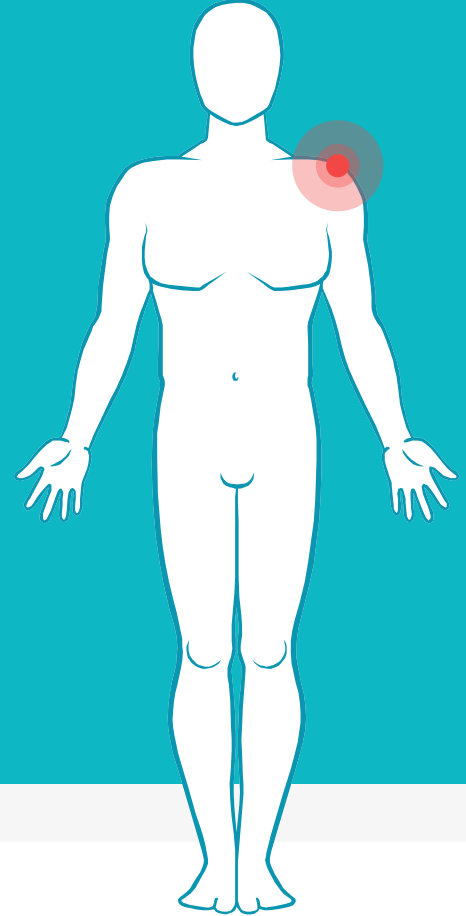


Estimation For Cancer Screening Model

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Mentor : Antonio Olivas



*Cancer is accounting for nearly
10,000,000 deaths in 2020, or nearly
one in six deaths.*

”

2,300,000

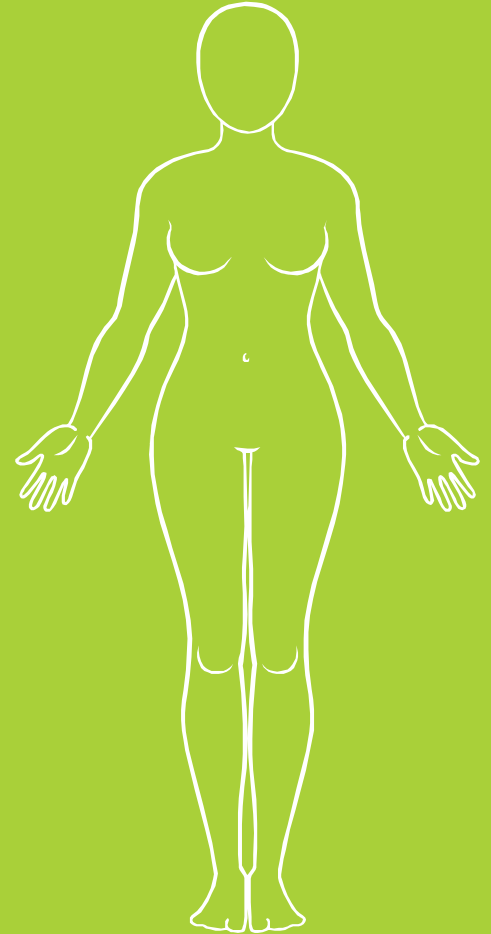
Women diagnosed in 2020

685,000

Deaths globally

40%

5 years survival rate in South Africa



How to reduce breast cancer mortality rate?

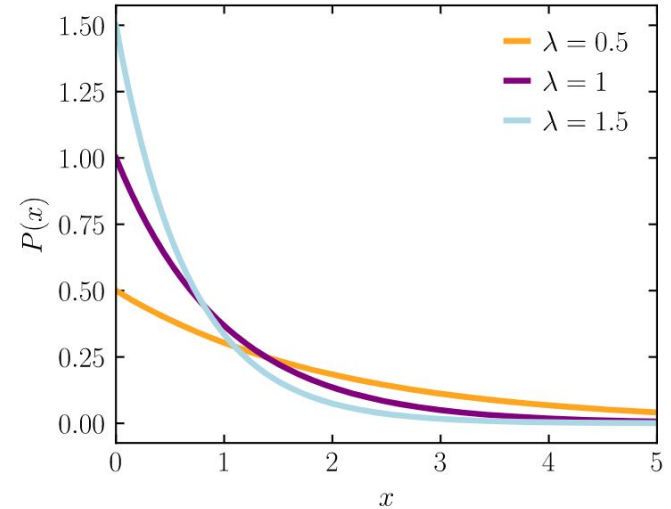
Early detection + treatment!



