

**Julia Brettschneider**

**Statistical methodology and data science  
in science and engineering:  
Point processes**

**1 Hawkes process modelling of the pandemic**

**2 Dead pixel formations on digital X-ray detectors**

**3 Microscopic image based modelling of biological processes**

## **Applied statistician/data scientists**

**Collaborators:** engineers, life scientists, clinicians...

**Domains:** genomics, microscopy, detectors, cancer, screening, finance, OR...

**Methodological topics:** data quality, spatial statistics, decision theory, concepts of probability and risk

## **Short biography**

- Reader (since 2021), Associate Professor (2010-2021), Assistant Professor (2007-2010), Dept of Statistics, University of **Warwick, UK**
- **Turing fellow** since 2017
- Assistant Professor, Dept of Math/Stats & Dept of Community Health/Epidemiology & Cancer Research Institute, **Queen's University, CN**
- Visiting Assistant Professor and Research Statistician, Dept of Statistics at **University of California at Berkeley, USA**
- Postdoctoral fellow in Computational Biology at **Eurandom, NL**
- **PhD (2001) in Mathematics**, thesis supervisor Prof H Föllmer, **Humboldt Uni Berlin, D**
- Masters in Mathematics (with Computer Sciences and Psychology), thesis supervisor Prof H Föllmer, **University Bonn, D**

# Point processes

## Definition: Point Process

Point processes are a class of random process whose realisations are a set of points on some given space.

i.e. A sequence of random variables  $t = \{t_1, t_2, \dots, t_d\}$  taking values in a subset of  $\mathbb{R}^d$ .

## Definition: Temporal Point Process (also called counting process)

Temporal Point process is a point process over time: It describes the occurrence of random events over time.

i.e. a sequence of events  $t = \{t_1, t_2, \dots, t_d\}$  s.t.  $0 \leq t_1 < t_2 < \dots < t_d$

# Example: Poisson point process

1d: Stochastic process  $N(t)$  ( $t \geq 0$ ) with

- $N(0) = 0$
- independent increments
- number of events at interval of length  $t$  is a Poisson random variable with mean  $\lambda t$

Higher d: Stochastic process  $N(A)$  ( $A \in \mathcal{B}(\mathbf{R}^d)$ ) with

- $N(\emptyset) = 0$
- $N(A)$  and  $N(B)$  are independent for disjoint sets  $A, B$
- $N(A)$  is a Poisson random variable with mean  $\mu(A)$

Interpretation:

Number of points in a set is distributed proportionally to the size of the set, i.e. the area (plane  $d=2$ ), volume (space  $d=3$ ), and what happens in a region does not effect what happens in a different regions (if there is no overlap).

## Example: Hawkes process

# ETAS Hawkes Process model

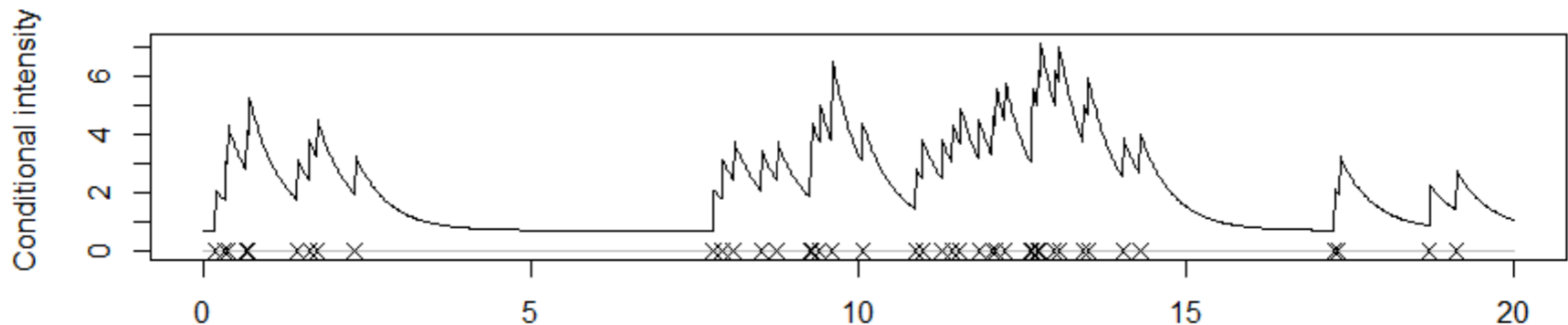
**ETAS** = Epidemic-type aftershock sequence

- Most widely used example of Hawkes Process.
- Model:

$$\lambda(t) = \mu + \sum_{t_i < t} \underbrace{\alpha e^{-\beta(t-t_i)}}_{\text{Exponential triggering function}}$$

Exponential triggering function

Example:



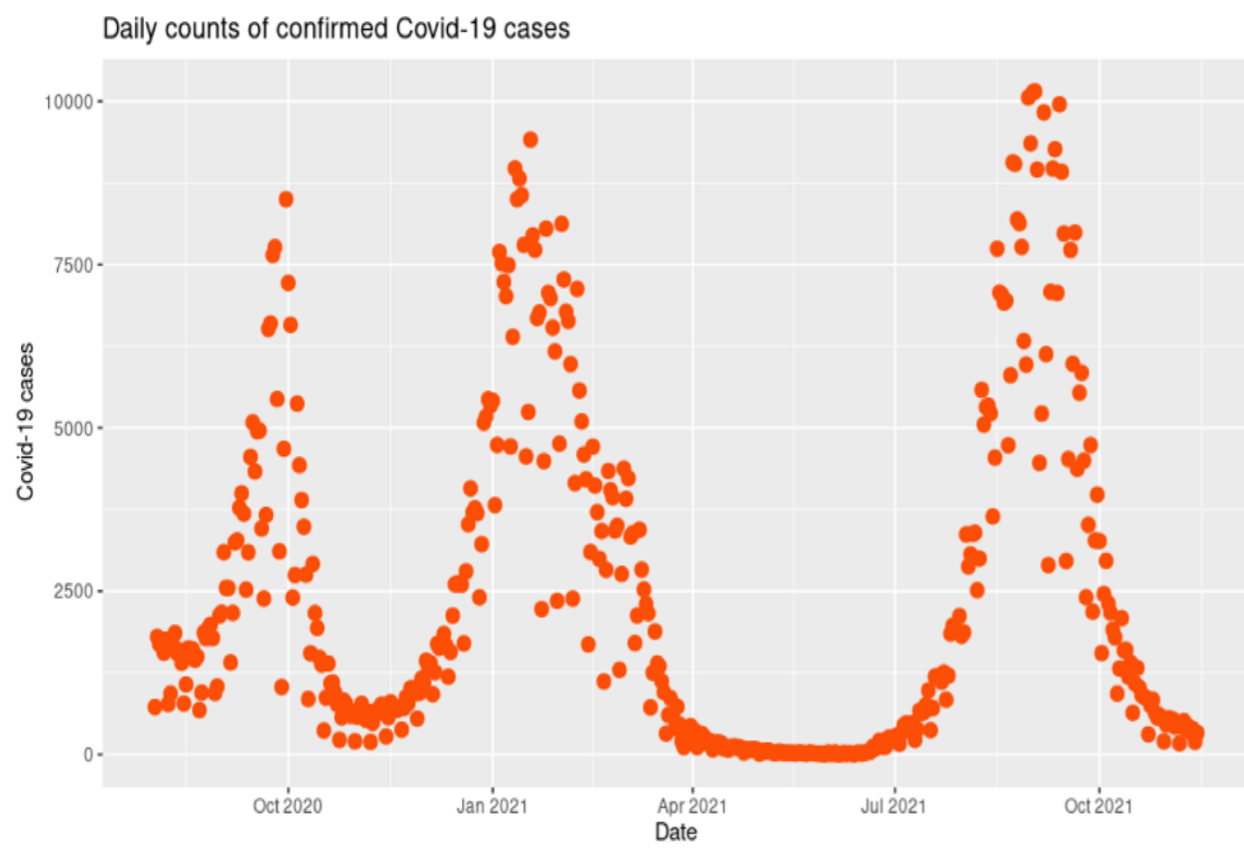
# Hawkes process modelling of the pandemic

Joint projects with integrated Master's students:

Marianna Mavroleftherou and Adam Davison

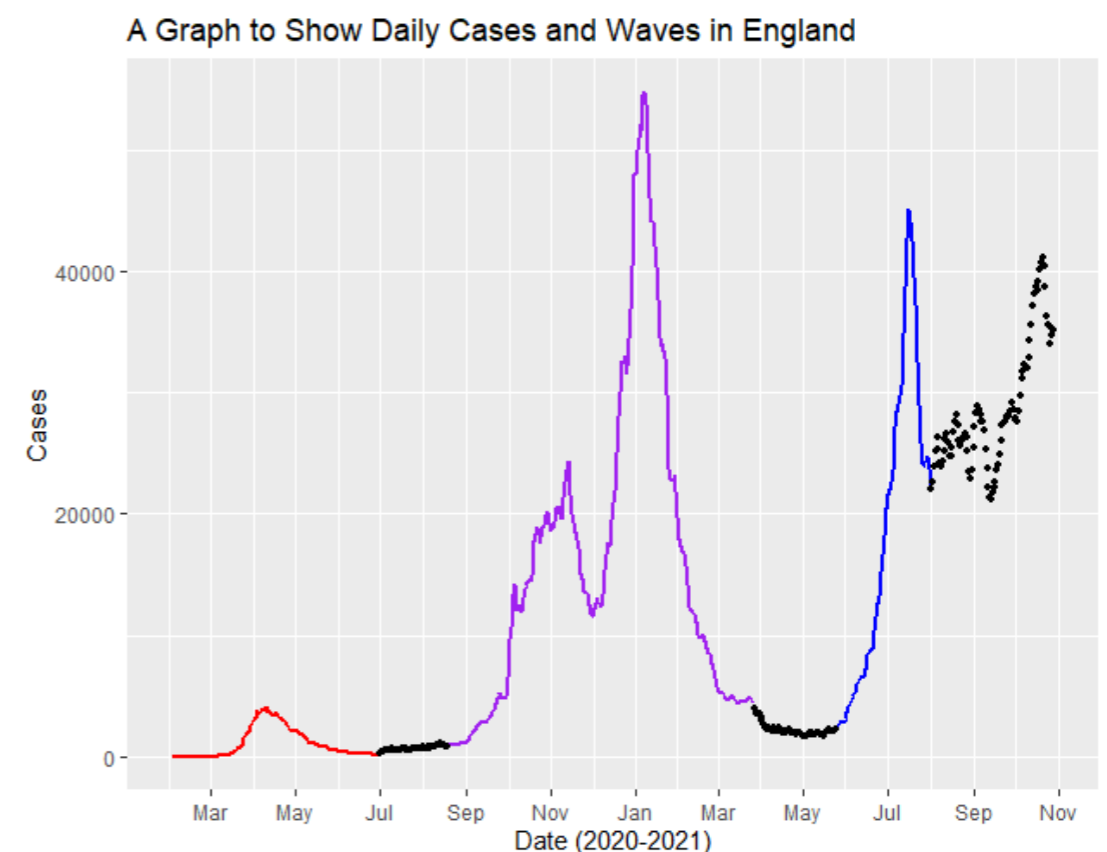
## 1. Data from Israel

Vaccine for data deal with Pfizer/BioNTech  
(Marianna Mavroleftherou's project)



## 2. Data from England

ONS/Oxford survey  
(Adam Davison's project)



# Hawkes process modelling of the pandemic

## Hawkes Process

Self-exciting temporal point process described by the conditional intensity function:

$$\lambda(t) = \underbrace{\mu}_{\substack{\text{Background intensity} \\ \text{Or} \\ \text{Baseline mean}}} + \underbrace{\alpha \sum_{i:t_i < t} y_{t_i} g(t - t_i)}_{\text{Excitation intensity}}$$

**Triggering kernel**  
**Or**  
**decay function**

The diagram shows the conditional intensity function  $\lambda(t) = \mu + \alpha \sum_{i:t_i < t} y_{t_i} g(t - t_i)$ . A blue bracket under  $\mu$  is labeled 'Background intensity Or Baseline mean'. A green bracket under the entire sum term is labeled 'Excitation intensity'. A purple bracket over  $g(t - t_i)$  is labeled 'Triggering kernel Or decay function'.

# Hawkes process modelling of the pandemic

## Model Setup

Number of daily cases (or deaths)  
[e.g. Rousseau et al 2020]

- It is a natural response to assume that  $Y(t)$  follows *Poisson*(  $\lambda(t)$  )

Since Poisson distribution is governed by one parameter  $\lambda$ , which is the expected number of times an event occurs in an interval of time or space.

