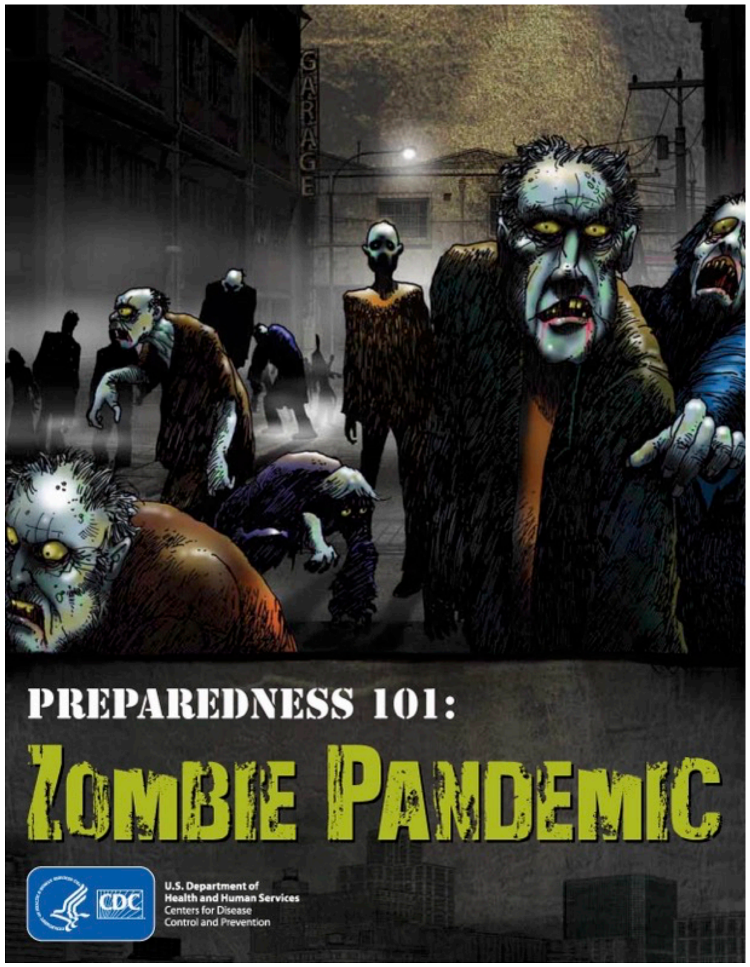
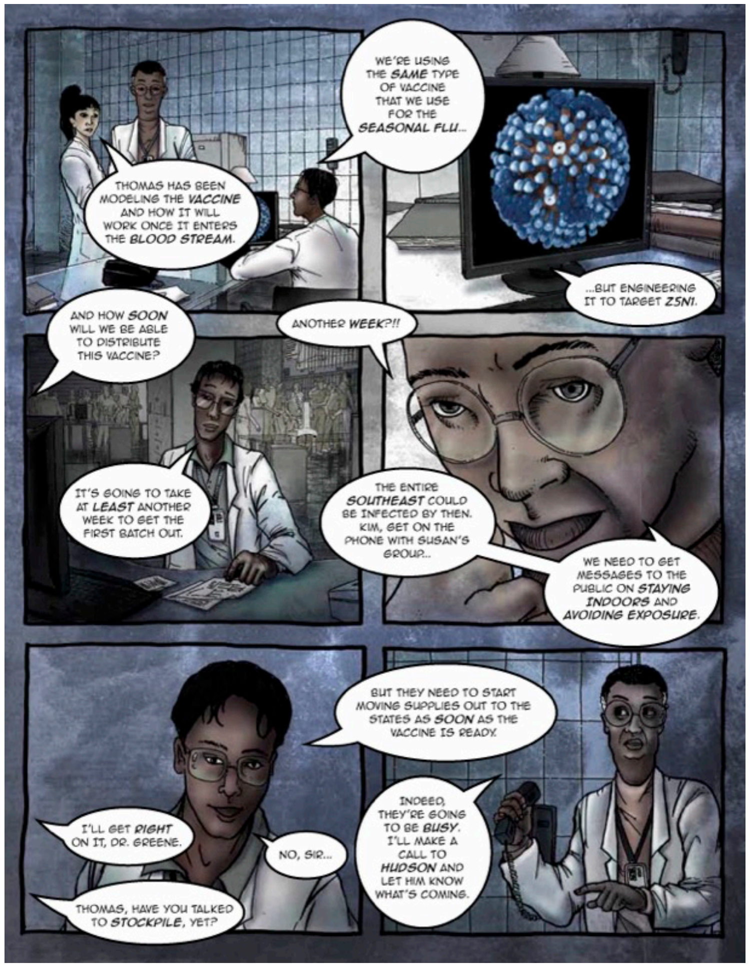
ZOMBIE PANDEMIC!