Cancer Screening Program

Three Questions to answer:

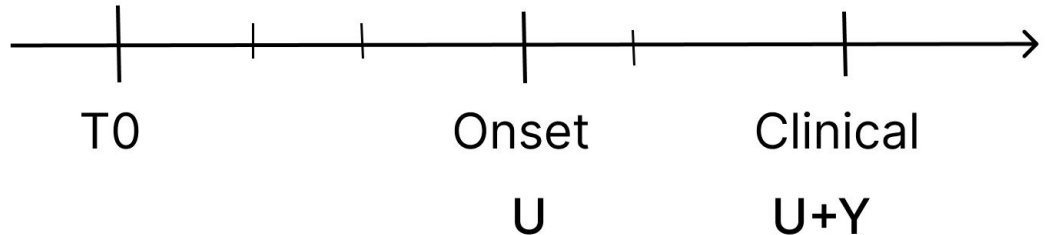
- ▶ When to start cancer screening?
 - ▶ $U \sim \text{Exp}(\lambda)$
- ▶ How often should the cancer screening be?
 - ▶ $Y \sim \text{Exp}(\gamma)$
- ▶ How accurate is the screening tool?
 - ▶ Sensitivity(β)



When and How Often to perform cancer screening?

- ▶ **T₀**: Minimum age to have cancer
- ▶ **Onset**: cancer appears in the body without symptoms
- ▶ **Clinical**: Symptoms emerge
- ▶ **U**: Age of onset $\sim \text{Exp}(\lambda) + T_0$
- ▶ **Y**: Sojourn time $\sim \text{Exp}(\gamma)$
- ▶ **U+Y**: Age of clinical

Natural History of Cancer

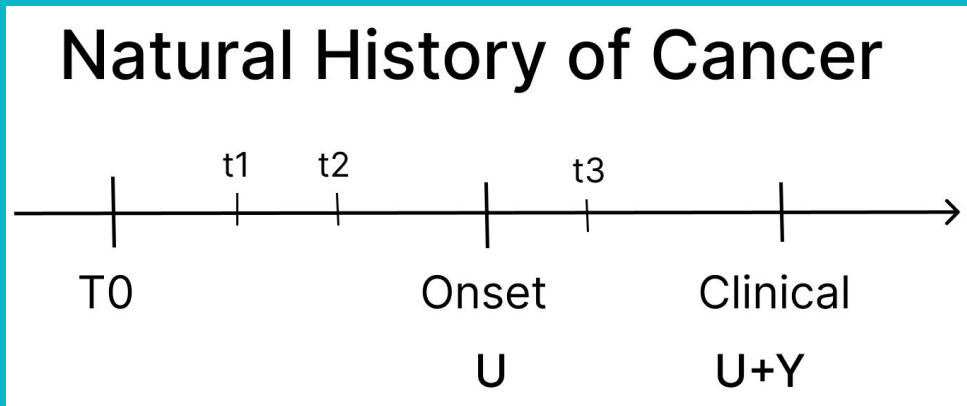


Accuracy of Screening Tool

- ▶ **Sensitivity:** β
 - ▶ Probability of detecting disease when there is disease
 - ▶ $1 - \beta$: failing to detect disease when there is disease
- ▶ **Specificity:** 100%
 - ▶ No False Positive

		Disease:		
		Sick	Healthy	
Test result:	Positive	True positive (TP)	False positive (FP)	→ PPV
	Negative	False negative (FN)	True negative (TN)	→ NPV
		↓ Sensitivity	↓ Specificity	

