is":6}, {"it":10,"is":2}, {"it":11,"is":3}, {"it":12,"is":4}, {"it":13,"is":5}, {"it":14,"is":6}], "O":[{"ot":1,"os":2}, {"ot":2,"os":3}, {"ot":3,"os":4}, {"ot":4,"os":5}, {"ot":5,"os":8}, {"ot":6,"os":5}, {"ot":7,"os":6}, {"ot":8,"os":7}, {"ot":9,"os":7}, {"ot":10,"os":7}, {"ot":11,"os":7}, {"ot":12,"os":7}, {"ot":13,"os":7}, {"ot":14,"os":8}]}
```

```
In [92]: ast.literal_eval(pyacset_s)
```

```
Out[92]: {'S': [{'sname': 'S', 'uid': 1},
                {'sname': 'I', 'uid': 2},
                {'sname': 'D', 'uid': 3},
                {'sname': 'A', 'uid': 4},
                {'sname': 'R', 'uid': 5},
                {'sname': 'T', 'uid': 6},
                {'sname': 'H', 'uid': 7},
                {'sname': 'E', 'uid': 8}],
          'T': [{'tname': 'alpha', 'uid': 10},
                {'tname': 'beta', 'uid': 11},
                {'tname': 'gamma', 'uid': 12},
                {'tname': 'delta', 'uid': 13},
                {'tname': 'epsilon', 'uid': 14},
                {'tname': 'mu', 'uid': 15},
                {'tname': 'zeta', 'uid': 16},
                {'tname': 'lamda', 'uid': 17},
                {'tname': 'eta', 'uid': 18},
                {'tname': 'rho', 'uid': 19},
                {'tname': 'theta', 'uid': 20},
                {'tname': 'kappa', 'uid': 21},
                {'tname': 'nu', 'uid': 22},
                {'tname': 'xi', 'uid': 23},
                {'tname': 'sigma', 'uid': 24},
                {'tname': 'tau', 'uid': 25}],
          'I': [{'it': 1, 'is': 1},
                {'it': 2, 'is': 2},
                {'it': 3, 'is': 2},
                {'it': 4, 'is': 2},
                {'it': 5, 'is': 3},
                {'it': 6, 'is': 4},
                {'it': 7, 'is': 4},
                {'it': 8, 'is': 5},
                {'it': 9, 'is': 6},
                {'it': 10, 'is': 2},
                {'it': 11, 'is': 3},
                {'it': 12, 'is': 4},
                {'it': 13, 'is': 5},
                {'it': 14, 'is': 6}],
          'O': [{'ot': 1, 'os': 2},
                {'ot': 2, 'os': 3},
                {'ot': 3, 'os': 4},
                {'ot': 4, 'os': 5},
                {'ot': 5, 'os': 8},
                {'ot': 6, 'os': 5},
                {'ot': 7, 'os': 6},
                {'ot': 8, 'os': 7},
                {'ot': 9, 'os': 7},
                {'ot': 10, 'os': 7},
                {'ot': 11, 'os': 7},
                {'ot': 12, 'os': 7},
                {'ot': 13, 'os': 7},
                {'ot': 14, 'os': 8}]}
```

5. Linking the annotations to the py-acset and paper info

Finally, we bring everything together: for every place and transition in the pyacset, let's map it to the annotations from earlier:

```
In [93]: dct3 = {"pyacset_str":pyacset_s, "annotations_str":full_json_str, "info_str":info_s}
r3 = requests.post(API_ROOT + "annotation/link_annos_to_pyacset/", params=dct3)
print(r3)
```

<Response [200]>