IDM modeling demo of a Zombie pandemic using the Starsim framework. When Zombies attack, based on information from the CDC and cutting edge research from resources including zombieresearchsociety.com and Zombiepedia.


GARAGE
PREPAREDNESS 101:
ZOMBIE PANDEMIC
CDC
U.S. Department of Health and Human Services
Centers for Disease Control and Prevention

UH... MRS. CLEMENTS YOU DON'T LOOK SO GOOD.
MAYBE YOU SHOULD GO LIE DOWN AND I'LL BRING SNOWBALL BACK FOR YOU.
AAARGH!
MRS. CLEMENTS!!
URRR!
?!!
IT'S ME TODD, YOUR NEIGHBOR!! YOU REALLY DON'T LOOK WELL!! WHY DON'T YOU GO BACK HOME...
...AND I'LL BRING SNOWBALL BY IN THE MORNING!
URRK!
AAH!!
OKAY, MAYBE NOT... !
GRRR!!
RROWWR!!


WE'RE USING THE SAME TYPE OF VACCINE THAT WE USE FOR THE SEASONAL FLU...
THOMAS HAS BEEN MODELING THE VACCINE AND HOW IT WILL WORK ONCE IT ENTERS THE BLOOD STREAM.
...BUT ENGINEERING IT TO TARGET Z5N1.
AND HOW SOON WILL WE BE ABLE TO DISTRIBUTE THIS VACCINE?
ANOTHER WEEK?!!
IT'S GOING TO TAKE AT LEAST ANOTHER WEEK TO GET THE FIRST BATCH OUT.
THE ENTIRE SOUTHEAST COULD BE INFECTED BY THEN. KIM, GET ON THE PHONE WITH SUSAN'S GROUP...
WE NEED TO GET MESSAGES TO THE PUBLIC ON STAYING INDOORS AND AVOIDING EXPOSURE.
BUT THEY NEED TO START MOVING SUPPLIES OUT TO THE STATES AS SOON AS THE VACCINE IS READY.
I'LL GET RIGHT ON IT, DR. GREENE.
NO, SIR...
INDEED, THEY'RE GOING TO BE BUSY. I'LL MAKE A CALL TO HUDSON AND LET HIM KNOW WHAT'S COMING.
THOMAS, HAVE YOU TALKED TO STOCKPILE, YET?

Let's start by importing some basic packages

- **Starsim** is our new agent-based disease modeling framework. Starsim source code is open source and freely available. See also our emerging online documentation and tutorials.

- **zombie** is all the stuff we'll need to do zombie simulations
- Other imports are for numerical operations (**numpy**, **pandas**), convenience (**sciris**), and plotting (**seaborn**, **matplotlib**)

In [ ]:
```
%matplotlib inline
%load_ext autoreload
%autoreload 2

import starsim as ss # starsim is the Starsim framwork
from zombie import * # zombie is a custom zombie library, see zombie.py

# Numerical librarires and utilities
import numpy as np
import pandas as pd
import sciris as sc

# Plotting libraries
import seaborn as sns
from matplotlib import pyplot
import matplotlib.pyplot as plt
pyplot.rcParams['figure.dpi'] = 120

import warnings
warnings.simplefilter(action='ignore', category=FutureWarning)
```

