Meeting Record for meeting with Chris Jewell 2015/6/25

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1 Meeting 6.28

```
probs[state==0] = beta_mat[:, state==0].sum(1)[state==0]
```

This is the python operation for the calculation all the columns that suitable for state==0 and get its sum. Then we only want the column that for state==0———may exist some error: we only sum for the Infectious pressure: means that we sum for state==1
so the correct code is

```
probs[state==0] = beta_mat[:, state==1].sum(1)[state==0]
```

or

```
probs[state==0] = beta_mat[state==1,:].sum(0)[state==0]
```

This is instead of the for loop

However, for some not-regular function there are no(??maybe) usual way to assign to instead two for loop. We need to use matrix computation to make the calculate fast. Here are code for distance between object i and j.

```
-2 * np.dot(X, X.T) + np.sum(np.square( X), 1).reshape(N, 1)
 + np.sum(np.square( X), 1).reshape(1, N)
```

because the distance between object i and object j is $\|p_i - p_j\|$, which is $\|p_i\|^2 + \|p_j\|^2 - 2\|p_i\|\|p_j\|$,$p_i = (x_i, y_i)$ which can show as follows

$$D = \begin{bmatrix} d_{11} & d_{11} & \cdots & d_{1n} \\ d_{21} & d_{22} & \cdots & d_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ d_{n1} & d_{n2} & \cdots & d_{nn} \end{bmatrix}$$

which $d_{ij} = \sqrt{x_i^2 + x_j^2 + y_i^2 + y_j^2 - 2x_ix_j - 2y_iy_j}$ So, $(D_{ij}) = -2(x_ix_j + y_iy_j) + (x_i^2 + y_i^2) + (x_j^2 + y_j^2)$ In this way, the code for this is followed the code show upon.
The vectorization tutorial $http : //uk.mathworks.com/help/matlab/matlab_prog/vectorization.html$ The deep numpy tutorial

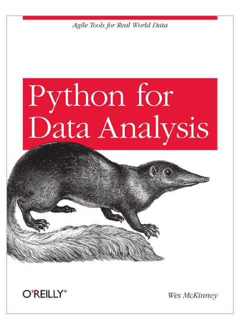

Figure 1: python for data analysis

2 Meeting 6.29

2.1 Correct version for R

The formula for R function is as follows

$$R = \frac{\beta \frac{I}{N} \frac{S}{N}}{\gamma \frac{I}{N}} \tag{1}$$

So, when the infection group is extremely small, so that the suspect group is almost the total population. Then we have

$$R = \frac{\beta}{\gamma} \tag{2}$$

as the baseline ratio.Which is an important parameter for epidemiology.

2.2 The basic assumption for infection

Here is a number axis which will show the time period

We assume that the probability(!) for a people(Pay attention to the infectious ratio,(or I called infect pressure) to the link of probability) get infected during time period t follows the exponential distribution with rate λ_i, in our model, the time period is a day so that the interval for integral is t to t+1 day.

$$Pr(I_i \leq t+1 | I_i > t) = 1 - e^{\int_t^{t+1} \lambda_j dt} = 1 - e^{\lambda_j} \tag{3}$$

which is like the cumulative survival function. And the rate λ_j is the "infection pressure" which can be describe as the

$$\lambda_j = \sum_{i \subseteq I(t)} \beta_0 e^{-d_{ij}/\phi} \tag{4}$$

2.3 Suggestion for debug

Set a random seeds so that get same results every time, for geo_data.
Save the map as a document, then update when ever needed.

2.4 likelihood

"Conditional Independence" Markov property
Another number axis for time here

$$L(x|\theta) = \prod_{t=1}^{N_t} [\prod_{j=S(t)} p_j^{1[I_i \leq t+1]} (1-p_i)^{1-1[I_j \leq t+1]} \prod_{i \subseteq I(t)} p_r^{1[R_i \leq t+1]} (1-p_r)^{1-1[r_i \leq t+1]}] \tag{5}$$

$$p_j(t) = 1 - e^{-\lambda_j(t)} \tag{6}$$

$$p_r = 1 - e^{-\gamma} \tag{7}$$

Calculate $L(x|\theta)$ naive way

Fixϕ,use scipy.optimize() to recover β, γ from simulated data. Consider about the parameter ϕ . Attention for the "flat" occur for the Likelihood: which will cause error for optimize function.