```
In [94]: ast.literal_eval(r3.text)
```



```

Out[94]: {'1': {'type': 'variable',
  'name': 'S',
  'id': 'v0',
  'text_annotations': ['Susceptible (uninfected)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ido:0000514', 'susceptible population']],
  'equation_annotations': {'\\delta(t)=-S(t)(a l(t)+\\theta D(t)+r A(t)+\\delta t(t)':
    ['S']}},
  'file': '41591_2020_Article_883.pdf',
  'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
  '2': {'type': 'variable',
  'name': 'I',
  'id': 'v1',
  'text_annotations': ['Infected (asymptomatic or pauci-symptomatic infected, undetecte
d)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']],
  'equation_annotations': {'{\\dot{A}}(t)=\\zeta I(t)-(\\theta+\\mu+\\kappa)A(t)':
    ['I']},
  '{\\hat{D}}(t)=\\varepsilon I(t)-(\\eta+\\rho)D(t)': ['I']},
  'file': '41591_2020_Article_883.pdf',
  'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
  '3': {'type': 'variable',
  'name': 'D',
  'id': 'v2',
  'text_annotations': ['Diagnosed (asymptomatic infected, detected)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']],
  'equation_annotations': {'{\\hat{D}}(t)=\\varepsilon I(t)-(\\eta+\\rho)D(t)': ['D'],
    '\\delta(t)=-S(t)(a l(t)+\\theta D(t)+r A(t)+\\delta t(t)': ['D']},
  'file': '41591_2020_Article_883.pdf',
  'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
  '4': {'type': 'variable',
  'name': 'A',
  'id': 'v3',
  'text_annotations': ['Ailing (symptomatic infected, undetected)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']],
  'equation_annotations': {'{\\dot{A}}(t)=\\zeta I(t)-(\\theta+\\mu+\\kappa)A(t)':
    ['A']},
  '\\delta(t)=-S(t)(a l(t)+\\theta D(t)+r A(t)+\\delta t(t)': ['A'],
  '{\\hat{T}}(t)=\\mu A(t)+\\nu R(t)-(\\sigma+\\tau){\\hat{T}}(t)': ['A']},
  'file': '41591_2020_Article_883.pdf',
  'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
  '5': {'type': 'variable',
  'name': 'R',
  'id': 'v4',
  'text_annotations': ['Recognized (symptomatic infected, detected)'],
  'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
    ['ncit:C28554', 'Dead']],
  'equation_annotations': {'{\\hat{T}}(t)=\\mu A(t)+\\nu R(t)-(\\sigma+\\tau){\\hat{T}}
(t)': []},
  'file': '41591_2020_Article_883.pdf',
  'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
  '6': {'type': 'variable',
  'name': 'T',
  'id': 'v5',
  'text_annotations': ['Threatened (infected with life-threatening symptoms, detecte
d)'],
  'dkg_annotations': [['ido:0000511', 'infected population'],
    ['ncit:C171133', 'COVID-19 Infection']],
  'equation_annotations': {'{\\hat{T}}(t)=\\mu A(t)+\\nu R(t)-(\\sigma+\\tau){\\hat{T}}
(t)': []},

```

```

'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'7': {'type': 'variable',
'name': 'H',
'id': 'v6',
'text_annotations': ['Healed (recovered)'],
'dkg_annotations': [['ncit:C171133', 'COVID-19 Infection'],
['ncit:C28554', 'Dead']],
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'8': {'type': 'variable',
'name': 'E',
'id': 'v7',
'text_annotations': ['Extinct (dead)'],
'dkg_annotations': [['ido:0000511', 'infected population'],
['ncit:C171133', 'COVID-19 Infection']],
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'10': {'type': 'variable',
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'id': 'v8',
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single contact multiplied by the average number of contacts per person)'],
'dkg_annotations': [],
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'11': {'type': 'variable',
'name': 'β',
'id': 'v9',
'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
'dkg_annotations': [['doid:0080928', 'dialysis-related amyloidosis'],
['vo:0005114', 'β-propiolactone-inactivated SARS-CoV vaccine']],
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'12': {'type': 'variable',
'name': 'γ',
'id': 'v10',
'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)'],
'dkg_annotations': [['askemo:0000013', 'recovery rate'],
['vo:0004915', 'vaccine specific interferon-γ immune response']],
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'13': {'type': 'variable',
'name': 'δ',
'id': 'v11',
'text_annotations': ['Transmission rate (the probability of disease transmission in a
single contact multiplied by the average number of contacts per person)ε'],
'dkg_annotations': [['askemo:0000011', 'progression rate'],
['vo:0005123', 'VSVΔG-MERS vaccine']],
'equation_annotations': {'\\delta(t)=-S(t)(a l(t)+\\theta D(t)+r A(t)+\\delta t(t)':
['δ']}},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'14': {'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'15': {'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'16': {'type': 'variable',
'name': 'ζ',
'id': 'v13',
'text_annotations': ['probability rate at which an infected subject not aware of bein
g infected develops clinically relevant symptoms'],

```