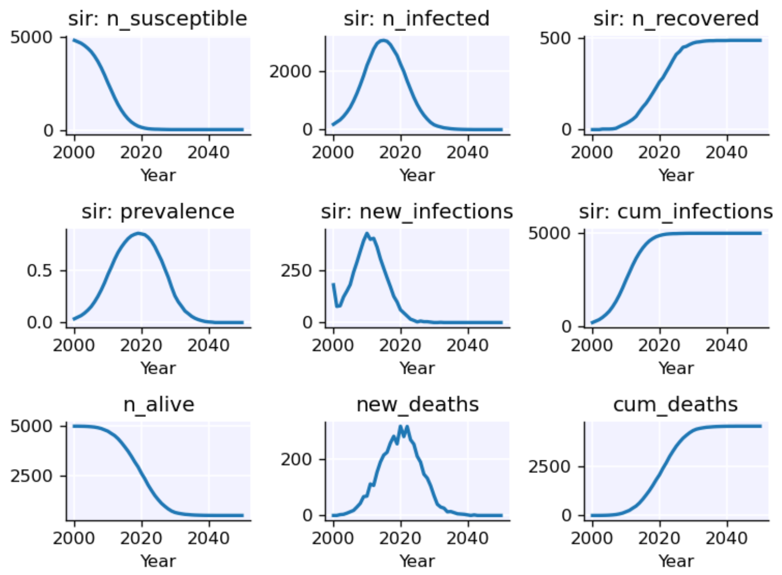
```
The autoreload extension is already loaded. To reload it, use:
  %reload_ext autoreload
```

Basic SIR simulation using the Starsim framework

- We represent the population using 5,000 agents
- 3% are selected at random to be "seed" infections.
- The disease will transmit on a "random" network in the sense that contacts between agents will be recreated on every time step. The number of contacts will be Poisson distributed with a mean of 4.
- The simulation runs in a fraction of a second.
- We then plot some default channels.

In [ ]:
```
people = ss.People(n_agents=5_000)

sir_pars = dict(
    beta = 0.1,
    init_prev = ss.bernoulli(p=0.03),
    dur_inf = ss.weibull(c=3, scale=10),
    p_death = ss.bernoulli(p=lambda _, sim, uids: sim.people.age[uids]/20),
)
sir = ss.SIR(sir_pars)

network = ss.RandomNet(n_contacts=ss.poisson(lam=4))
sim = ss.Sim(people=people, diseases=sir, networks=network)
sim.run()
sim.plot();
```

```
Initializing sim with 5000 agents
  Running 2000.0 ( 0/51) (0.02 s)  ———————————————————— 2%
  Running 2010.0 (10/51) (0.04 s)  ••••———————————————— 22%
  Running 2020.0 (20/51) (0.07 s)  ••••••••———————————— 41%
  Running 2030.0 (30/51) (0.09 s)  ••••••••••••———————— 61%
  Running 2040.0 (40/51) (0.10 s)  ••••••••••••••••———— 80%
  Running 2050.0 (50/51) (0.11 s)  •••••••••••••••••••• 100%
```



But we want ZOMBIES!!!

Zombie is an extension of the SIR disease that adds some important features:

- **p_fast** is the probability of zombie being fast, choosing 10% here based on my research. Fast zombies more contacts than slow zombies.
- **dur_fast** is the duration of a zombie being fast before reverting to slow, default 1000 years.

- **dur_inf** is the duration of zombie infection, default is 1000 years. Once a zombie, always a zombie!
- **p_symptomatic** is the probability of showing symptoms, default assumption is 100%
- **p_death_on_zombie_infection** is the probability of death when converting to a zombie, 50% might be a bit high based on my research!

A deep meta-analysis of recent and historical literature reveals that there are at least three ways to become a zombie:

1. Be attacked by a zombie, and survive!
2. Die of natural causes and be transformed into a zombie upon death
3. Acquire zombiism congenitally through pre-natal transmission.

DeathZombies is an extension of the base **Deaths** demographic class that captures people at natural death and potentially makes them zombies

- **p_zombie_on_natural_death** is the probability of becoming a zombie on death due to natural causes

