Probability Generating Functions

Joel C. Miller
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Context

Consider the spread of a disease starting from a single infected individual in a large population:

- A new disease emerges from some animal reservoir.
- A disease is introduced from some other population.

Focus on early spread, before saturation effects matter.

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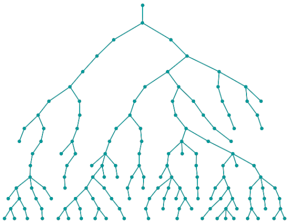

http://images.math.cnrs.fr/La-probabilite-d-extinction-d-une.html

Outline

- Quick taste of PGF properties
- Overview of things we can calculate with PGFs (and inference implications)
- A Python implementation

Probability Generating Functions

Joel Miller @joel_c_miller · Mar 14

Everything you ever wanted to know about using #ProbabilityGeneratingFunctions to study #InfectiousDisease : arxiv.org/abs/1803.05136 (I am contemplating turning this into a textbook on PGFs if I find interested collaborators who use PGFs in other biological systems)

5 28 54

Joel Miller @joel_c_miller · Mar 14

Apparently I'm the only person who thinks Probability Generating Functions deserve a hashtag!! 😀

2 5

Christophe Fraser
@ChristoPhraser

Following

Replying to @joel_c_miller

Definitely happy to follow #ProbabilityGeneratingFunctions ! They rock, though I still haven't quite got past the 'this is just weird magic' stage

Demagickifying PGFs — Alea iacta est

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- Then

$$\mu(x) = \sum P(i)x^i = \frac{1}{6}(x + x^2 + x^3 + x^4 + x^5 + x^6)$$

encodes the distribution of the infections caused.

PGF for multiple infectors

- Now consider two such individuals. The PGF of the combined number of infections caused

	⚀	⚁	⚂	⚃	⚄	⚅
⚀	2	3	4	5	6	7
⚁	3	4	5	6	7	8
⚂	4	5	6	7	8	9
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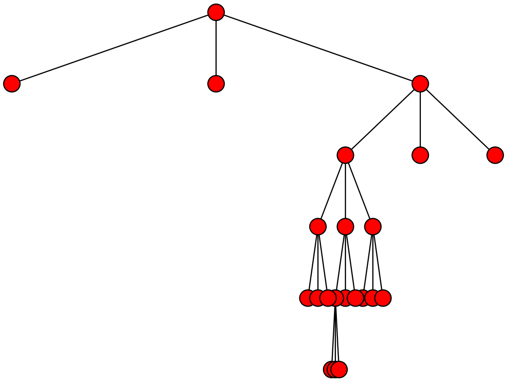
- The PGF of the number of infections caused by n individuals is given by $[\mu(x)]^n$.

PGF for multiple generations



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- The big takeaway is that composition of PGFs shows up naturally in getting from one generation to the next.

Other distributions

- Assume each individual causes a Poisson-distributed number of infections with rate parameter $\mathcal{R}_0$.

$$\mu(x) = \sum_{i=0}^{\infty} P(i) x^i = \sum_{i=0}^{\infty} \frac{\mathcal{R}_0{}^i e^{-\mathcal{R}_0}}{i!} x^i$$

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- Many commonly-used distributions have compact, closed-form PGFs.

Making predictions from the PGF

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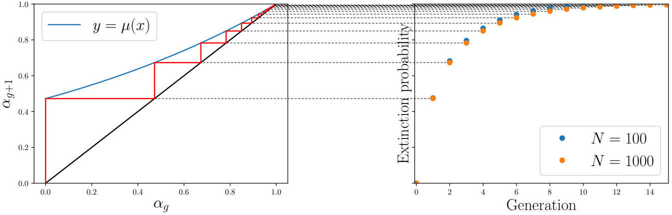
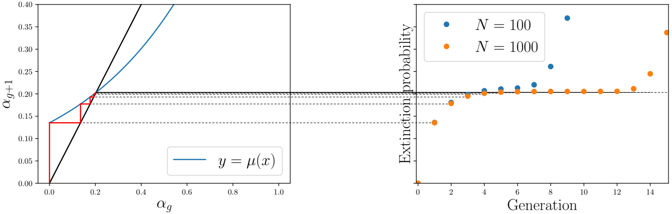
Poisson $\mathcal{R}_0 = 0.75$



Poisson $\mathcal{R}_0 = 2$



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- If only there were an efficient way to calculate the coefficient of arbitrary x^i for $\mu^{[g]}(x)$...
- Given a PGF $f(x)$, we can quickly approximate the coefficient of x^n in its Taylor Series by

$$r_n \approx \frac{1}{M} \sum_{m=0}^{M} \frac{f(e^{2\pi i m/M})}{\left(e^{2\pi i m/M}\right)^n}$$

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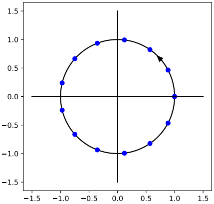

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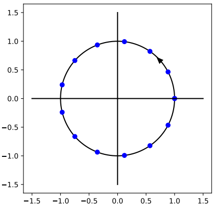

- This is really "just" a result from Complex Analysis about calculating residues through contour integration.