Hence, we set:

$$P(Y(t) = y \mid \lambda(t)) = \frac{\lambda(t)^y e^{-\lambda(t)}}{y!}$$

- Further to this:

we choose the triggering kernel  $\mathbf{g}()$  to be the **geometric** excitation kernel:

$$g(t - t_i \mid \beta) = \beta(1 - \beta)^{t - t_i - 1}$$

Since it can be shown to be the generalization of the exponential distribution in discrete time.

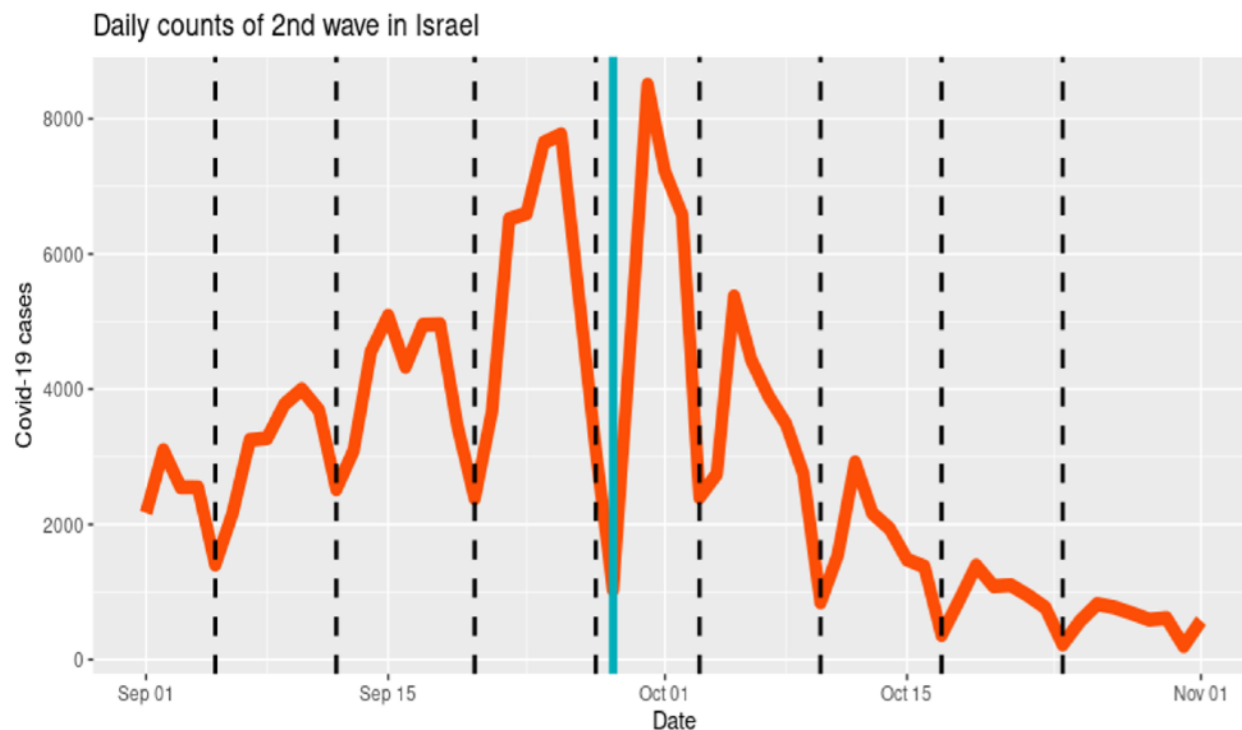


# Hawkes process modelling of the pandemic

## Model fitting steps in practice:

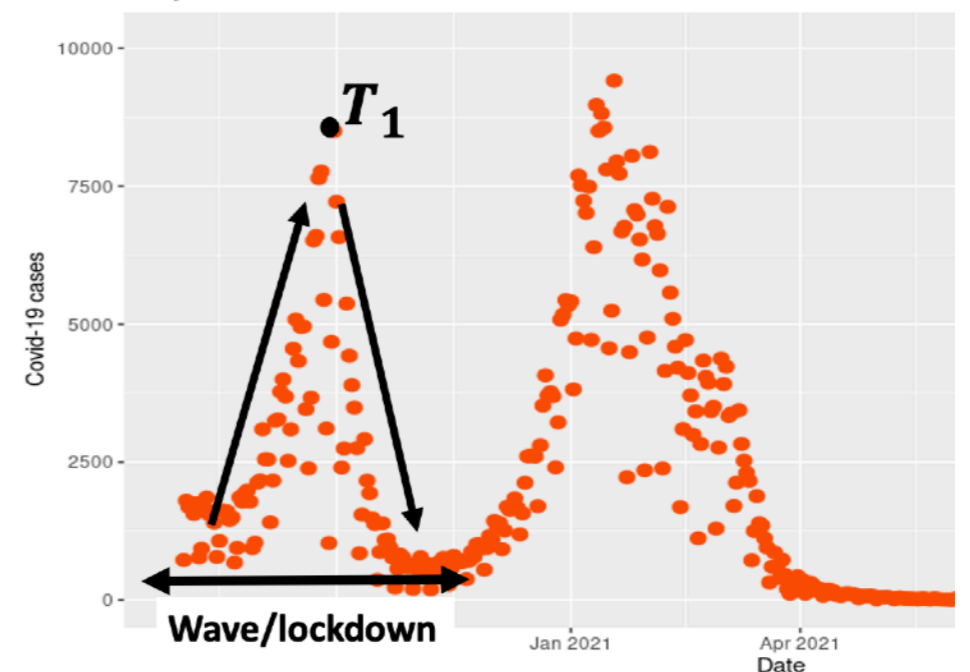
### 1. Data preprocessing

Small counts, smoothing



### 2. Waves

Piecewise fitting, piques



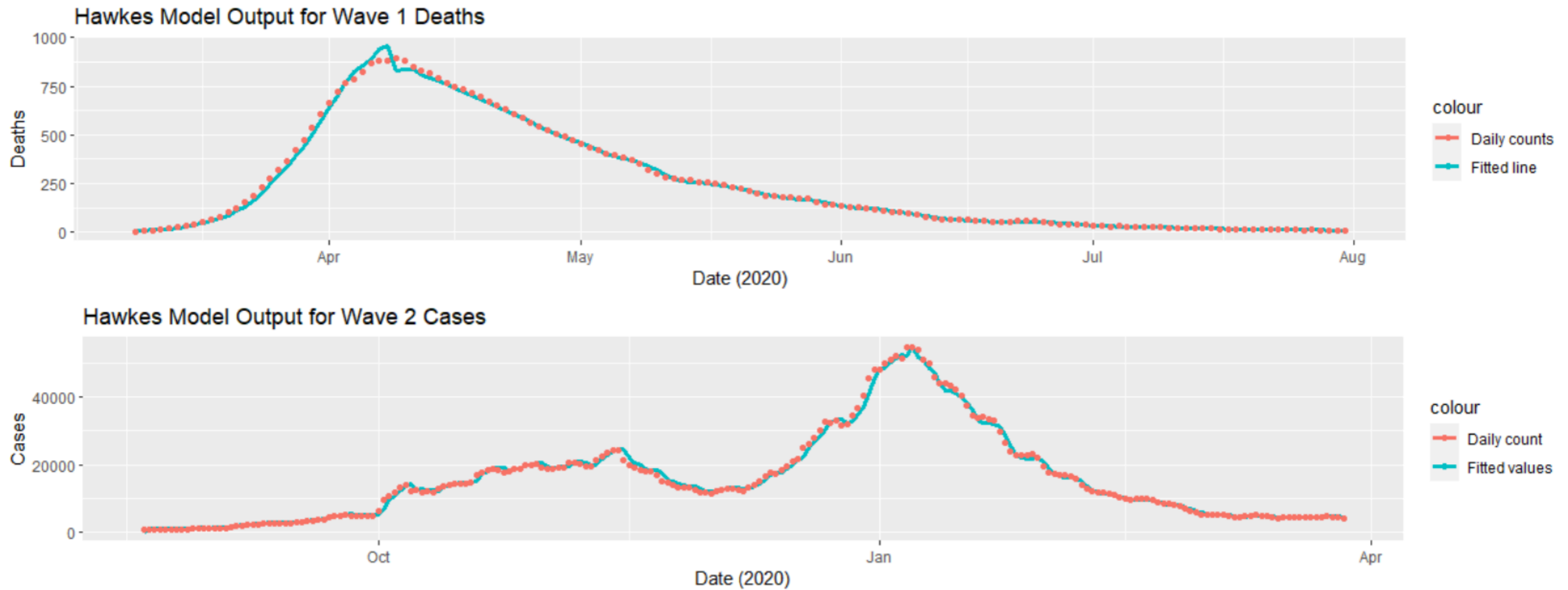
### 3. Likelihood function

### 4. Inference

- ML with Nelder-Mead
- Bayesian posterior MCMC

# Hawkes process modelling of the pandemic

## English data:



# Hawkes process modelling of the pandemic

## Further and future work:

- Models including age
- Including vaccination rates
- Testing coverage/reliability
- Behavioural indicators (e.g. google searches or mobility)
- Lockdown effects
- Events (e.g. football, holidays) and interaction with other factors
- Mixture population
- Regional models

# Dead pixel formations on digital X-ray detectors

## Inside-out

### Statistical Methods for Computed Tomography Validation of Complex Structures in Additive Layer Manufacturing

EPSRC grant  
3 years

10/2013 -  
9/2016

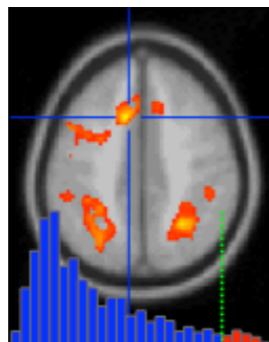
PI: Prof W Kendall

Other investigators: Prof M A Williams, Dr G J Gibbons,  
Dr J Brettschneider, Prof T Nichols

EP/K031066/1

Further team members: Clair Barnes, Jay Warnett, Audrey Kueh

Industrial partners: Nikon Metrology, Remishaw, EOS systems



# Spatial analysis of dead pixels

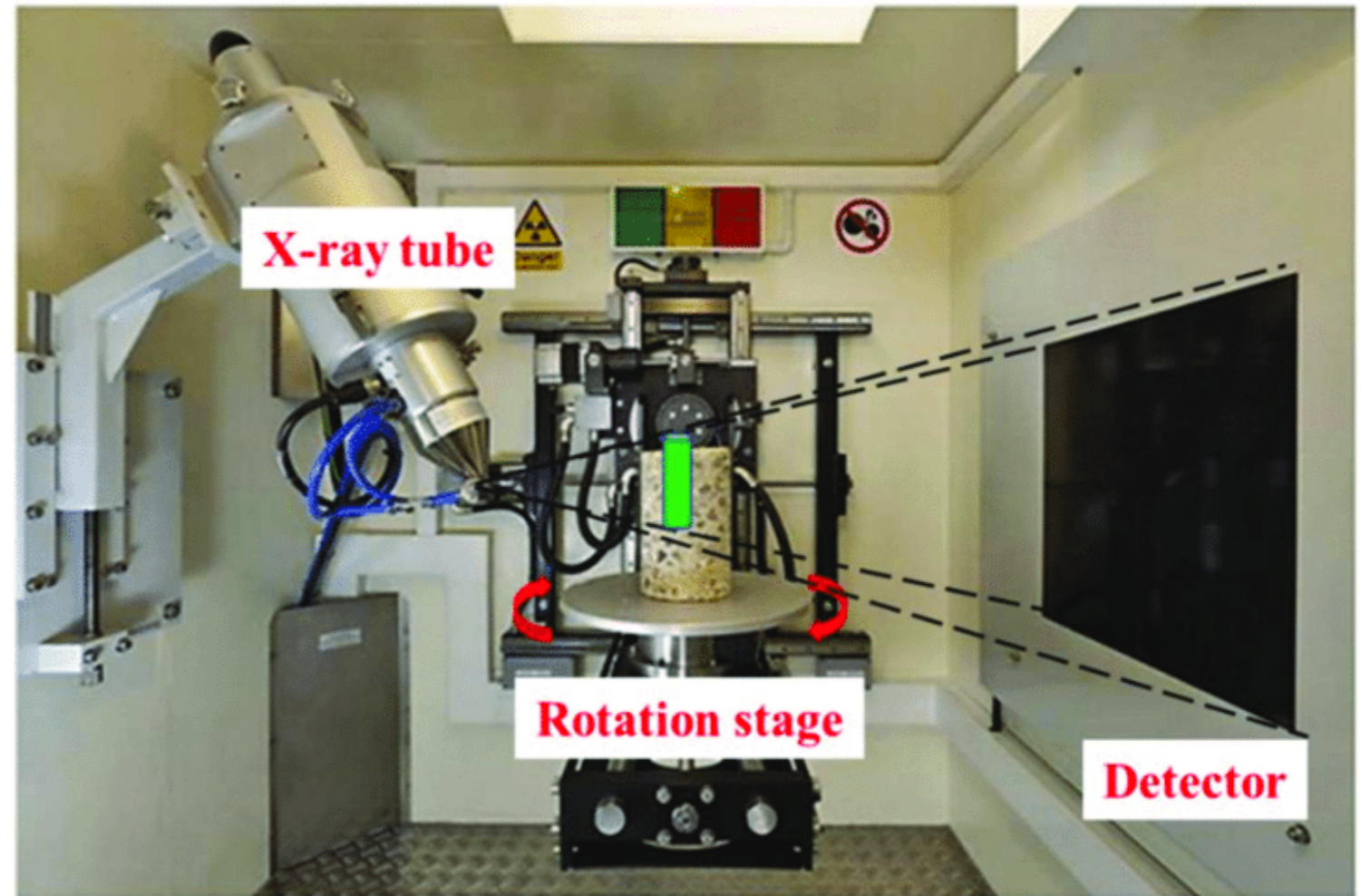
## **Objectives:**

- Feedback about state of detector through spatial pixel damage analysis
- Detector data repository