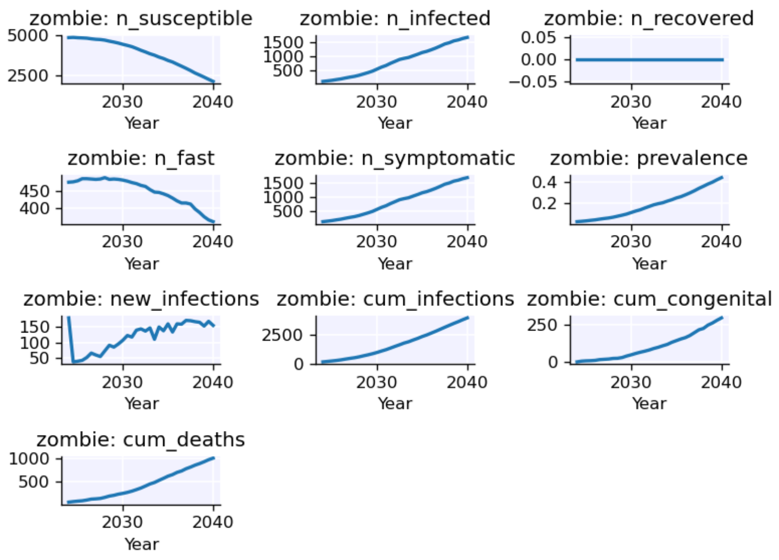
The **Pregnancy** and **MaternalNet** modules work together to simulate pregnancy, forming network connections between mothers and pre-birth children on which disease (zombie) transmission can occur.

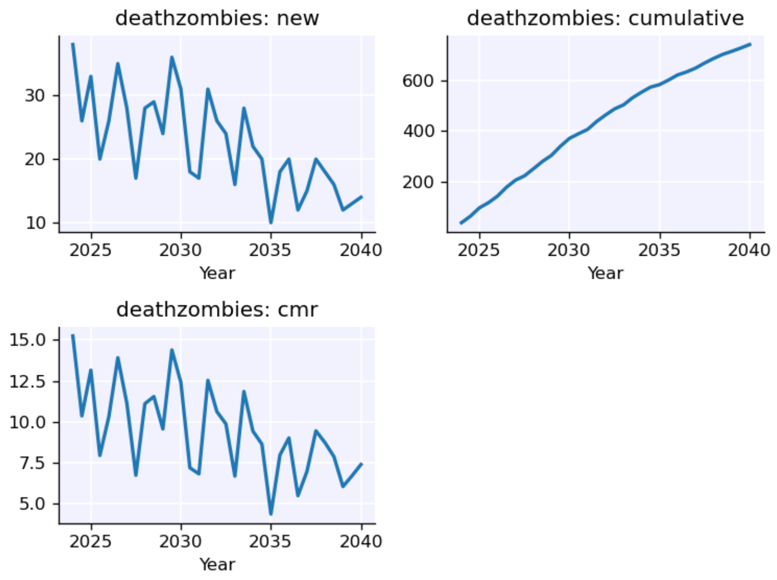
We include an intervention, **KillZombies** that kills only *symptomatic* zombies at a rate of 0.5/year.

Configuring and running the simulation from 2024 to 2040 takes less than one second. Showing built-in plots, although it is easy to generate alternative figures stored in sim.results.

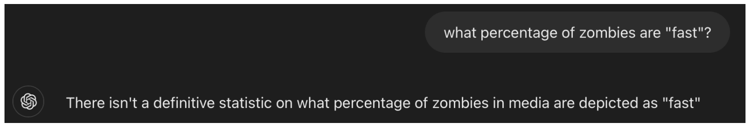
In [ ]:

```python
people = ss.People(n_agents=5_000) # People, as before

# Configure and create an instance of the Zombie class
zombie_pars = dict(
    init_prev = 0.03,
    beta = {'random': 0.05, 'maternal': 10},
    p_fast = ss.bernoulli(p=0.1),
    p_death_on_zombie_infection = ss.bernoulli(p=0.25),
    p_symptomatic = ss.bernoulli(p=1.0),
)
zombie = Zombie(zombie_pars)

# This function allows the lambda parameter of the poisson distribution usec
# n_contacts to vary based on agent characteristics, a key feature of Starsi
def choose_degree(self, sim, uids):
    mean_degree = np.full(fill_value=4, shape=len(uids)) # Default value is
    is_fast = (sim.diseases['zombie'].infected[uids]) & (sim.diseases['zombi
    mean_degree[is_fast] = 50 # Fast zombies get 50
    return mean_degree

# We create two network layers, random and maternal
networks = [
    ss.RandomNet(n_contacts=ss.poisson(lam=choose_degree)),
    ss.MaternalNet()
]

# Configure and create demographic modules
death_pars = dict(
    death_rate = 15, # per 1,000
    p_zombie_on_natural_death = ss.bernoulli(p=0.2),
)
deaths = DeathZombies(**death_pars)
births = ss.Pregnancy(fertility_rate=175) # per 1,000 women 15-49 annually
demog = [births, deaths]

# Create an intervention that kills symptomatic zombies
interventions = KillZombies(year=2024, rate=0.1)

# And finally bring everything together in a sim
sim_pars = dict(start=2024, end=2040, dt=0.5, verbose=0)
sim = ss.Sim(sim_pars, people=people, diseases=zombie, networks=networks, de

# Run the sim and plot results
sim.run()
sim.plot('zombie')
sim.plot('deathzombies');
```