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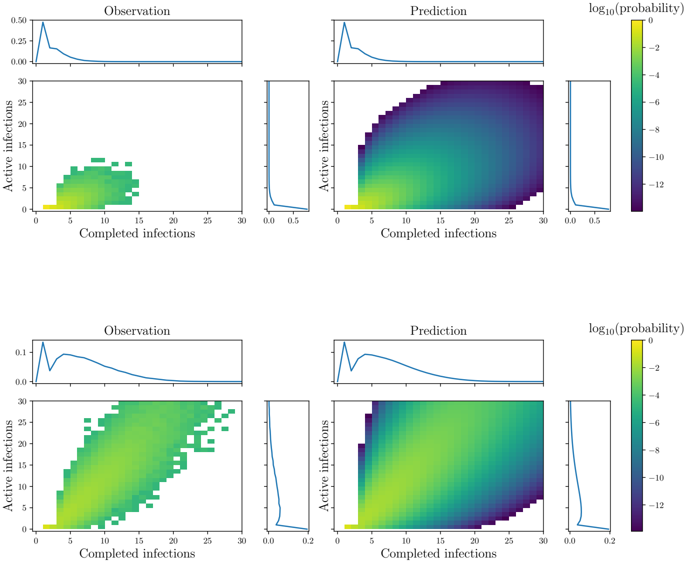
- Similar contour integrations works.

Comparison with simulation (Poisson, third generation)

$\mathcal{R}_0 = 0.75$

$\mathcal{R}_0 = 2$



Final sizes

It can be shown (the proof is beautiful) that $P(\text{Final size} = j)$ equals $1/j$ times the coefficient of x^{j-1} in $[\mu(x)]^j$.

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Distribution	**PGF**	**Probability of j infections**
Poisson	$e^{\mathcal{R}_0(x-1)}$	$\frac{(j\mathcal{R}_0)^{j-1}}{j!}e^{-j\mathcal{R}_0}$
Uniform	$x^{\mathcal{R}_0}$	$\begin{cases} 1 & j=1,\ \mathcal{R}_0=0 \\ 0 & \text{otherwise} \end{cases}$
Binomial	$(q+px)^n$	$\frac{1}{j}\binom{nj}{j-1}p^{j-1}q^{nj-j+1}$
Geometric	$p/(1-qx)$	$\frac{1}{j}\binom{2j-2}{j-1}p^j q^{j-1}$
Negative Binomial	$\left(\frac{q}{1-px}\right)^r$	$\frac{1}{j}\binom{rj+j-2}{j-1}q^{rj}p^{j-1}$

Inference

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- Bayesian inference allows us to infer improved parameter values.
- See:
  - Downgrading disease transmission risk estimates using terminal importations **bioRxiv**
  - Inference of R0 and Transmission Heterogeneity from the Size Distribution of Stuttering Chains. **PLoS One**
  - Characterizing the Transmission Potential of Zoonotic Infections from Minor Outbreaks. **PLoS Comp Bio**

Python Implementation

I have created a Python package that does most of this:
https://github.com/joelmiller/Invasion_PGF

(currently not compatible with python 2.x — just need to test and push new version to github)

Example

```
>>> import Invasion_PGF as pgf
>>> def mu(x):
...     return (1. + x + x**2 + x**3)/4
...
>>> pgf.R0(mu)
1.5000001241105565
>>> #probabilities of extinction up to generation 3
>>> pgf.extinction_prob(mu, 3, intermediate_values = True)
array([ 0.        ,  0.25      ,  0.33203125,  0.36972018])
>>> #possible states in generation 3
>>> pgf.active_infections(mu, 3, 5)
array([ 0.36972018,  0.05259718,  0.07178445,  0.09609134,  0.07393309])
>>> pgf.completed_infections(mu, 3, 5)
array([ -2.04281037e-17,   2.50000000e-01,   6.25000000e-02,
         7.81250000e-02,   9.76562500e-02])
>>> pgf.active_and_completed(mu, 3, 5, 5)
array([[ 0.        ,  0.25      ,  0.0625    ,  0.03125   ,  0.015625  ],
       [ 0.        ,  0.        ,  0.        ,  0.015625  ,  0.015625  ],
       [ 0.        ,  0.        ,  0.        ,  0.015625  ,  0.01953125],
       [ 0.        ,  0.        ,  0.        ,  0.015625  ,  0.0234375 ],
       [ 0.        ,  0.        ,  0.        ,  0.        ,  0.01171875]])
```

Summary

- PGFs allow us to magically calculate a lot of properties of small outbreaks.
- We've implemented many of the relevant functions in python.
- Detailed tutorial (effectively a short textbook) available at https://arxiv.org/abs/1803.05136