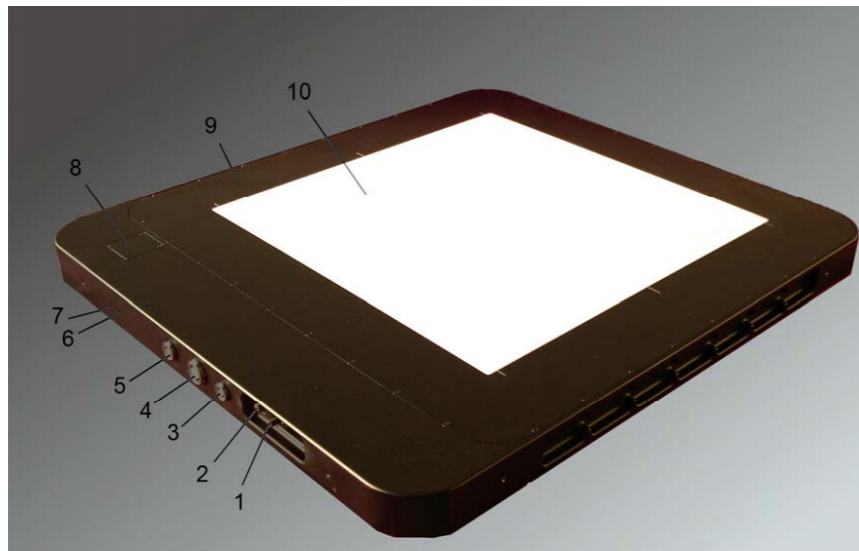
## **Applications:**

- Identify poor quality regions (patches with high dead pixels density) through density thresholding
- Remaining area CSR means no special causes of poor quality
- Identify causes of poor quality
- Monitor over time
- Conclusions for usage modes
- Conclusions about weakness of detector construction

# X-ray chamber

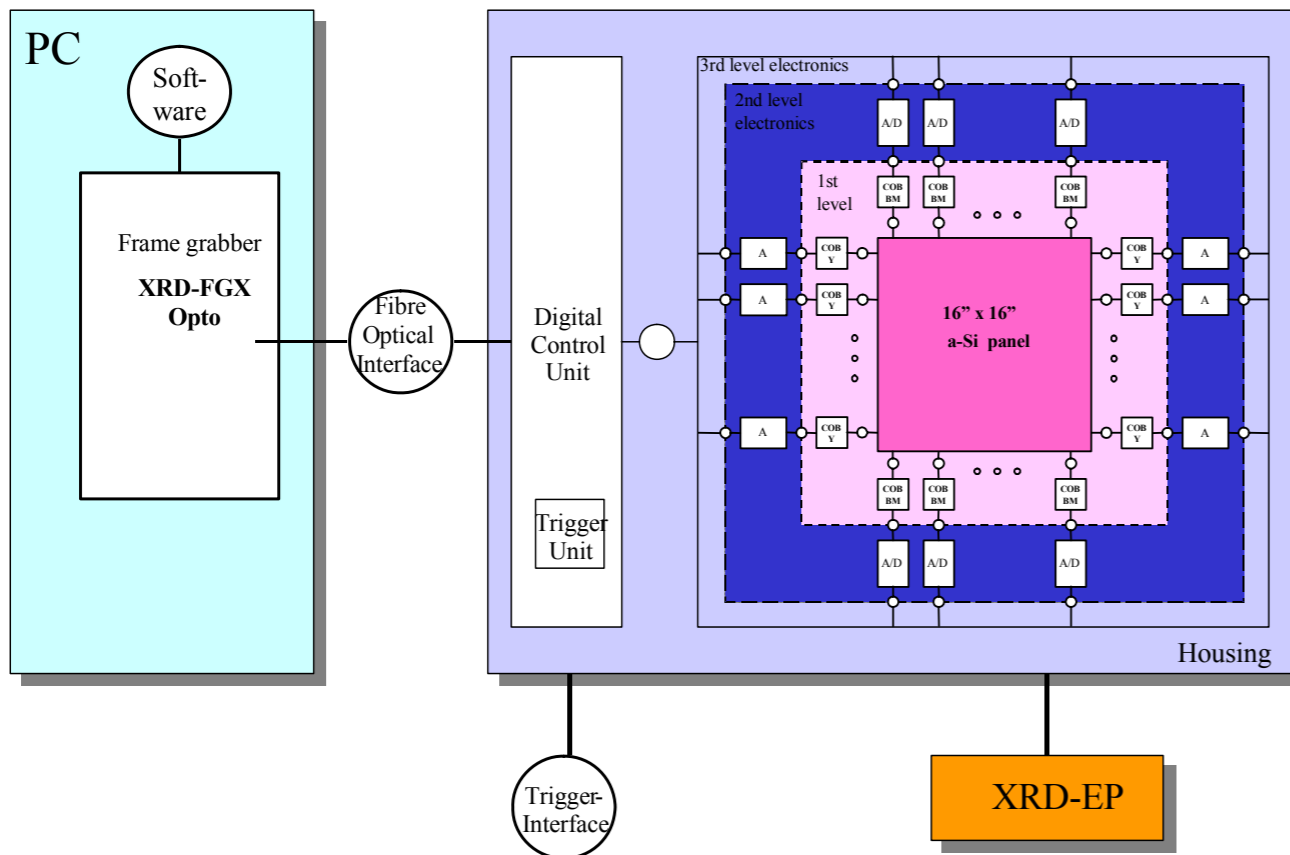


# X-ray detector



Perkin Elmer  
XRD 1621

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32



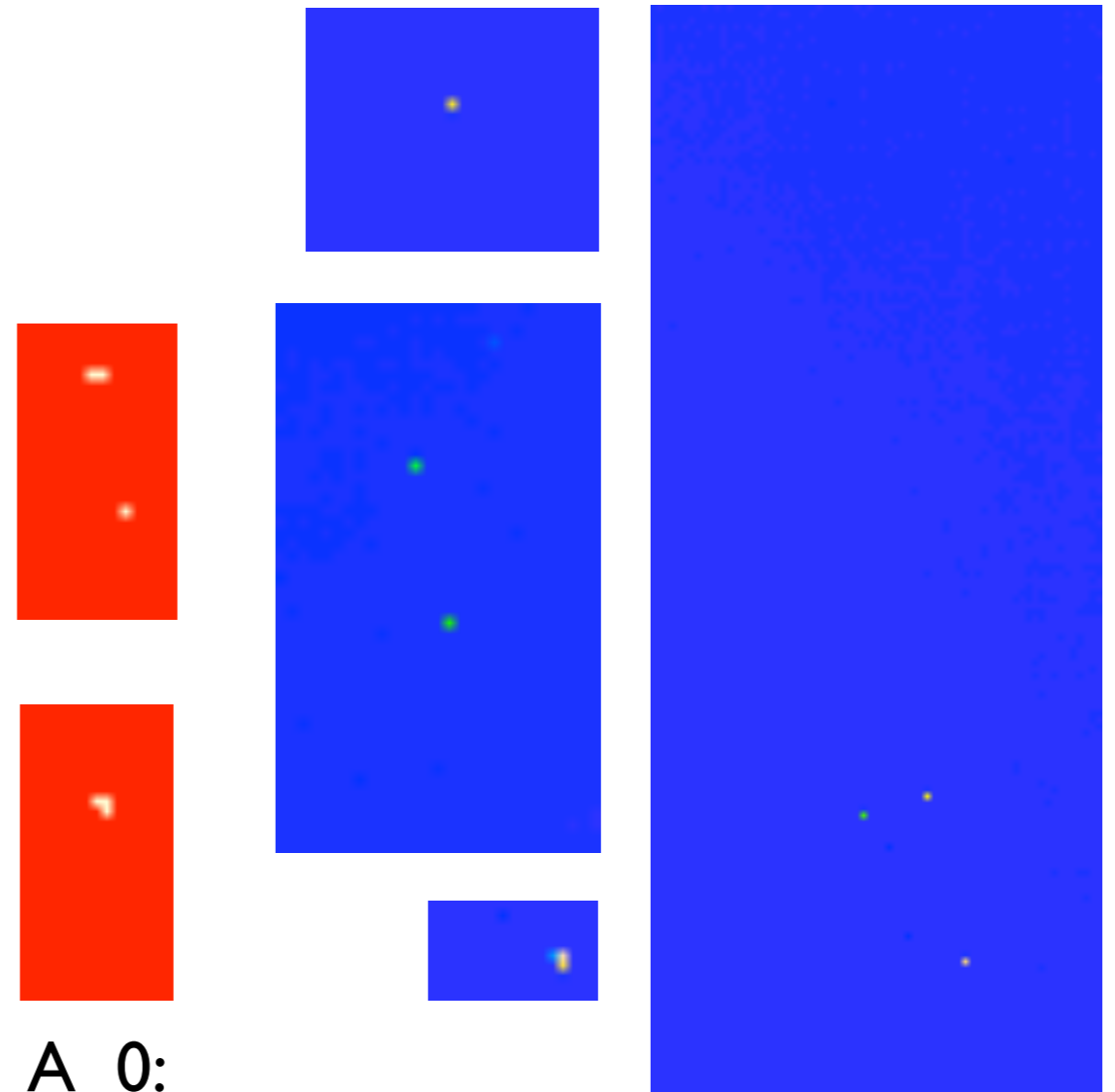
**Readout groups (ROG):**  
 Upper groups transferred first, starting read out from the upper row.  
 Lower groups starting from the last row.