Estimating the Parameters: λ , γ , β



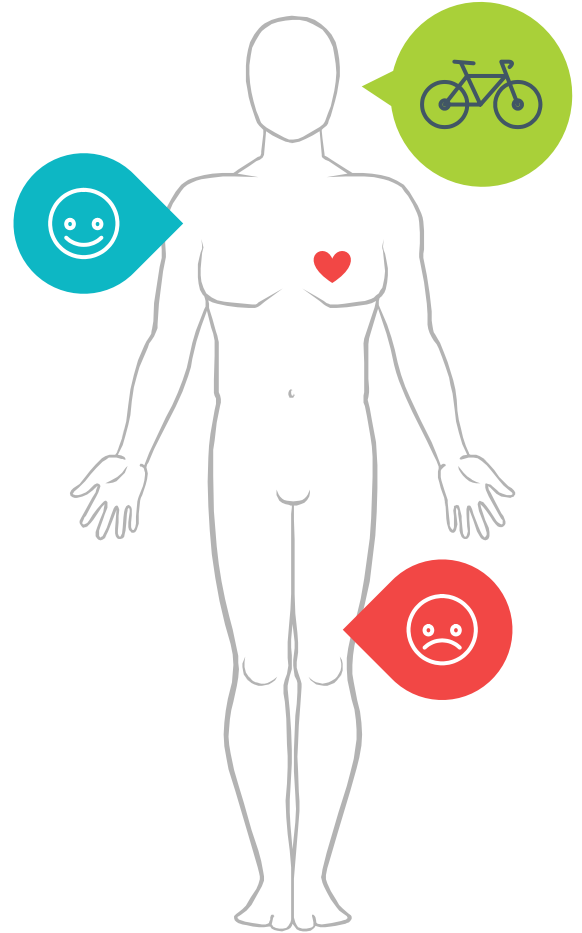
What do we hope to gain?

Recall: the expected value $E[X]$ of an exponential distribution is 1 over the parameter

- Mean sojourn time

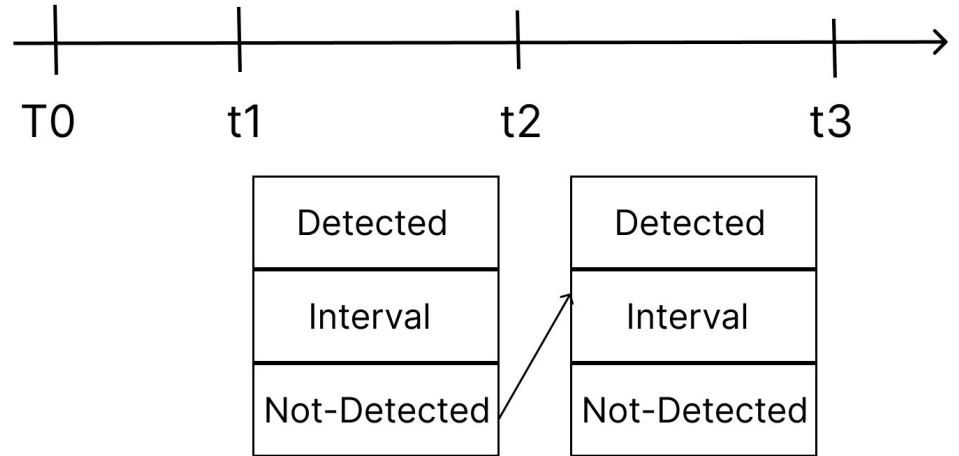
Maximum Likelihood Estimation

A method that determines the parameter of a function



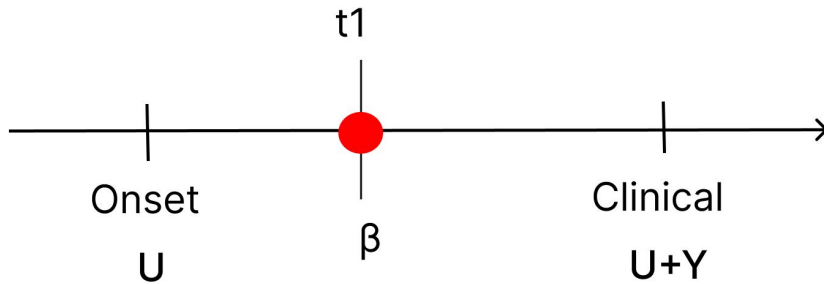
Model

- ▶ Multinomial
 - ▶ Screen-detected cases
 - ▶ Interval-detected cases
 - ◆ Rapid development between screenings
 - ▶ Not-detected cases