But what do we actually know about zombies?



what percentage of zombies are "fast"?

There isn't a definitive statistic on what percentage of zombies in media are depicted as "fast"

Empirical data on Zombies is sparse. Here we compare default assumptions (same as above) to several alternatives:

	Scenario Name	Configuration
0	Default assumptions	Same as above
1	More fast zombies	75% of zombies are fast, as opposed to 25%
2	Fast-->slow zombies	75% of zombies start fast, but slow down after about 2y
3	Shorter infectious period	Zombies remain infectious for about 5y
4	All zombies asymptomatic	Zombies are asymptomatic (hmm?!)
5	Less death on zombie infection	10% die on zombie infection, down from 25%
6	Half zombie on natural death	50% of natural deaths transform into a zombie
7	REALLY BAD	A worst case scenario

Define the scenarios

In [ ]:
```
scens = {
    'Default assumptions': {},
    'More fast zombies': {'zombie_pars': dict(p_fast=ss.bernoulli(p=0.75))},
    'Fast-->Slow zombies': {'zombie_pars': dict(p_fast=ss.bernoulli(p=0.75),
    'Shorter infectious period': {'zombie_pars': dict(dur_inf=ss.normal(loc=
    'All zombies asymptomatic': {'zombie_pars': dict(p_symptomatic=ss.bernou
    'Less death on zombie infection': {'zombie_pars': dict(p_death_on_zombie
    'Half zombie on natural death': {'death_pars': dict(p_zombie_on_natural_
    'REALLY BAD': {'zombie_pars': dict(p_fast=ss.bernoulli(p=1.0), p_sympton
                   'death_pars': dict(p_zombie_on_natural_death=ss.bernoulli
}
```

Now make a function that configures and runs a zombie

simulation, taking inputs from the user. When the run is complete, results are returned as a dataframe.

```
In [ ]: def run_zombies(scen, rand_seed, zombie_pars=None, death_pars=None, intvs=[]
            people = ss.People(n_agents=5_000) # People

            # Zombies
            zombie_defaults = dict(
                init_prev = 0.03,
                beta = {'random': 0.05, 'maternal': 10},
                p_fast = ss.bernoulli(p=0.1),
                p_death_on_zombie_infection = ss.bernoulli(p=0.25),
                p_symptomatic = ss.bernoulli(p=1.0),
            )
            zombie_pars = sc.mergedicts(zombie_defaults, zombie_pars) # Override def
            zombie = Zombie(zombie_pars)

            # Networks
            networks = [
                ss.RandomNet(n_contacts=ss.poisson(lam=choose_degree)),
                ss.MaternalNet()
            ]

            # Deaths
            death_defaults = dict(
                death_rate = 15, # per 1,000 per year
                p_zombie_on_natural_death = ss.bernoulli(p=0.2),
            )
            death_pars = sc.mergedicts(death_defaults, death_pars)
            deaths = DeathZombies(**death_pars)

            # Births
            births = ss.Pregnancy(fertility_rate=175) # per 1,000 women 15-49 per ye
            demog = [births, deaths]

            # Interventions
            interventions = KillZombies(year=2024, rate=0.1)
            interventions = [interventions] + sc.promotetolist(intvs) # Add interver

            # Create and run the simulation
            sim_pars = dict(start=2024, end=2040, dt=0.5, rand_seed=rand_seed, label
            sim = ss.Sim(sim_pars, people=people, diseases=zombie, networks=networks
            sim.run()

            # Package results
            df = pd.DataFrame( {
                'Year': sim.yearvec,
                'Population': sim.results.n_alive,
                'Zombies': sim.results.zombie.n_infected,
                'Zombie Prevalence': sim.results.zombie.prevalence,
                'Congential Zombies (cum)': sim.results.zombie.cum_congenital,
                'Zombie-Cause Mortality': sim.results.zombie.cum_deaths,
            })
            df['rand_seed'] = rand_seed
            df['Scen'] = scen
            for key, val in kwargs.items():
                df[key] = val

            return df
```