# Local defects: Isolated dead pixels

Singles, doubles, small clusters



A\_0: Grey image [R]

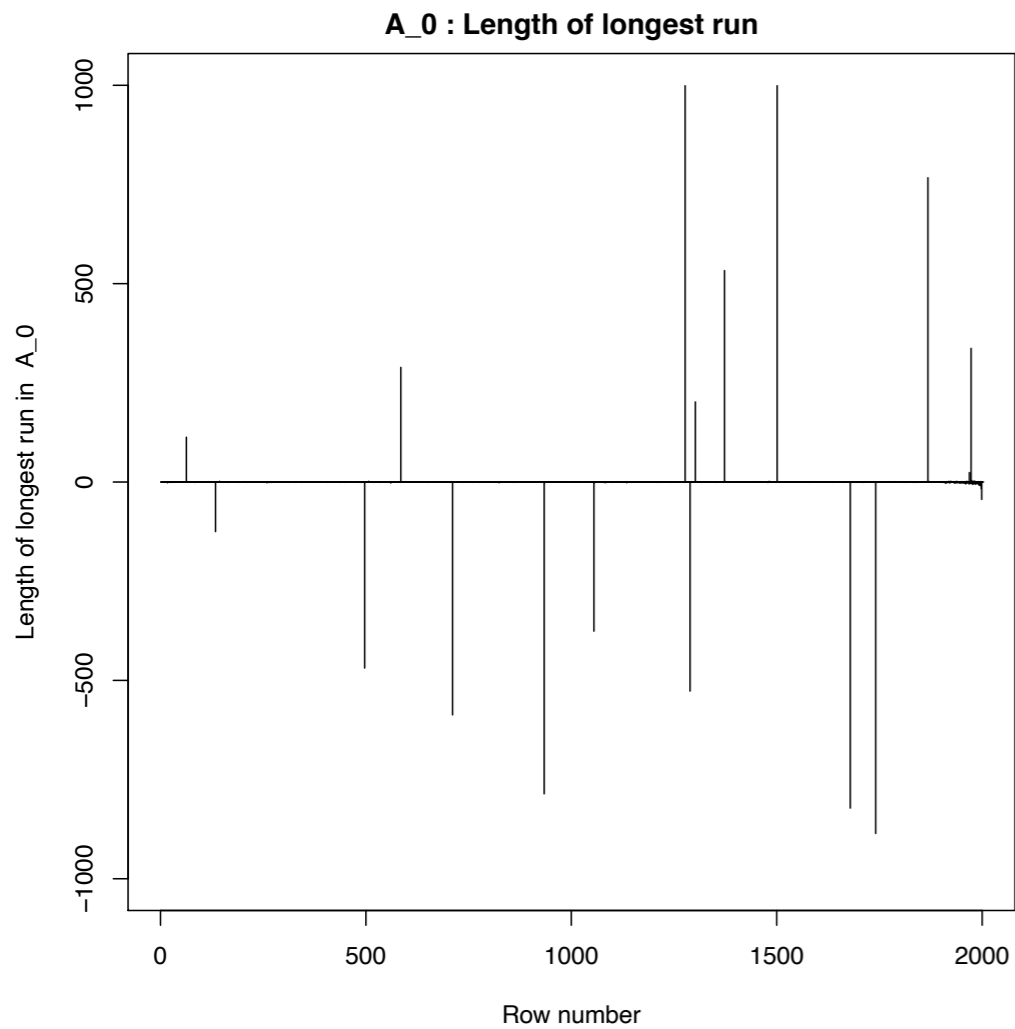


A\_0:  
bp binary  
image [R]

A\_0: Black  
image [R]



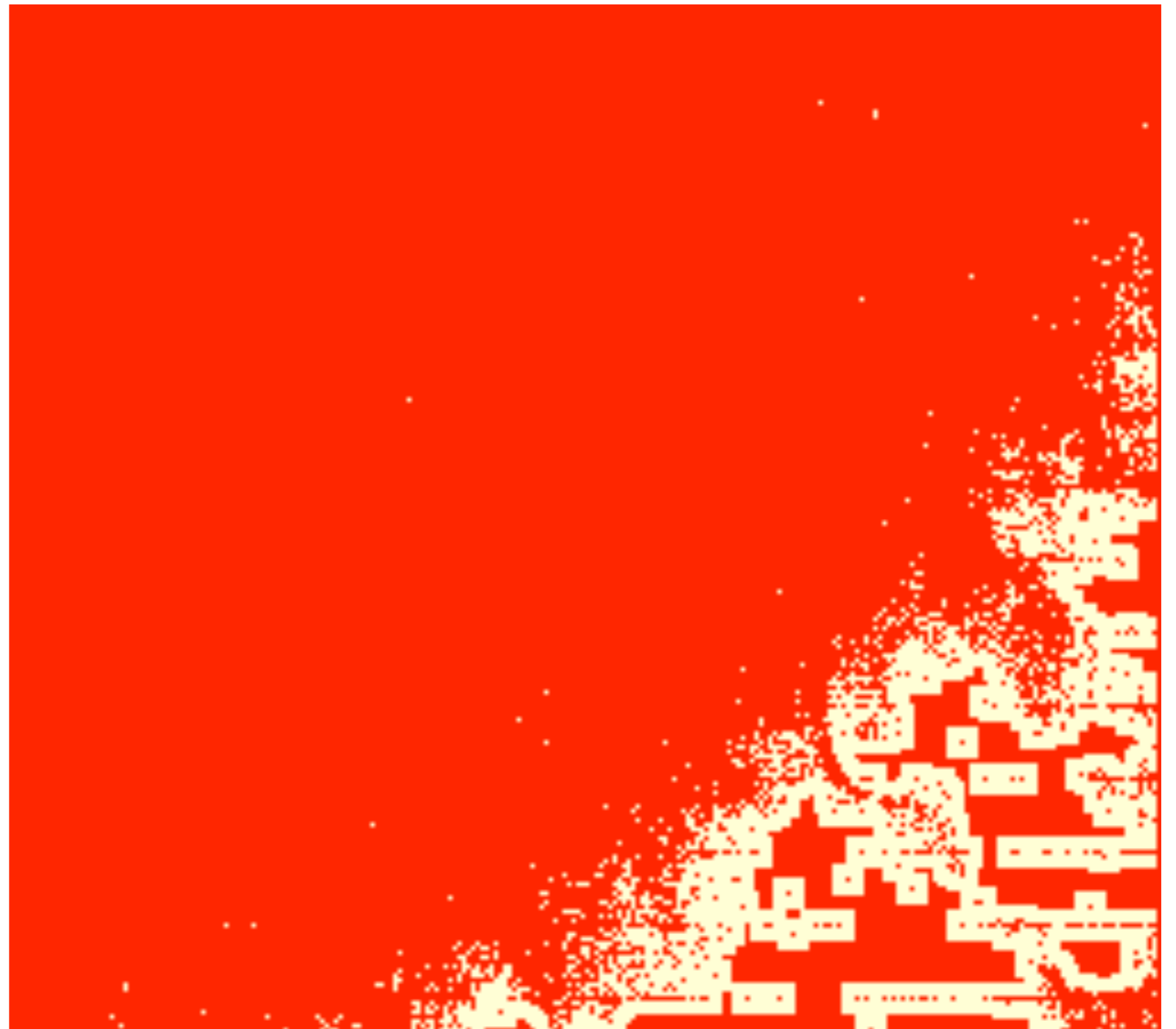
# Local defects: Dead lines



A\_0: Graph of  
bad pixel images

A\_0: Bad pixel image

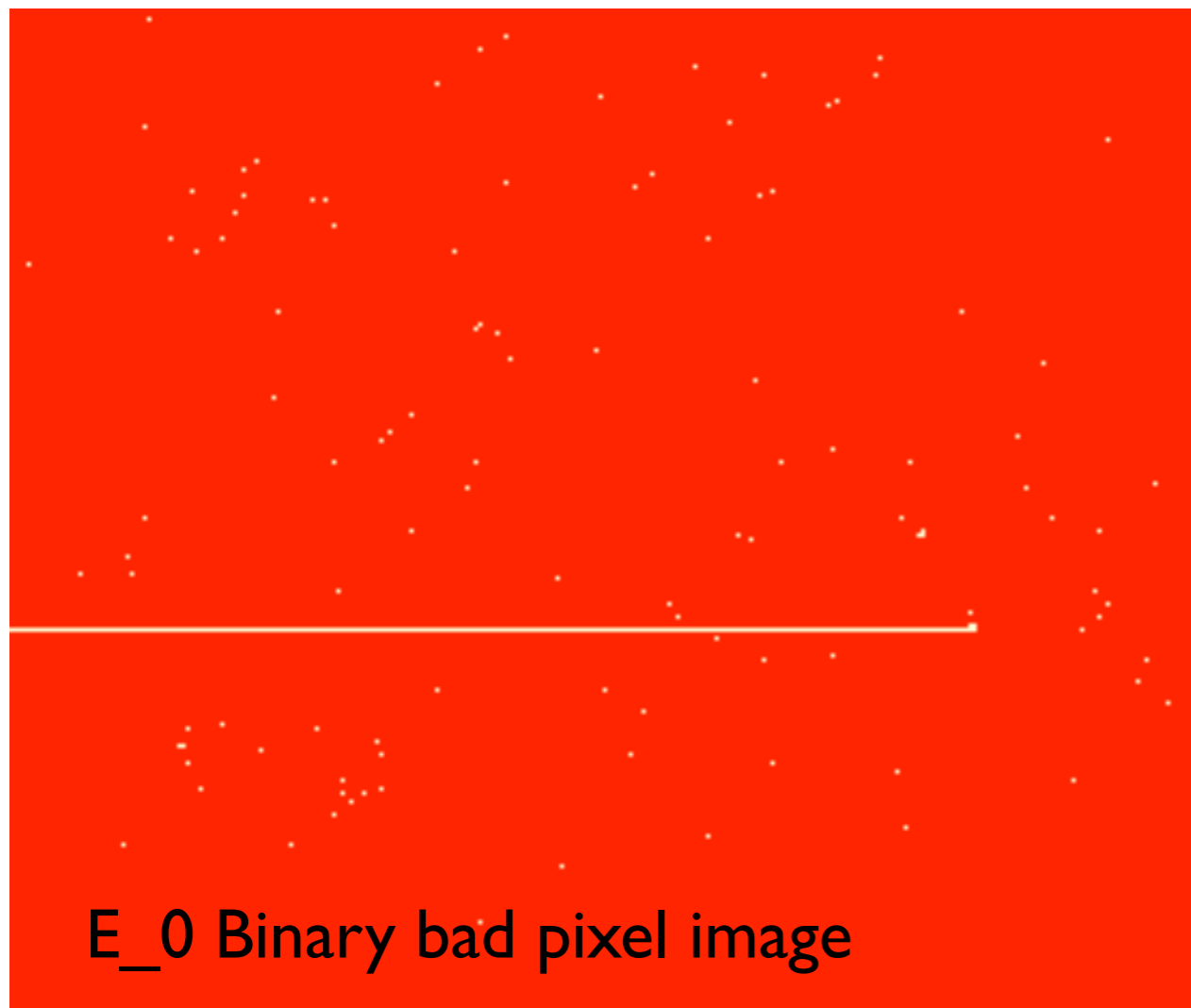
# Local defects: Corners



B\_0: Binary bad pixel image [R]

# Local defects: Patches

- Areas with high density area of bad pixels



# Spatial model for dead pixels

## Dead pixel set as point process

Detector is based on a lattice, but **our interest** is in **locations** of *dead pixels and these are relatively few*. Hence, use a *spatial point pattern* model, but with reduced resolution (given by the detector lattice).

Point pattern  $X$ : random locations of dead pixels (2 dimensional)

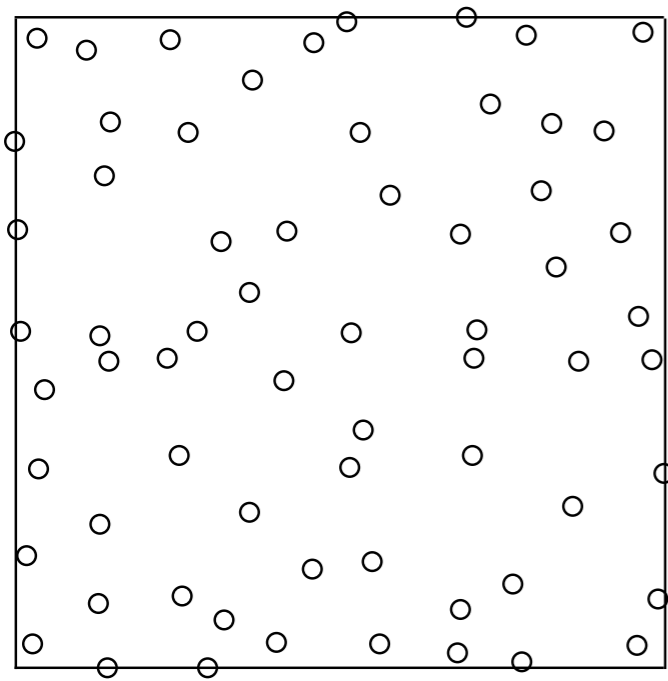
### Objectives:

- describe spatial distribution of dead pixels
- hypothesise causes for dead pixels

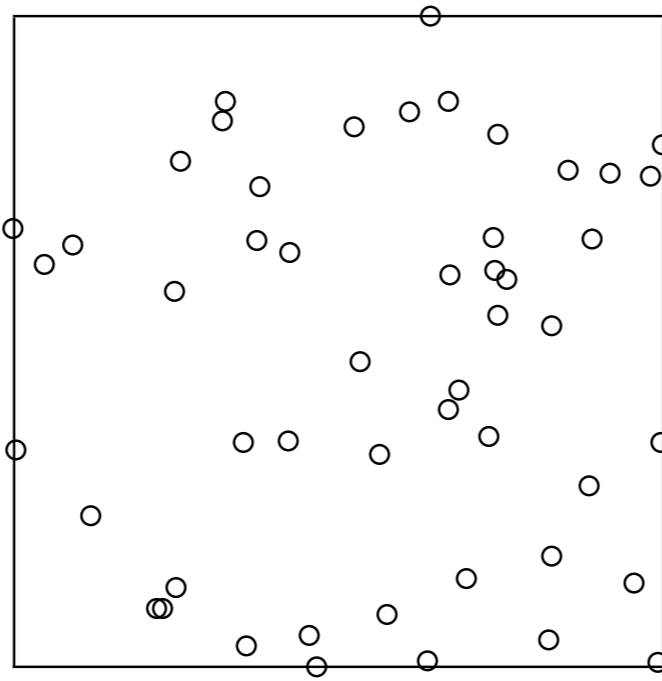
For example, look at CSR...