```

'dkg_annotations': [],
'equation_annotations': {'{\dot{A}}(t)=\zeta I(t)-(\theta+\mu+\kappa)A(t)':
['\zeta']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'17': {'type': 'variable',
'name': '\lambda',
'id': 'v17',
'text_annotations': ['Rate of recovery for infected subjects'],
'dkg_annotations': [],
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'18': {'type': 'variable',
'name': '\eta',
'id': 'v14',
'text_annotations': ['probability rate at which an infected subject aware of being in
fected develops clinically relevant symptoms\mu']},
'dkg_annotations': [],
'equation_annotations': {'R(t)=\eta D(t)+\theta A(t)-(\nu+\xi)R(t)': ['\eta']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'19': {'type': 'variable',
'name': '\rho',
'id': 'v20',
'text_annotations': ['Rate of recovery for infected subjects'],
'dkg_annotations': [],
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'20': {'type': 'variable',
'name': '\theta',
'id': 'v12',
'text_annotations': ['probability rate of detection relative to symptomatic cases'],
'dkg_annotations': [],
'equation_annotations': {'{\dot{A}}(t)=\zeta I(t)-(\theta+\mu+\kappa)A(t)':
['\theta']},
'H(t)=i I(t)+\theta b(t)+\kappa d(t)+i R(t)+\sigma T(t)': ['\theta'],
'R(t)=\eta D(t)+\theta A(t)-(\nu+\xi)R(t)': ['\theta'],
'\delta(t)=-S(t)(a l(t)+\theta D(t)+r A(t)+\delta t(t)': ['\theta']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'21': {'type': 'variable',
'name': '\kappa',
'id': 'v18',
'text_annotations': ['Rate of recovery for infected subjects'],
'dkg_annotations': [],
'equation_annotations': {'{\dot{A}}(t)=\zeta I(t)-(\theta+\mu+\kappa)A(t)':
['\kappa']},
'H(t)=i I(t)+\theta b(t)+\kappa d(t)+i R(t)+\sigma T(t)': ['\kappa']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'22': {'type': 'variable',
'name': 'v',
'id': 'v15',
'text_annotations': ['Rate at which detected infected subjects develop life-threateni
ng symptoms'],
'dkg_annotations': [],
'equation_annotations': {'R(t)=\eta D(t)+\theta A(t)-(\nu+\xi)R(t)': ['v'],
'{\hat{T}}(t)=\mu A(t)+\nu R(t)-(\sigma+\tau){\hat{T}}(t)': ['v']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'},
'23': {'type': 'variable',
'name': '\xi',
'id': 'v19',
'text_annotations': ['Rate of recovery for infected subjects'],

```

```

'dkg_annotations': [],
'equation_annotations': {'R(t)=\\eta D(t)+\\theta A(t)-(\\nu+\\xi)R(t)': ['\\xi']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7',
'24': {'type': 'variable',
'name': '\\sigma',
'id': 'v21',
'text_annotations': ['Rate of recovery for infected subjectsNone'],
'dkg_annotations': [],
'equation_annotations': {'H(t)=i I(t)+\\theta b(t)+\\kappa d(t)+i R(t)+\\sigma T(t)':
['\\sigma'],
'\\hat{T}(t)=\\mu A(t)+\\nu R(t)-(\\sigma+\\tau)\\hat{T}(t)': ['\\sigma']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7',
'25': {'type': 'variable',
'name': '\\tau',
'id': 'v16',
'text_annotations': ['Mortality rate for infected subjects with life-threatening symptoms'],
'dkg_annotations': [],
'equation_annotations': {'\\hat{T}(t)=\\mu A(t)+\\nu R(t)-(\\sigma+\\tau)\\hat{T}(t)': ['\\tau']},
'file': '41591_2020_Article_883.pdf',
'doi': 'https://doi.org/10.1038/s41591-020-0883-7'}}

```

Data in this format can be ingested, visualized and edited by TA4! 

6. Interacting with the University of Arizona codepaths

The University of Arizona team can also produce an annotated py-acset as an output. We can integrate the two outputs by matching on the names of places and transitions, to get a more complete picture of the model. The metadata extracted by both teams can then be accessible by using the associated uid of each place/transition as a key into the metadata JSON file.