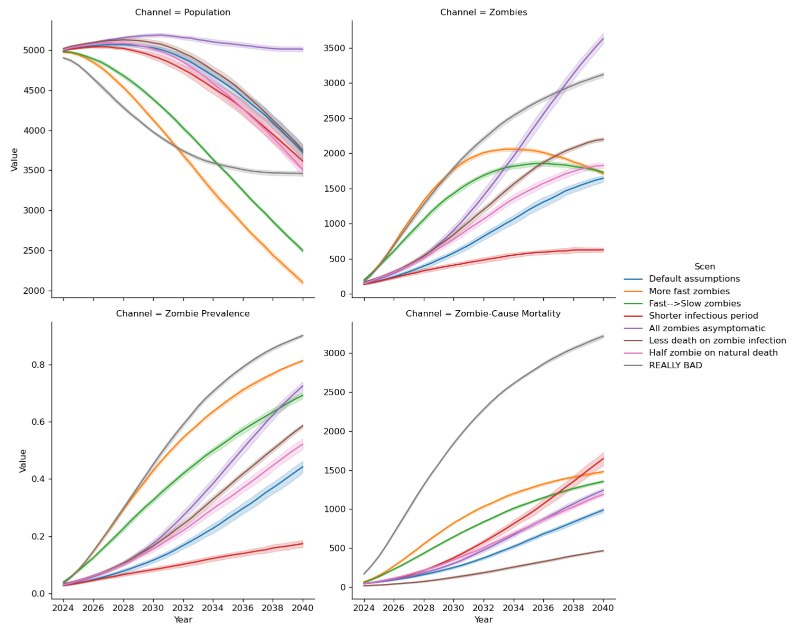
Now run all the scenarios in parallel, repeating each configuration 10 times.

```
In [ ]: # Now run all the scenarios in parallel, repeating each configuration 10 tim
        n_repeats = 10

        results = []
        cfgs = []

        for skey, scen in scens.items():
            for rand_seed in range(n_repeats):
                cfgs.append({'scen': skey, 'rand_seed':rand_seed} | scen)

        T = sc.tic()
        results += sc.parallelize(run_zombies, iterkwargs=cfgs)
        print(f'Completed {len(cfgs)} sims in {sc.toc(T, output=True):.1f}s')
        df = pd.concat(results).replace(np.inf, np.nan)

        # Display the top of the results data frame
        display(df.head())
```

```
Completed 80 sims in 5.1s
```

	Year	Population	Zombies	Zombie Prevalence	Congential Zombies (cum)	Zombie-Cause Mortality	rand_seed	S
0	2024.0	4984.0	139.0	0.027889	2.0	51.0	0	Def assumpti
1	2024.5	4994.0	158.0	0.031638	6.0	62.0	0	Def assumpti
2	2025.0	5010.0	174.0	0.034731	7.0	68.0	0	Def assumpti
3	2025.5	5011.0	198.0	0.039513	10.0	76.0	0	Def assumpti
4	2026.0	5022.0	237.0	0.047192	14.0	95.0	0	Def assumpti

```
In [ ]: # Manipulate the data and create a plot using the Seaborn library
        dfm = df.melt(id_vars=['Scen', 'Year', 'rand_seed'], value_vars=['Populatior
        g = sns.relplot(kind='line', data=dfm, col='Channel', x='Year', y='Value', h
```



That's alarming! What can we do to slow the spread of zombies?