# Complete spatial randomness (CSR)

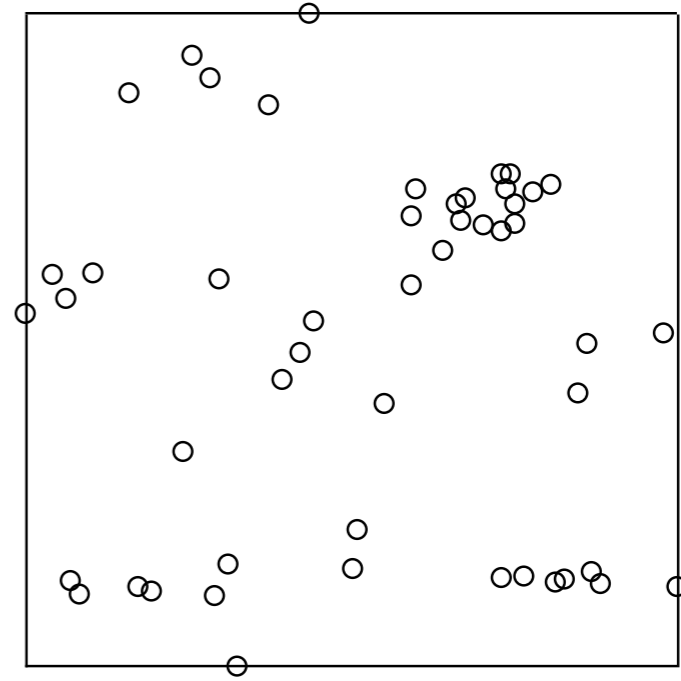
CSR: Points are distributed independently and homogeneously, as in a homogenous Poisson process.



Regular (nearly)



CSR



Clustering

# Exploring CSR using F- and G-functions

## **Nearest neighbour function G:**

Cumulative distribution function of the distance from an arbitrary point to its nearest point

Under CSR:  $G(r) = 1 - \exp(-\lambda\pi r^2)$

## **Empty space function F:**

Cumulative distribution function of the distance from an arbitrary location to its nearest point

Under CSR:  $F(r) = 1 - \exp(-\lambda\pi r^2)$

# Exploring CSR using Ripley's K-function

## **K-function:**

expected number of extra points in circle of radius  $r$  rescaled by density

$$K(r) = \lambda^{-1} E[N_0(r)]$$

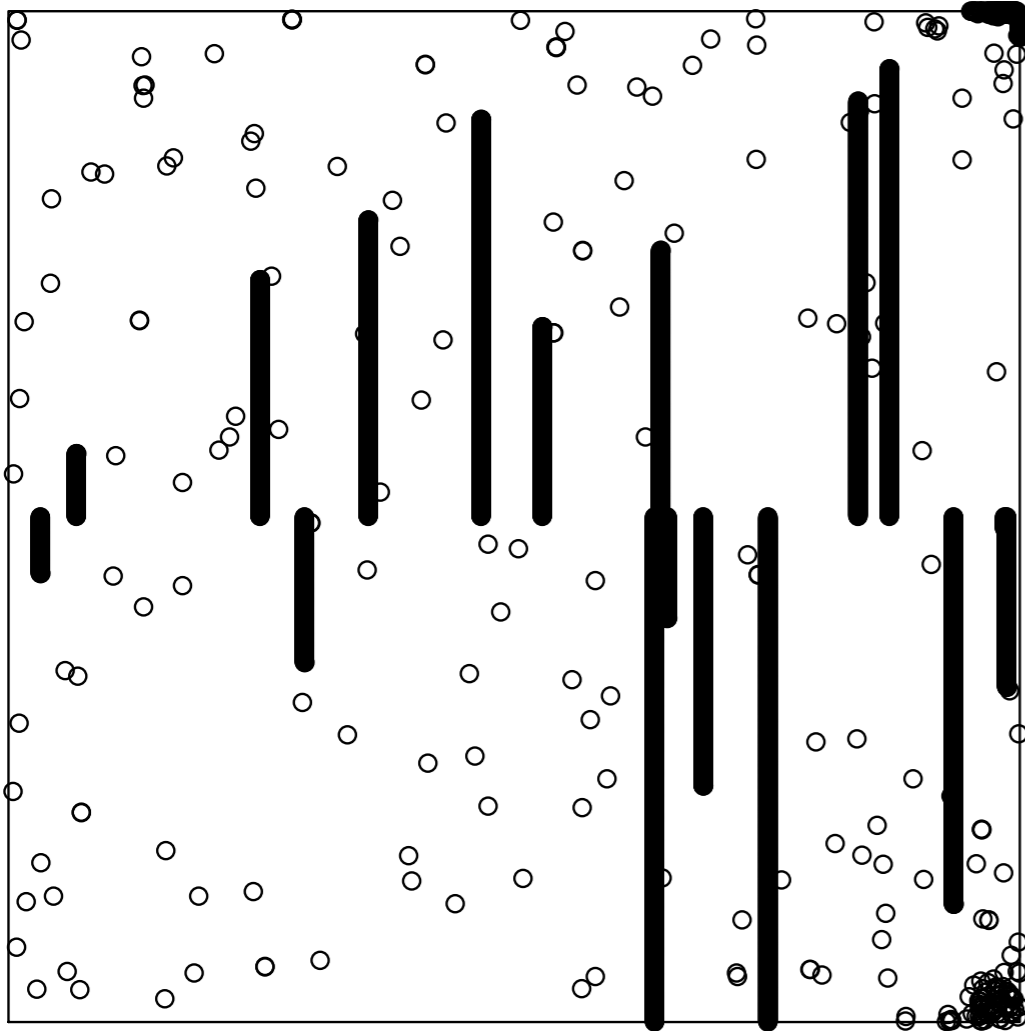
$N_0(r)$  number of points within distance  $r$  from arbitrary point

