fig setup

April 5, 2022

1 Figure: Experimental setup and inference procedure

```
[1]: import numpy as np
  import pandas as pd
  import scipy.stats as stats
  import scipy.optimize as optimize
  import pymc3 as pm
  import arviz as az
  import theano.tensor as tt

import matplotlib.pyplot as plt
  import matplotlib.gridspec as gridspec
  import matplotlib.patches as mpatches
  import matplotlib.lines as mlines
  import seaborn as sns; sns.set_theme(style='ticks', context='paper');

%reload_ext watermark
%watermark -a "Mathieu Baltussen" -d -t -u -v -iv
```

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Python implementation: CPython Python version : 3.9.5 IPython version : 7.28.0

seaborn: 0.11.1pandas: 1.2.4arviz: 0.11.4scipy: 1.6.2pymc3: 3.11.4

sys : 3.9.5 | packaged by conda-forge | (default, Jun 19 2021, 00:32:32)

[GCC 9.3.0]

matplotlib: 3.4.2
numpy : 1.20.3
theano : 1.1.2

1.1 Helper functions for plotting

```
[2]: XSIZE = 7 \#inch
     YSIZE = XSIZE/np.sqrt(2) #inch
     def savefig(name):
         """Helper function to save figures in desired formats"""
         plt.savefig(f"../figures/{name}.svg")
         plt.savefig(f"../figures/{name}.png", dpi=300)
     def generate_figure(n_col, n_row):
         """ Helper function to generate gridspec figures"""
         DX = XSIZE/n_col
         DY = YSIZE/n_col
         YLENGTH = n_row*DY
         fig = plt.figure(figsize=(XSIZE, YLENGTH), constrained_layout=True)
         gs = fig.add_gridspec(n_row, n_col)
         return fig, gs
     def plot_reactor(ax, input_substrates, output_substrates, enzymes, r_enzymes=0.
      \hookrightarrow 1):
         """ Helper function to plot reactor schematics with inputs, outputs, an_{\!\!\perp}
      ⇔encapsulated enzymes"""
         WIDTH = 0.55
         HEIGHT = 0.45
         reactor = mpatches.FancyBboxPatch(
             ((1 - WIDTH) / 2, (1 - HEIGHT) / 2),
             width=WIDTH,
             height=HEIGHT,
             fill=False,
             edgecolor="black",
             linewidth=3,
             boxstyle=mpatches.BoxStyle("Round", pad=0.0, rounding_size=0.15),
         )
         reactor.set clip on(False)
         ax.add_patch(reactor)
         for i, substrate in enumerate(input_substrates):
             ax.annotate(
                 text=substrate,
                 xy = ((1 - WIDTH) / 2, 0.5 - (len(input_substrates) - 1) * 0.1/2 + i *_{\sqcup}
      \rightarrow 0.1),
                 xytext=(0.1, 0.5 - (len(input_substrates)-1) * 0.1/2 + i * 0.1),
                 arrowprops={"lw": 2, "arrowstyle": "-", "color": "black"},
                 verticalalignment="center",
                 horizontalalignment='right',
```

```
fontsize=12,
           fontweight="medium",
   for i, substrate in enumerate(output_substrates):
       ax.annotate(
           text=substrate,
           xy=((1 + WIDTH) / 2, 0.5 - (len(output_substrates)-1) * 0.1/2 + i *_{\sqcup}
\rightarrow 0.1),
           xytext=((1 + WIDTH) / 2 + 0.15, 0.5 - (len(output_substrates)-1) *_{\sqcup}
0.1/2 + i * 0.1,
           arrowprops={
                        "arrowstyle": "<-",'connectionstyle':"arc3",</pre>
                        "lw": 2, "color": "black",
           },
           verticalalignment="center",
           horizontalalignment='left',
           fontsize=12,
           fontweight="medium",
       )
   enzyme_colors = {'HK': "CO", 'GDH': "C1", "G6PDH": "C2", 'Tr': 'C3' }
   indices = np.arange(0, len(enzymes), dtype=float) + 0.5
   r = np.sqrt(indices/len(enzymes))
   theta = np.pi * (1 + 5**0.5) * indices
   if len(enzymes) == 1:
       x_{coords} = np.array([0.5])
       y_coords = np.array([0.5])
   else:
       x_{coords} = r*np.cos(theta)*WIDTH/2.9 + 0.5
       y_coords = r*np.sin(theta)*HEIGHT/2.9 + 0.5
   for i, enzyme in enumerate(enzymes):
       with sns.color_palette("Pastel1"):
           if len(enzyme) > 3:
               FS = (12-len(enzyme))
           else:
               FS = 12
           enzyme_patch = mpatches.Circle((x_coords[i], y_coords[i]),__
→radius=r_enzymes, edgecolor="black",linewidth=1, fc=enzyme_colors[enzyme])
           enzyme_patch.set_clip_on(False)
           enzyme_label = ax.annotate(enzyme, xy=(x_coords[i], y_coords[i]),__
→va='center_baseline', ha='center', fontsize=FS, fontweight="medium")
           ax.add_patch(enzyme_patch)
   return ax
```