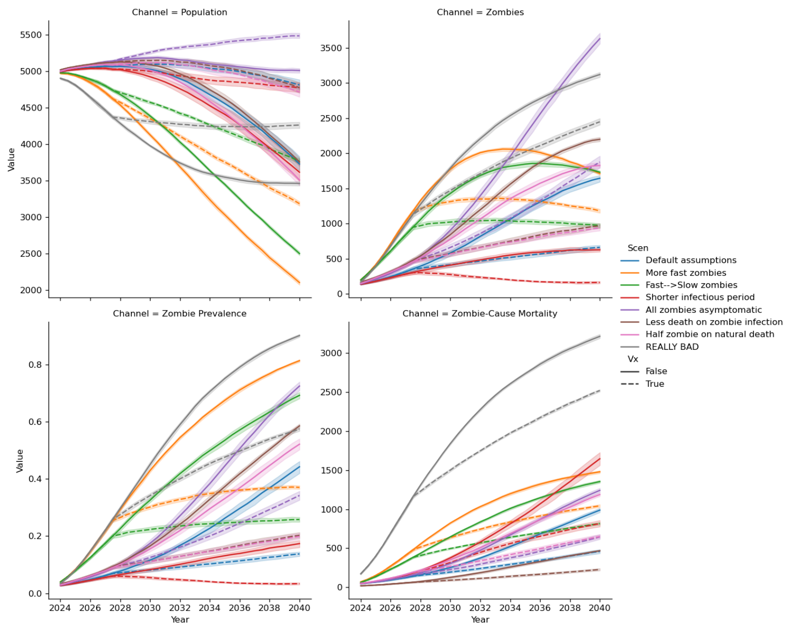
Let's consider a vaccine intervention, and see how well it works in each scenario.

In [ ]:
```
# Create a vaccine intervention
antizombie_vx = zombie_vaccine(efficacy = 0.95)
vx_intv = ss.campaign_vx(
    product = antizombie_vx,
    years = [2028],  # Begin year
    prob = [0.6],    # Coverage
)

# Revise scenarios to see impact of the vaccine
scens_vx = {}
for skey, scen in scens.items():
    scens_vx[skey] = scen.copy()
    scens_vx[skey]['intvs'] = [vx_intv]
```

In [ ]:
```
results = []
cfgs = []

for skey, scen in scens_vx.items():
    for rand_seed in range(n_repeats):
        cfgs.append({'scen': skey,'rand_seed':rand_seed} | scen) # Merge dic

T = sc.tic()
results += sc.parallelize(run_zombies, iterkwargs=cfgs)
print(f'That took: {sc.toc(T, output=True):.1f}s')
df_vx = pd.concat(results)

# Combine results
df['Vx'] = False
df_vx['Vx'] = True
df_all = pd.concat([df, df_vx])
```

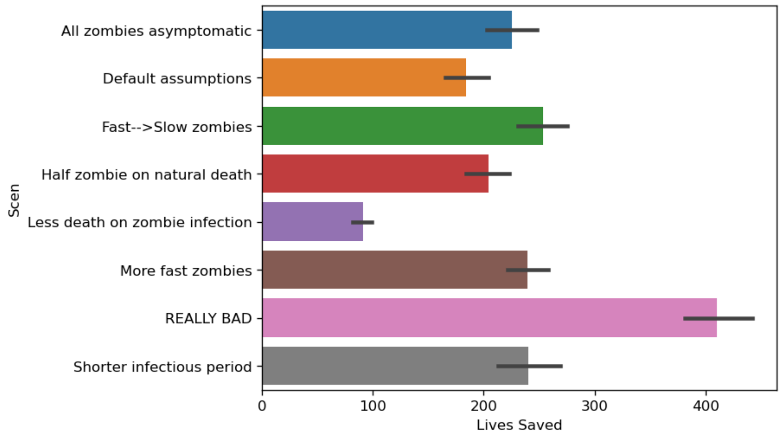
```
That took: 5.0s
```

In [ ]:
```
dfm = df_all.melt(id_vars=['Scen', 'Vx', 'Year', 'rand_seed'], value_vars=['
g = sns.relplot(kind='line', data=dfm, col='Channel', x='Year', y='Value', h
```



How many lives are we saving with vaccine?