$\lambda$  globally estimated density

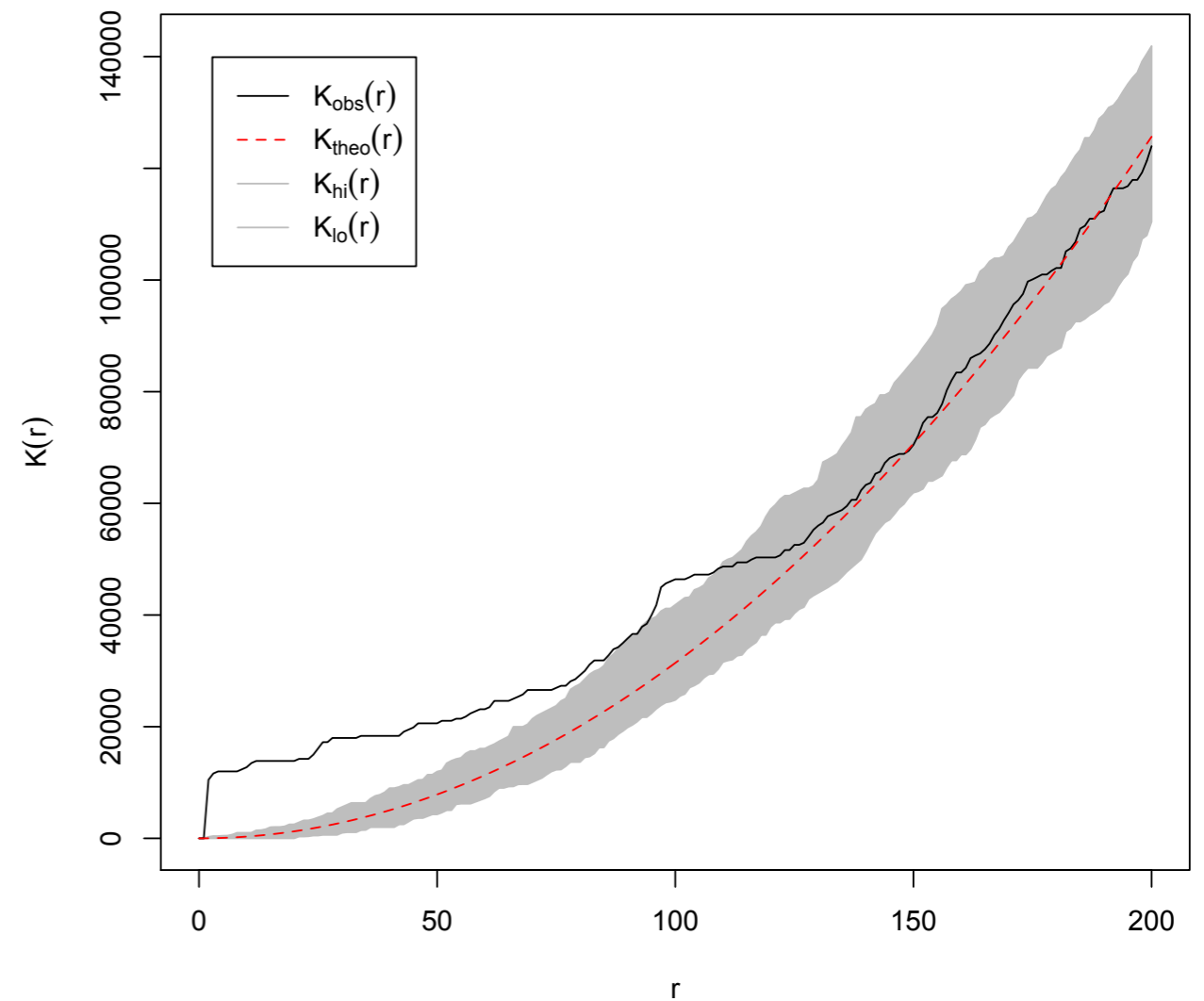
Under CSR:  $K(r) = \pi r^2$

# Point pattern and K-function

Point pattern A\_0



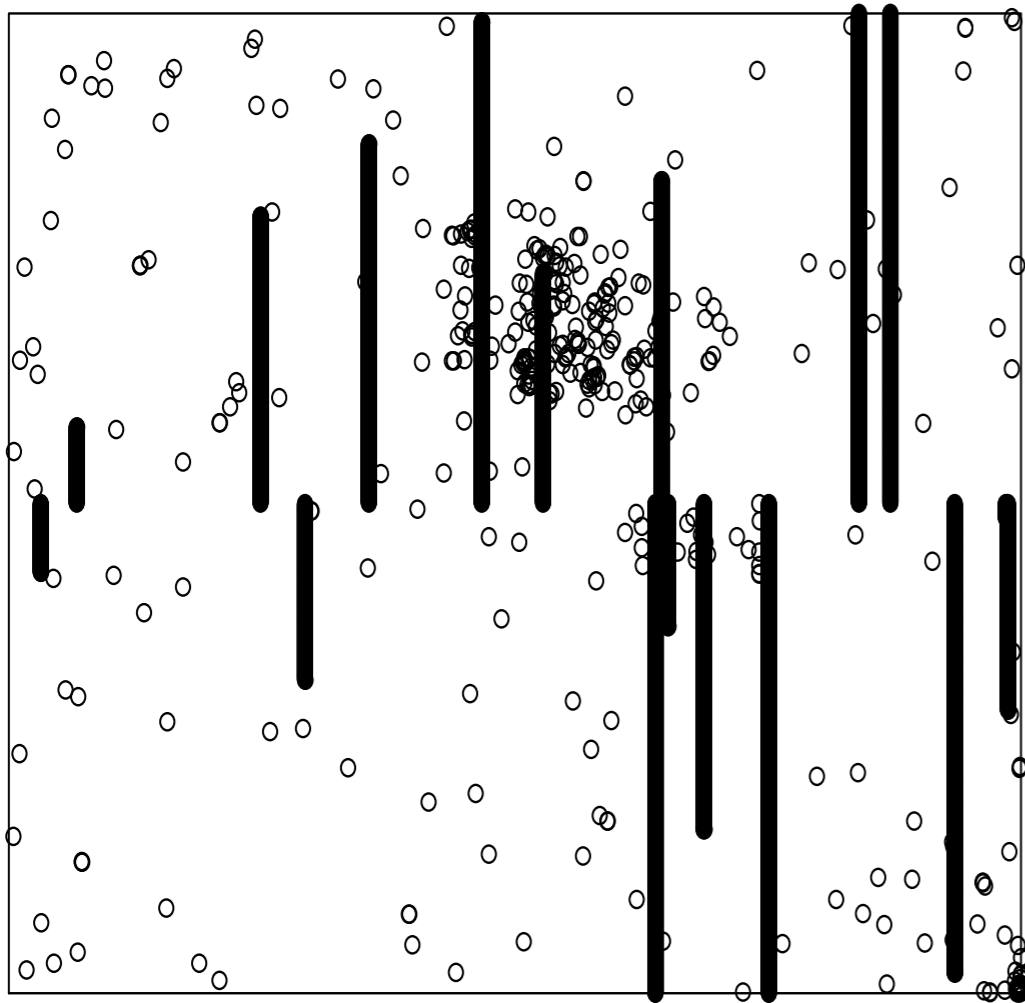
K function A\_0 cropped



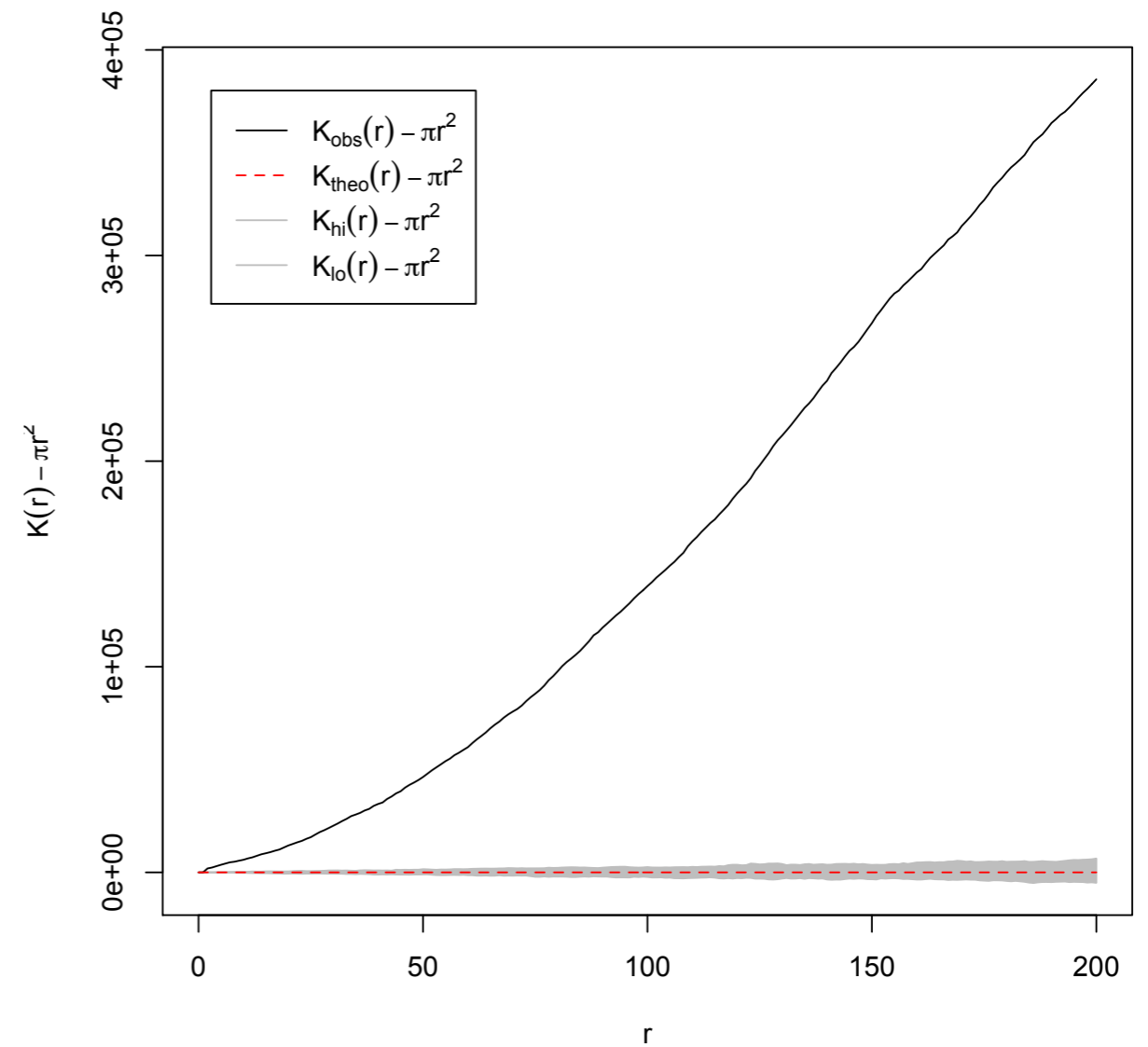


# Point pattern and K-function

Point pattern E\_0



K function normed E\_0 cropped



# Are we asking the right question?

**Modified question: Is it CSR after we remove all specific (known) problems?**

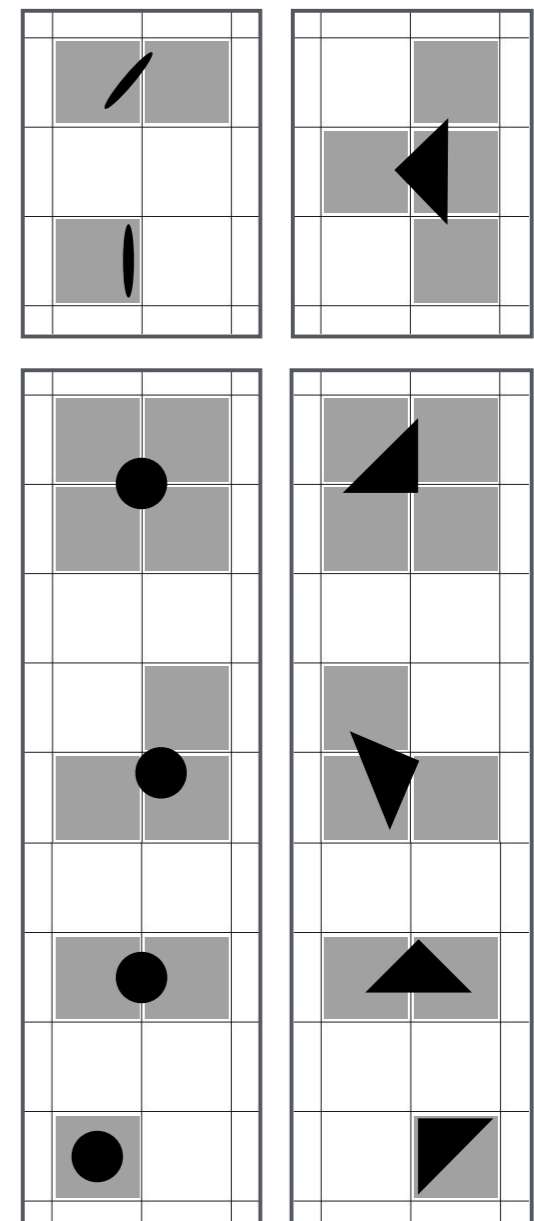
## Step 1:

Convert point process into *event process* by

- Reducing a line to one endpoint
- Reducing a clusters to its centre point

## Step 2:

- Fit inhomogeneous density
- Cut out areas above threshold

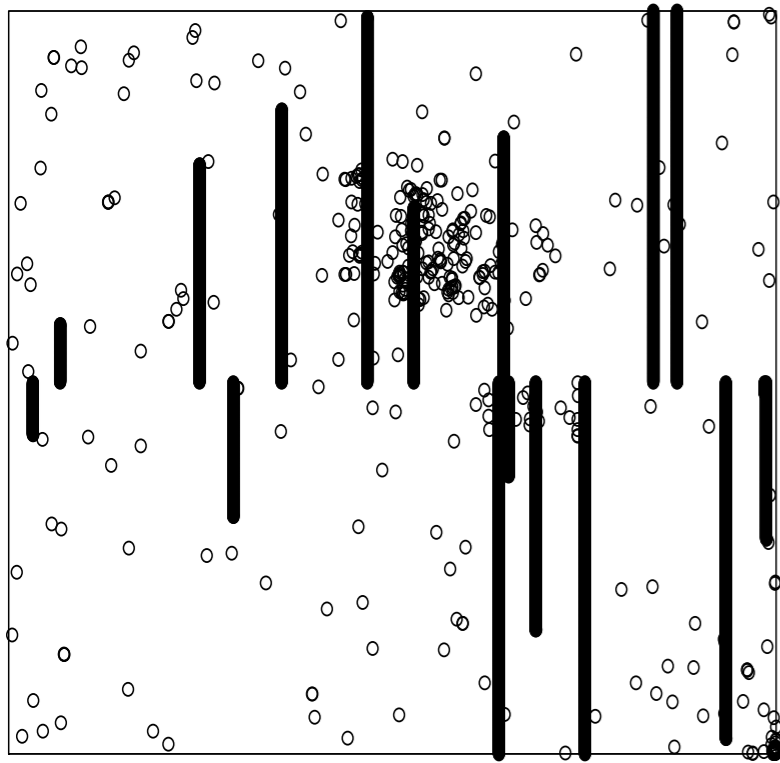


# Modified process: K-function

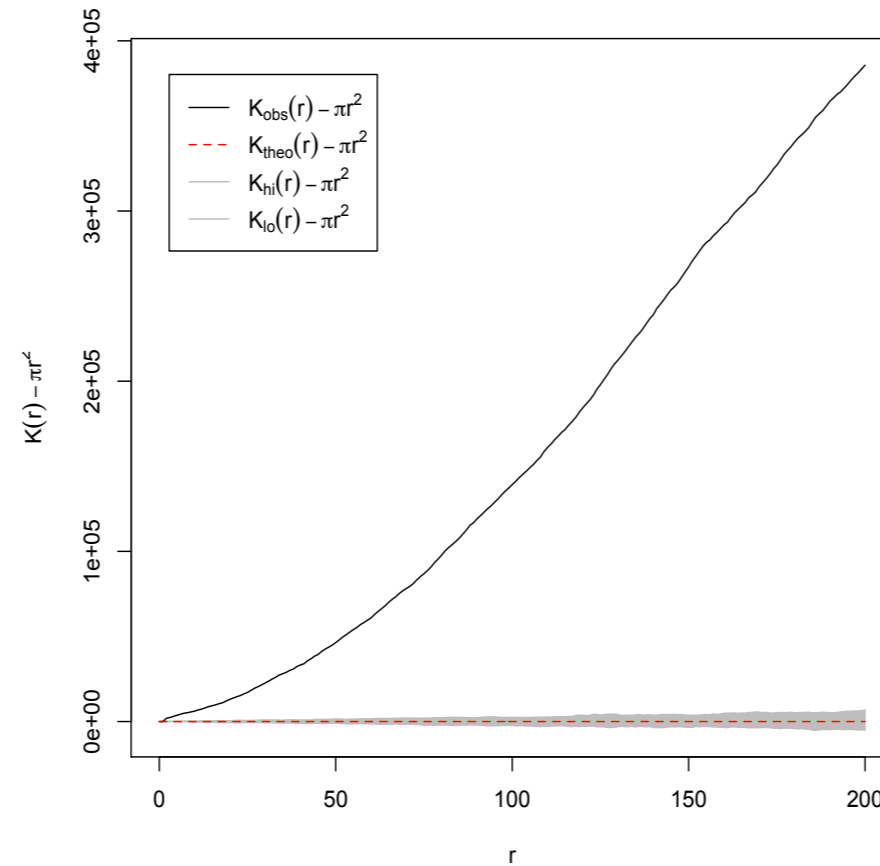
Pixel level

Event level

Point pattern E\_0

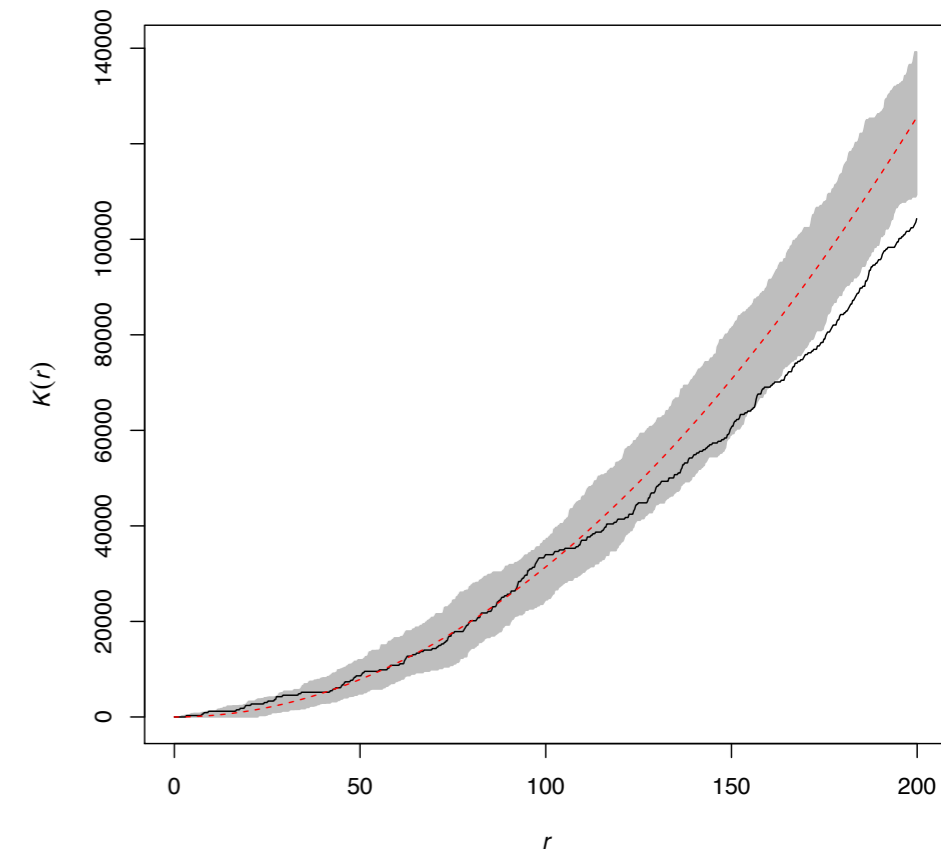


K function normed E\_0 cropped



Not CSR

K-function, Events, nsim=100

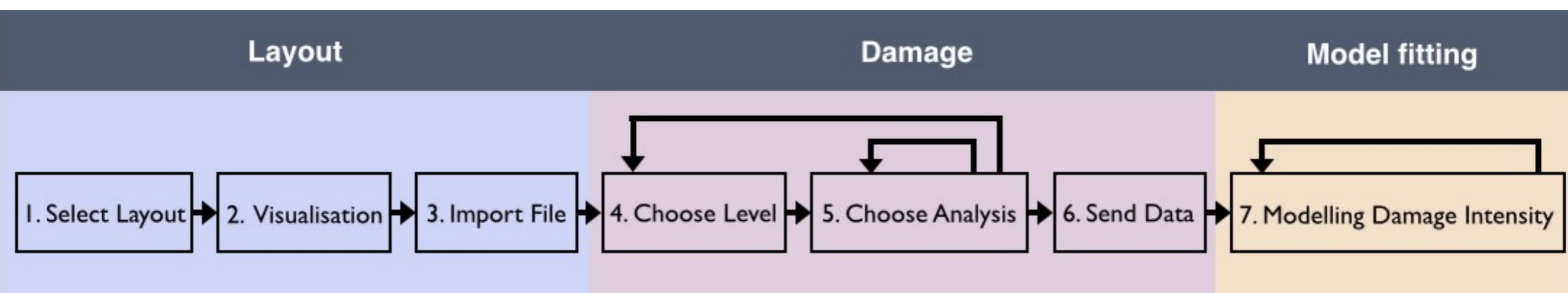


CSR

# Seed funding for a software project with Turing

- Working with Turing Research Software Engineer Group
- *DetectorChecker* R package for statistical analysis of pixel damage in CT scanners available at <https://github.com/alan-turing-institute/DetectorChecker>
- *DetectorCheckerWebApp* for useful initial graphical/analysis, available at <https://detectorchecker.azurewebsites.net>
- Facility to upload data in different formats (crowd sourcing)

*Brettschneider, Giles, Kendall, Lausaskas, (2020). DetectorChecker: analyzing patterns of defects in detector screens. Journal of Open Source Software, 5(56), 2474*



# Microscopic image based modelling of biological processes

## Quantifying spatial abundance of proteins in living cells

Confocal fluorescent laser microscopy (live cells)

Electron microscopy (dead cells, higher resolution)

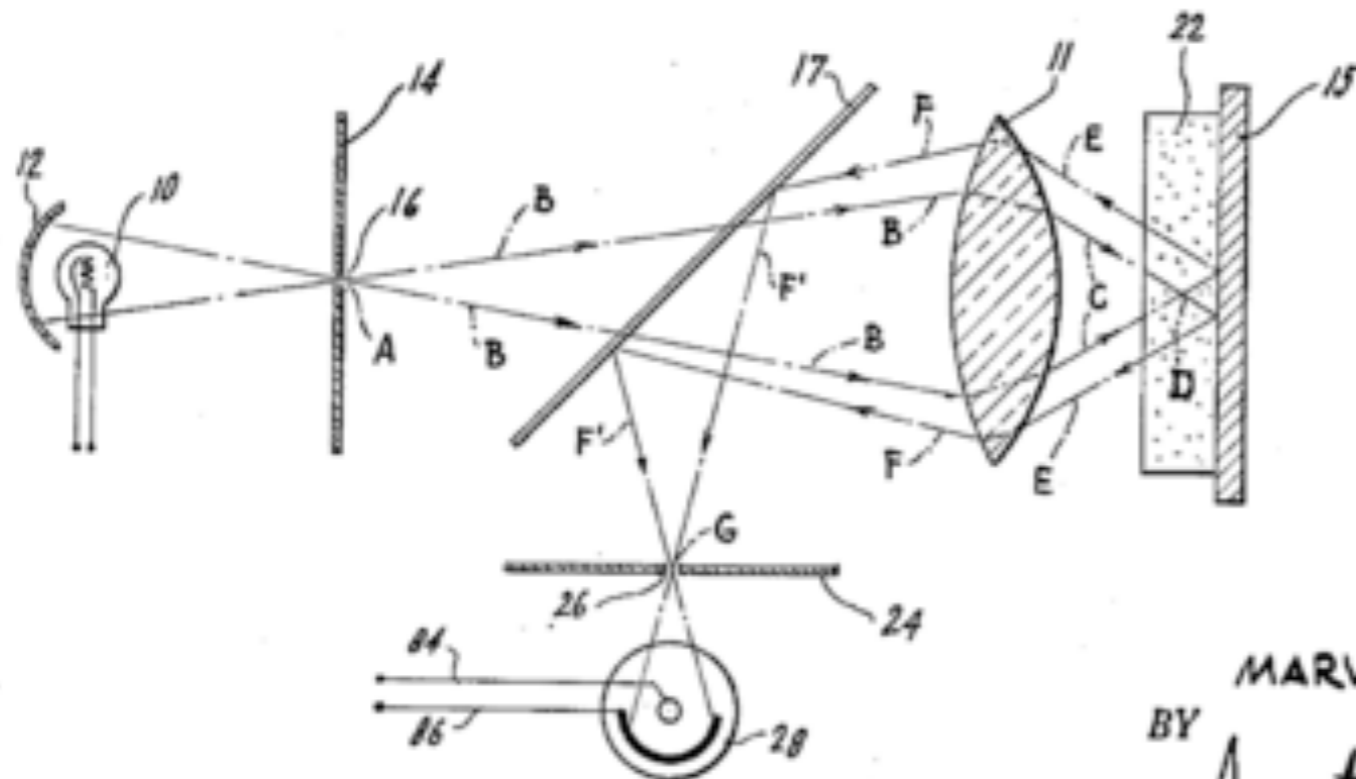
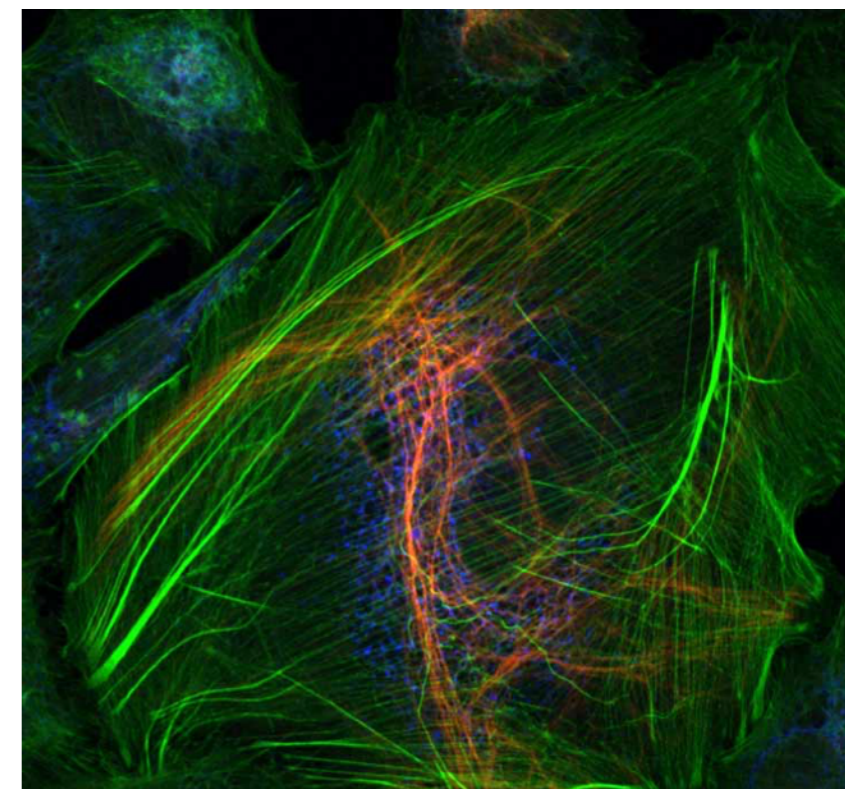
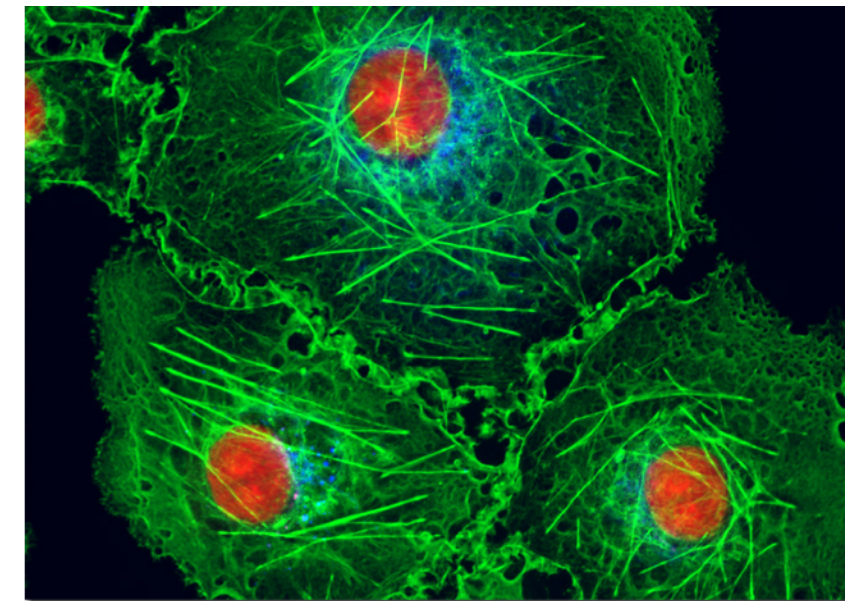


FIG. 3 .