1.2 Data loading

```
[4]: """ Time-series data (selected subset)"""

CEKS33_timedata = pd.read_csv("../data/CEKS33_time.csv")

period_1 = CEKS33_timedata.time.between(2500, 24300)

CEKS33_timedata = CEKS33_timedata[period_1]

CEKS33_timedata = CEKS33_timedata.assign(time = CEKS33_timedata/60)

""" Steady-state data (selected subset, no inhibitor)"""

data = pd.read_csv("../data/CEKS33.csv")

kf = 0.125  # minute^-1

E = 0.012

data = data.assign(kf=kf, Tr=E)

data = data[data.AAA == 0]
```

1.3 Probabilistic model (PyMC3)

```
[5]: with pm.Model() as model:
         k_cat = pm.Uniform("k_cat", 0, 500)
         K_M = pm.Uniform("K_M", 0, 500)
         sigma = pm.Exponential("sigma", 10)
         S in = data["R"].values
         P_obs = data["AMC"].values
         S_{obs} = S_{in} - P_{obs} \# Substrate concentration inside reactor determined_{\square}
      →via stoichiometric conservation at steady-state
         E = data["Tr"].values
         kf = data["kf"].values
         # Inference of probabilistic model at steady-state conditions
         P = pm.Normal(
             "obs", mu=k_cat * E * S_obs / (kf * (K_M + S_obs)), sigma=sigma,__
      \rightarrowobserved=P_obs
         idata = pm.sample(
             1000,
             tune=1000,
             cores=4,
             step=pm.NUTS(target_accept=0.95),
             return_inferencedata=True,
         )
```

```
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [sigma, K_M, k_cat]
<IPython.core.display.HTML object>
```

Sampling 4 chains for 1_000 tune and 1_000 draw iterations (4_000 + 4_000 draws total) took 5 seconds.

The number of effective samples is smaller than 25% for some parameters.

1.4 Statistical model (SciPy)

```
[6]: kf = 0.125 \# minute^{-1}
     E = 0.012
     S_{in\_range} = np.linspace(0, 600, 100)
     def steady_state_model(S_in, k_cat,K_M):
         V_M = k_cat * E
         Vk = V_M/kf
         # Explicit equation form of steady-state product-concentration is used.
         return 0.5*(Vk + K_M + S_{in}) - 0.5*np.sqrt((Vk + K_M + S_{in})**2 - 4*Vk*S_{in})
     popt, pcov = optimize.curve_fit(steady_state_model, data["R"], data["AMC"])
     perr = np.sqrt(np.diag(pcov))
     residuals = data["AMC"] - steady_state_model(data["R"], *popt)
     ss_residuals = np.sum(residuals**2)
     ss_total = np.sum((data["AMC"] - np.mean(data["AMC"]))**2)
     r_squared = 1 - (ss_residuals/ss_total)
     print("=== Least-squares kinetic parameter values ===")
     print(f''k_cat = \{popt[0]:.1f\} +- \{perr[0]:.1f\}'')
     print(f''K_M = \{popt[1]:.1f\} +- \{perr[1]:.1f\}'')
     print(f"R^2 = \{r\_squared:.5f\}")
    === Least-squares kinetic parameter values ===
    k_cat = 102.6 +- 4.3
    K_M = 121.7 + 14.4
    R^2 = 0.99236
```