In [ ]:
```
dfp = df_all.pivot(index=['Year', 'Scen', 'rand_seed'], columns='Vx', values
dfp['Lives Saved'] = dfp[False] - dfp[True]
g = sns.barplot(data=dfp.reset_index(), x='Lives Saved', y='Scen')
```



We can also look at multiplie zombie "variants"

- Separate fast and slow zombies in to separate diseases
- Being infected with one gives immunity to the other, using a "connector"
- Main difference is that fast (slow) create new fast (slow) zombies on infection, instead of just random

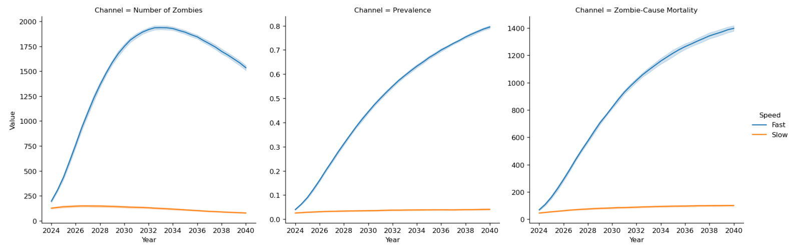
In [ ]:
```
def run_multizombie(rand_seed):
    people = ss.People(n_agents=5_000) # People

    # Start with parameters for slow zombies
    slow_zombie_pars = dict(
        init_prev = 0.03,
        beta = {'random': 0.05, 'maternal': 10},
        p_fast = ss.bernoulli(p=0), # <--- Notice NONE are fast
        p_death_on_zombie_infection = ss.bernoulli(p=0.25),
        p_symptomatic = ss.bernoulli(p=1.0),
    )
    slow_zombie = Zombie(slow_zombie_pars, name='slow_zombie')

    # Now create fast zombies
    fast_zombie_pars = slow_zombie_pars.copy()
    fast_zombie_pars['p_fast'] = ss.bernoulli(p=1) # <-- Notice ALL are fast
    fast_zombie = Zombie(fast_zombie_pars, name='fast_zombie')

    zombies = [fast_zombie, slow_zombie]

    connector = ZombieConnector() # Interaction between slow and fast zombie

    def choose_degree(self, sim, uids):
        mean_degree = np.full(fill_value=4, shape=len(uids))
        is_fast = ((sim.diseases['fast_zombie'].infected[uids]) & (sim.disea
                  ((sim.diseases['slow_zombie'].infected[uids]) & (sim.disease
        mean_degree[is_fast] = 50
        return mean_degree

    networks = [
        ss.RandomNet(n_contacts=ss.poisson(lam=choose_degree)),
        ss.MaternalNet()
    ]

    death_pars = dict(
        death_rate = 15, # per 1,000 per year
        p_zombie_on_natural_death = ss.bernoulli(p=0.2),
    )
    deaths = DeathZombies(**death_pars)
    births = ss.Pregnancy(fertility_rate=175) # per 1,000 women 15-49 per ye
    demog = [births, deaths]

    killzombies = KillZombies(year=2024, rate=0.1)

    sim_pars = dict(start=2024, end=2040, dt=0.5, rand_seed=rand_seed, label
    sim = ss.Sim(sim_pars, people=people, diseases=zombies, networks=network
    sim.run()

    # Package results by zombie speed
    dfs = []
    for speed in ['Fast', 'Slow']:
        res = sim.results.fast_zombie if speed == 'Fast' else sim.results.sl
        df = pd.DataFrame( {
            'Year': sim.yearvec,
            'Number of Zombies': res.n_infected,
            'Prevalence': res.prevalence,
            'Zombie-Cause Mortality': res.cum_deaths,
        })
        df['rand_seed'] = rand_seed
        df['Speed'] = speed
        dfs.append(df)

    return pd.concat(dfs)
```

Run variant simulations and plot results

In [ ]:
```
T = sc.tic()
results = sc.parallelize(run_multizombie, iterkwargs={'rand_seed':range(n_re
print(f'That took: {sc.toc(T, output=True):.1f}s')
df = pd.concat(results)
```

```
That took: 0.9s
```

In [ ]:
```
# Manipulate the data and create a plot using the Seaborn library
ch = df.columns.drop(['Year', 'Speed', 'rand_seed'])
dfm = df.melt(id_vars=['Year', 'Speed', 'rand_seed'], value_vars=ch, var_nam
g = sns.relplot(kind='line', data=dfm, col='Channel', hue='Speed', x='Year',
```



Thanks!