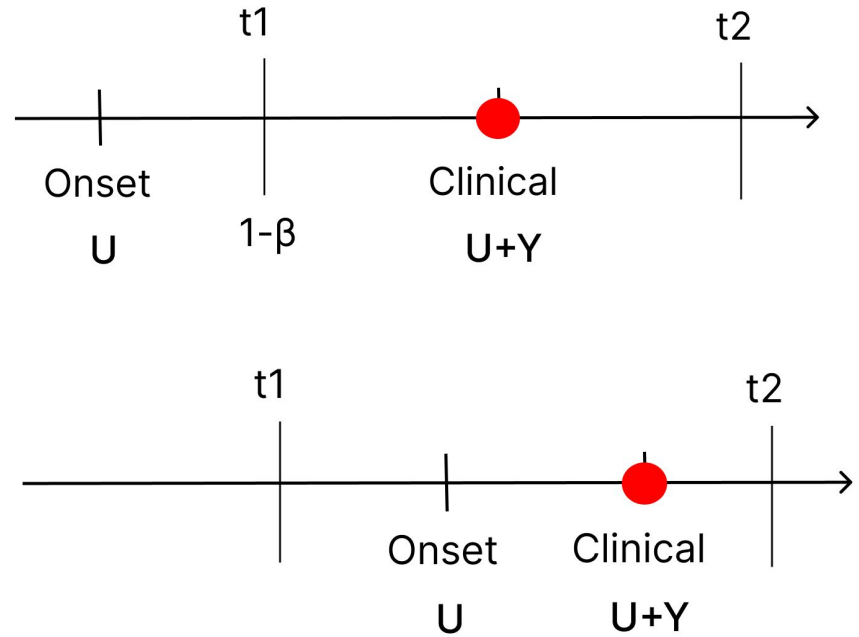


$$t1 \leq a < t2$$

Screen-Detected Case

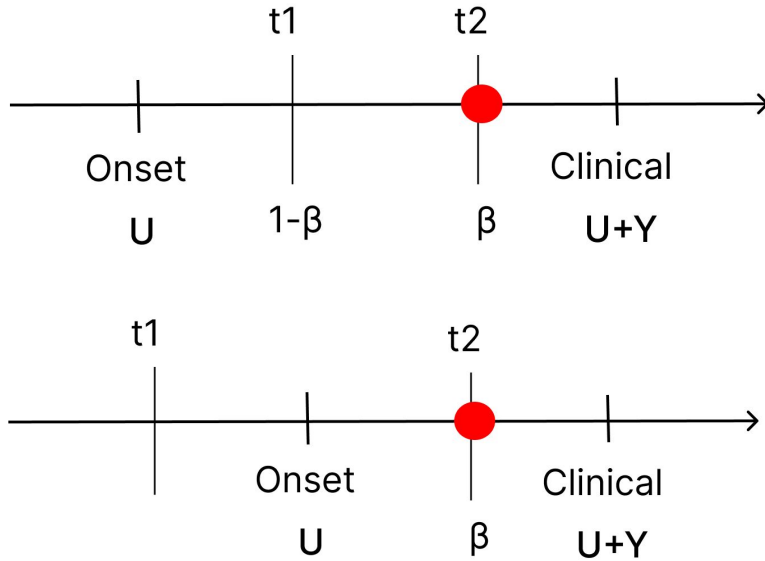


Interval-Detected Case

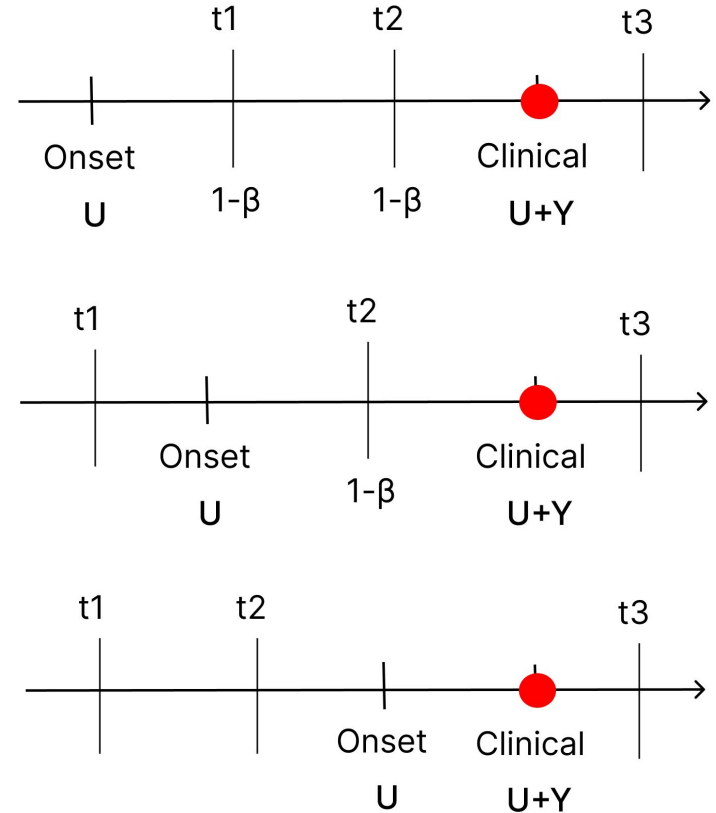


$$t_2 \leq a < t_3$$

Screen-Detected Case



Interval-Detected Case



Model

Detected
Interval
Not-Detected

- ▷ S_i = screen detected at t_i
- ▷ I_i = interval cases between t_i and t_{i+1}
- ▷ s_i = number of screen-detected at t_i
- ▷ i_i = number of interval cases between t_i and t_{i+1}
- ▷ n_i = total number of screened at t_i

$$\triangleright L(\lambda, \gamma, \beta) = P(S_1)^{s_1} * P(I_1)^{i_1} * (1 - S_1 - I_1)^{n_1 - s_1 - i_1} * P(S_2)^{s_2} * P(I_2)^{i_2} * (1 - S_2 - I_2)^{n_2 - s_2 - i_2}$$

$$\triangleright \ell(\lambda, \gamma, \beta) = s_1 \ln(P(S_1)) + i_1 \ln(P(I_1)) + (n_1 - s_1 - i_1) \ln((1 - S_1 - I_1)) + \\ s_2 \ln(P(S_2)) + i_2 \ln(P(I_2)) + (n_2 - s_2 - i_2) \ln((1 - S_2 - I_2))$$

Application to Real Data

Web Table 1

Screening round	No. of women	Screen-detected cases	Interval-detected cases
1	19711	142	15
2	17669	66	10
3	17347	43	9
4	17193	54	9
5	9876	28	5

CNBSS-2. Grouped data from the Canadian Breast Cancer Screening Study-2 [3]. "No. of women" is the number of women who attended all screening rounds up to and including the current round.