1.5 Sampling of the posterior predictive distribution

<IPython.core.display.HTML object>

1.6 Creation of the figure

```
[8]: fig, gs = generate_figure(3,3)
     ax_1 = fig.add_subplot(gs[0,0])
     ax 2 = fig.add subplot(gs[0,1:])
     ax_3 = fig.add_subplot(gs[1,0])
     ax_4 = fig.add_subplot(gs[1,1])
     ax_1.axis("off")
     ax_1.set_ylim(0.1,0.9)
     ax_1.set_aspect("equal")
     ax_1.text(-0.5, 1.0, 'A', transform=ax_1.transAxes, weight="bold", size=12)
     plot_reactor(ax_1, ['R-AMC'], ['AMC'], ['Tr'], r_enzymes=0.12)
     ax_2.text(-0.15, 1.0, 'B', transform=ax_2.transAxes, weight="bold", size=12)
     ax_2.plot(CEKS33_timedata.time, CEKS33_timedata.signal)
     ax_2.set_xlabel("Time (min.)")
     ax_2.set_ylabel("Signal (a.u.)")
     ax_2.set_xlim(40)
     ax 2.set ylim(0)
     ax_2.fill_betweenx([0,200], 5000/60, 5600/60, alpha=0.2, color='black')
     ax_2.fill_betweenx([0,200], 9200/60, 9600/60, alpha=0.2, color='black')
     ax_2.fill_betweenx([0,200], 12730/60, 13240/60, alpha=0.2, color='black')
     ax_2.fill_betweenx([0,200], 23560/60, 24300/60, alpha=0.2, color='black')
     ax_2.fill_betweenx([0,200], 20000/60, 20200/60, alpha=0.2, color='black')
     sns.despine(ax=ax_2)
     ax_3.text(-0.4, 1.0, 'C', transform=ax_3.transAxes, weight="bold", size=12)
     ax_3.scatter(data.R, data.AMC, ec='black')
     ax_3.plot(S_in_range, steady_state_model(S_in_range, *popt), "--", color="C3")
     ax_3.set_xlim(0, 600)
     ax_3.set_ylim(0, 10)
     ax_3.set_xlabel(r"$[$R-AMC$]_{in}^(\mu M)$")
     ax_3.set_ylabel(r"$[$AMC$]_{ss}^(\mu M)$")
     sns.despine(ax=ax_3)
     ax_4.text(-0.4, 1.0, 'D', transform=ax_4.transAxes, weight="bold", size=12)
     ax_4.scatter(data.R, data.AMC, ec='black',zorder=10)
     ax_4.fill_between(S_in_range, post_pred_qs[0], post_pred_qs[4], color="C4", __
     \rightarrowalpha=0.6)
     ax_4.fill_between(S_in_range, post_pred_qs[1], post_pred_qs[3], color="C4", __
     \rightarrowalpha=0.8)
     ax_4.plot(S_in_range, post_pred_qs[2], "--", color="black", )
     ax_4.set_xlim(0, 600)
     ax_4.set_ylim(0, 10)
```

```
ax_4.set_xlabel(r"$[$R-AMC$]_{in}^(\mu M)$")
ax_4.set_ylabel(r"$[$AMC$]_{ss}^(\mu M)$")
sns.despine(ax=ax_4)
ax_5 = fig.add_subplot(gs[1,2])
sns.kdeplot(data=posterior_df,
            x='k_cat', y='K_M', fill=True, cmap="Purples"
ax 5.set ylim(80, 180)
ax_5.set_xlim(80, 130)
ax_5.set_ylabel(r"$K_{M}^{(\underline{M} M)}")
ax_5.set_xlabel(r"$k_{cat}^{min^{-1}})$")
ax_5.text(-0.3, 1.0, 'E', transform=ax_5.transAxes, weight="bold", size=12)
print(f''k_cat = \{popt[0]:.1f\} +- \{perr[0]:.1f\}'')
print(f"K_M = {popt[1]:.1f} +- {perr[1]:.1f}")
print(f"R^2 = \{r\_squared:.5f\}")
ax_5.errorbar(popt[0], popt[1], perr[0], perr[1], color='C3', capsize=2.0, __
\rightarrowms=200, mfc='C3', mec='C3')
ax_6 = fig.add_subplot(gs[2,0])
ax_7 = fig.add_subplot(gs[2,1])
ax_8 = fig.add_subplot(gs[2,2])
sns.kdeplot(posterior_df["k_cat"], ax=ax_6, fill=True, color='C4')
ax_6.vlines(popt[0], 0, 1, linestyles="--", colors='C3')
sns.despine(ax=ax_6)
ax_6.set_xlim(0, 200)
ax 6.set ylim(0, 0.10)
ax_6.set_ylabel(r"$P(k_{cat})$")
ax_6.set_xlabel(r"$k_{cat}^{min^{-1}}\mu L^{-1})$")
sns.kdeplot(posterior_df["K_M"], ax=ax_7, fill=True, color='C4')
sns.despine(ax=ax 7)
ax_7.vlines(popt[1], 0, 1, linestyles="--", colors='C3')
ax_7.set_ylim(0, 0.03)
ax_7.set_xlim(0)
ax_7.set_ylabel(r"$P(K_{M})$")
ax_7.set_xlabel(r"$K_{M}^{(\underline{M})^{"}})
sns.kdeplot(posterior_df["sigma"], ax=ax_8, fill=True, color='C4')
sns.despine(ax=ax_8)
ax_8.set_xlim(0)
ax_8.set_ylabel(r"$P(\sigma)$")
```

```
ax_8.set_xlabel(r"$\sigma~(\mu M)$")
ax_6.text(-0.4, 0.95, 'F', transform=ax_6.transAxes, weight="bold", size=12)
savefig("fig_setup")
plt.show()
```

 $k_cat = 102.6 +- 4.3$ $K_M = 121.7 +- 14.4$ $R^2 = 0.99236$