re-parametrize the λ as $\beta^* e^{\frac{-(d_i j - c)}{\phi *}}$ or consider as "Normalization" with $c = E_{d_{ij}}[d_{ij}]$

2.5 Discussion

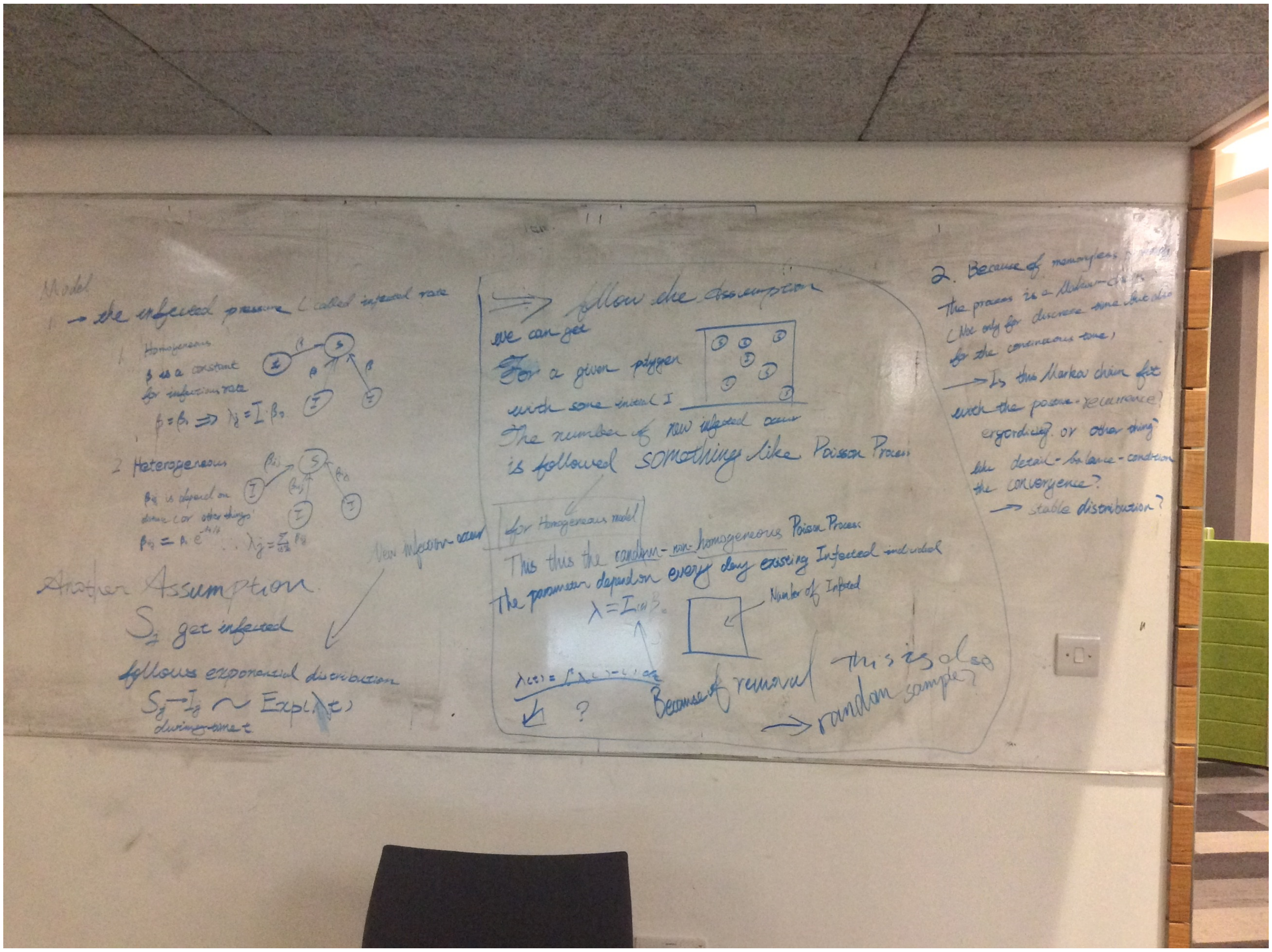

Figure 2: Thinking