Result

```
`` `{r}  
data <- rbind(c(142, 15, 19711-142-15), c(66, 10, 17669-66-10))  
known <- data.frame(t0 = 45, t1 = 50, t2 = 51, t3 = 52)  
known <- cbind(known,  
              s1 = data[1, 1],  
              r1 = data[1, 2],  
              n1 = data[1, 3],  
              s2 = data[2, 1],  
              r2 = data[2, 2],  
              n2 = data[2, 3])  
esti <- maxLik(logLik = max_likelihood, start = c(0.001, 0.01, 0.6),  
              method = "NR", input = known)
```

```
coef(esti)
```

```
````  
[1] 0.00317097 0.19592243 0.72099802
```

Web Table 2

| $\psi$ | $\hat{\lambda}$ | 95% CI    | $\hat{w}$ | 95% CI        | $\hat{\beta}$ | 95% CI    | $\chi^2$ | P-value |
|--------|-----------------|-----------|-----------|---------------|---------------|-----------|----------|---------|
| 0.00   | 0.30            | 0.10-0.47 | 0.0031    | 0.0023-0.0036 | 0.81          | 0.44- NA  | 6.20     | 0.7984  |
| 0.05   | 0.30            | 0.09-0.48 | 0.0029    | 0.0023-0.0034 | 0.75          | 0.41-0.96 | 7.03     | 0.7226  |
| 0.10   | 0.28            | 0.09-0.48 | 0.0028    | 0.0023-0.0032 | 0.69          | 0.40-0.90 | 7.74     | 0.6546  |
| 0.20   | 0.26            | 0.11-0.48 | 0.0026    | 0.0022-0.0030 | 0.59          | 0.39-0.79 | 8.23     | 0.6061  |
| 0.40   | 0.34            | 0.16-0.62 | 0.0024    | 0.0022-0.0027 | 0.51          | 0.38-0.64 | 8.39     | 0.5905  |

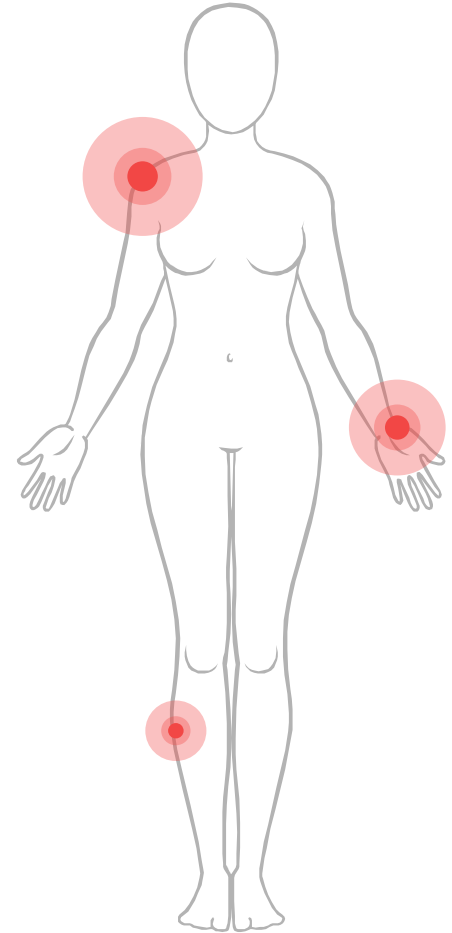
**CNBSS-2: Parameter estimation and goodness of fit for constrained mixture model.** The mixture model with fixed fraction of indolent cancers  $\psi$  is fit to the CNBSS-2 data (see Web Table 1). Onset of preclinical disease is assumed to be negligible before age  $\Delta_0 = 45$  years.

- ▷  $\lambda \approx 0.00317$ 
  - ▶ 1% women have breast cancer at 48.2 years old
- ▷  $\gamma \approx 0.1959$ 
  - ▶ Average sojourn time = 5 years
- ▷  $\beta \approx 0.721$



# Next Steps

- ▶ Further evaluate our result to produce a meaningful conclusion.
- ▶ Perform simulations to validate our model
- ▶ Consider other possible distributions



# Thank you for listening!

Special thanks to my mentor Antonio and the DRP!

# Reference

“Breast Cancer.” *World Health Organization*, World Health Organization, <https://www.who.int/news-room/fact-sheets/detail/breast-cancer>

“Cancer.” *World Health Organization*, World Health Organization, <https://www.who.int/news-room/fact-sheets/detail/cancer>

Ryser MD, Gulati R, Eisenberg MC, Shen Y, Hwang ES, Etzioni RB. Identification of the Fraction of Indolent Tumors and Associated Overdiagnosis in Breast Cancer Screening Trials. *Am J Epidemiol*. 2019 Jan 1;188(1):197-205. doi: 10.1093/aje/kwy214. PMID: 30325415; PMCID: PMC6321806.

<https://www.omnicalculator.com/statistics/sensitivity-and-specificity>

## CREDITS

Special thanks to all the people who made and released these awesome resources for free:

- ▶ Presentation template by [SlidesCarnival](#)
- ▶ Photographs by [Unsplash](#)