INVENTOR.  
MARVIN MINSKY  
BY  
Ameter & Levy  
ATTORNEYS



# Confocal microscope

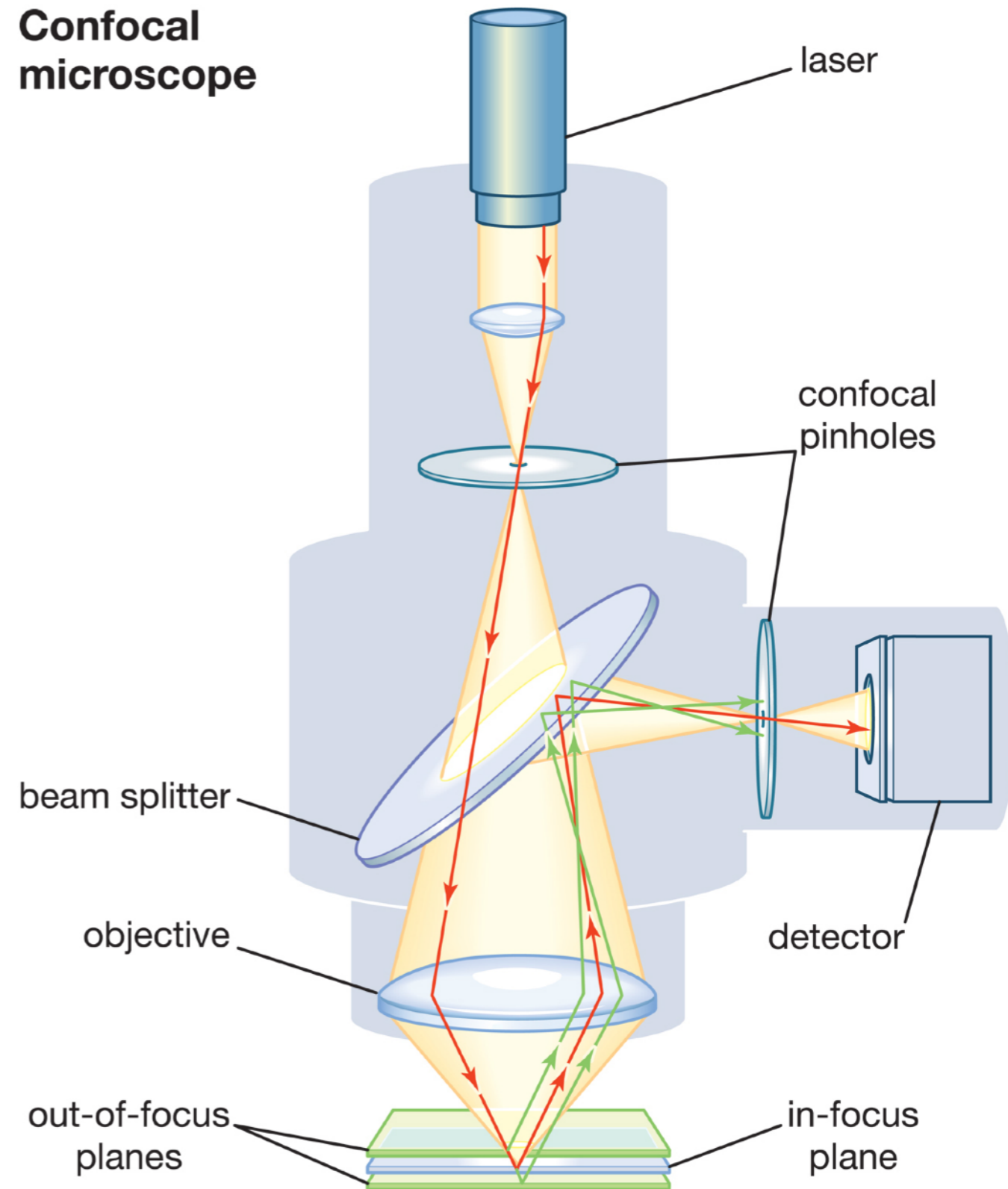
## Wide-field microscopy:

- All of specimen excited at the same time
- Large unfocused background

## Confocal microscope:

- Field of view limited by geometric optics
- Pinhole in front of the detector to eliminate out-of-focus signal
- Long exposure required
- Scanning arrangement to build up image of larger region
- Better resolution

Confocal microscope



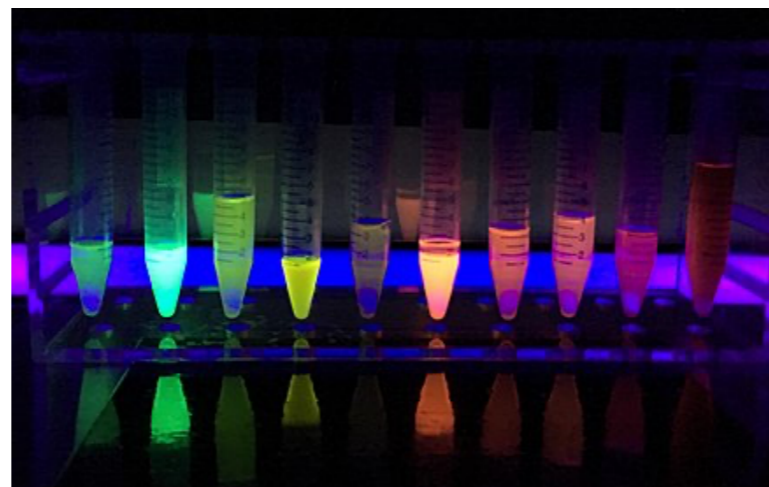
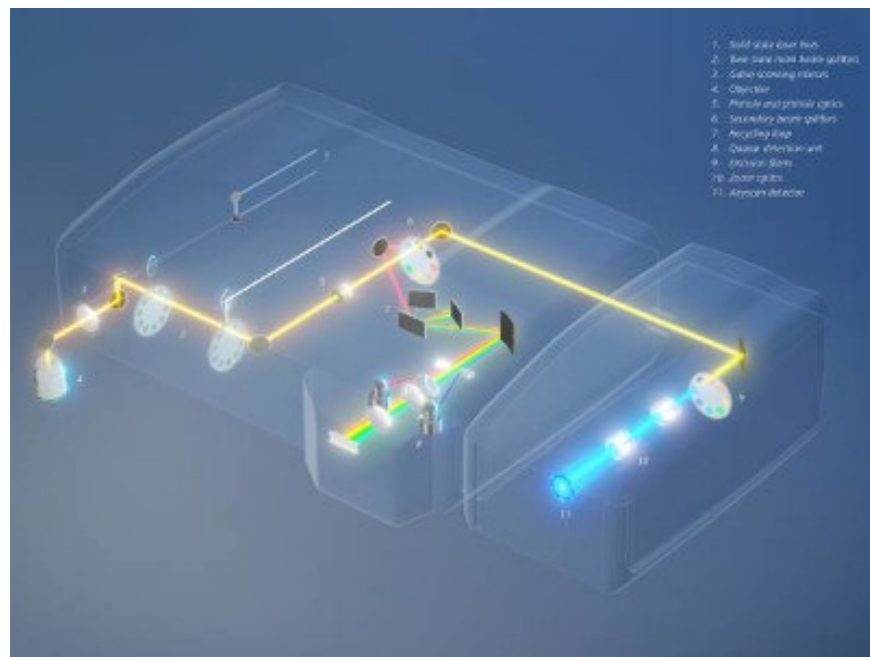
© 2012 Encyclopædia Britannica, Inc.

<https://www.britannica.com/technology/microscope/Confocal-microscopes>

# Confocal fluorescent laser microscope

## Fluorescent confocal microscope:

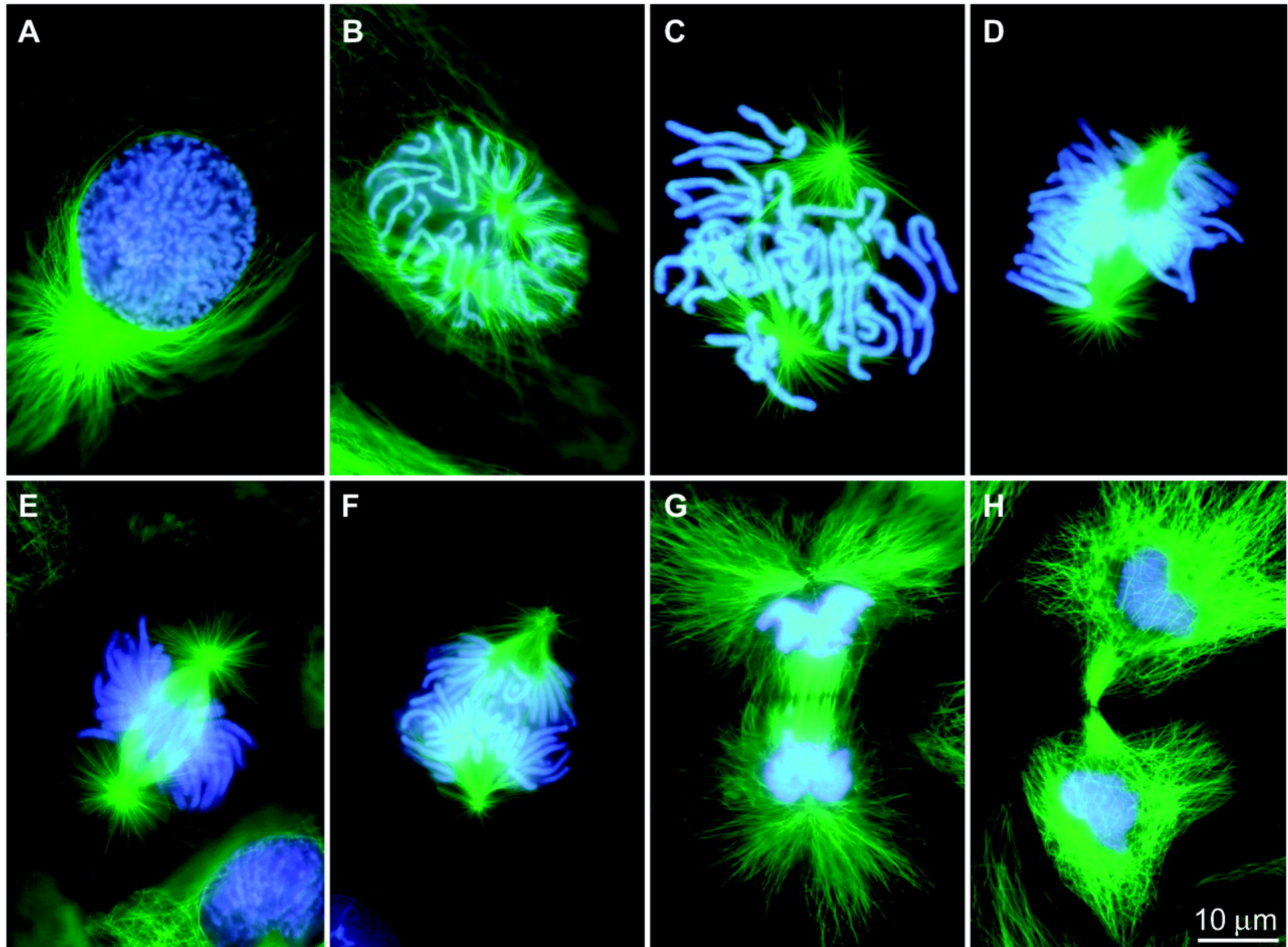
- Combination of two ideas in microscopy technology
- High resolution images
- Life cells
- 2D or 3D through scanning schemes
- Multi-channel through use of range of fluorescent proteins



[https://www.biocompare.com/25608-Microscopes-and-Cell-Imaging-Systems/14617250-ZEISS-LSM-980-Confocal-Laser-Scanning-Microscope/?pda=25608|14617250\\_0\\_1|2254289,2254327|1|&dfp=true](https://www.biocompare.com/25608-Microscopes-and-Cell-Imaging-Systems/14617250-ZEISS-LSM-980-Confocal-Laser-Scanning-Microscope/?pda=25608|14617250_0_1|2254289,2254327|1|&dfp=true)

[https://en.wikipedia.org/wiki/Green\\_fluorescent\\_protein#/media/File:Fluorescence\\_from\\_Fluorescent\\_Proteins.jpg](https://en.wikipedia.org/wiki/Green_fluorescent_protein#/media/File:Fluorescence_from_Fluorescent_Proteins.jpg)

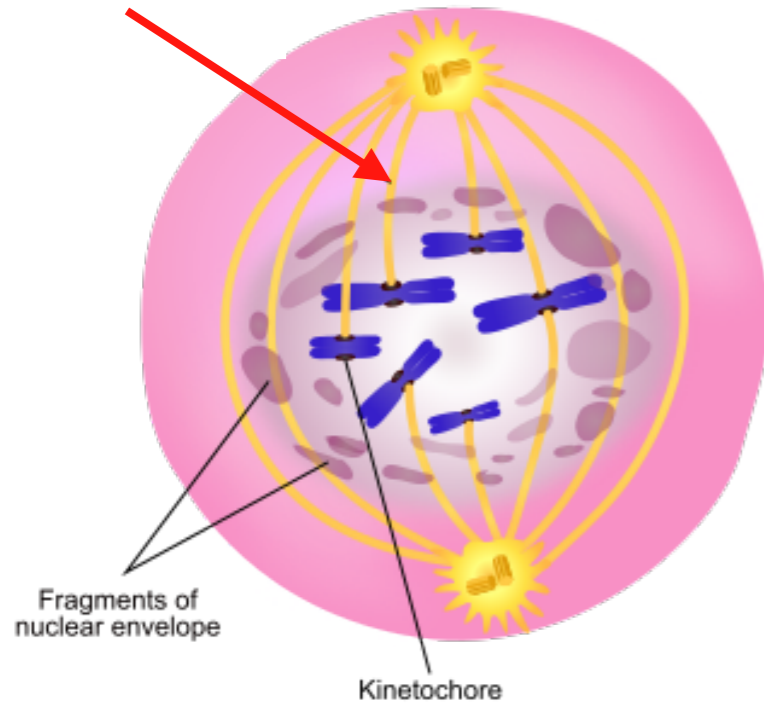
# Microtubules formation during mitosis





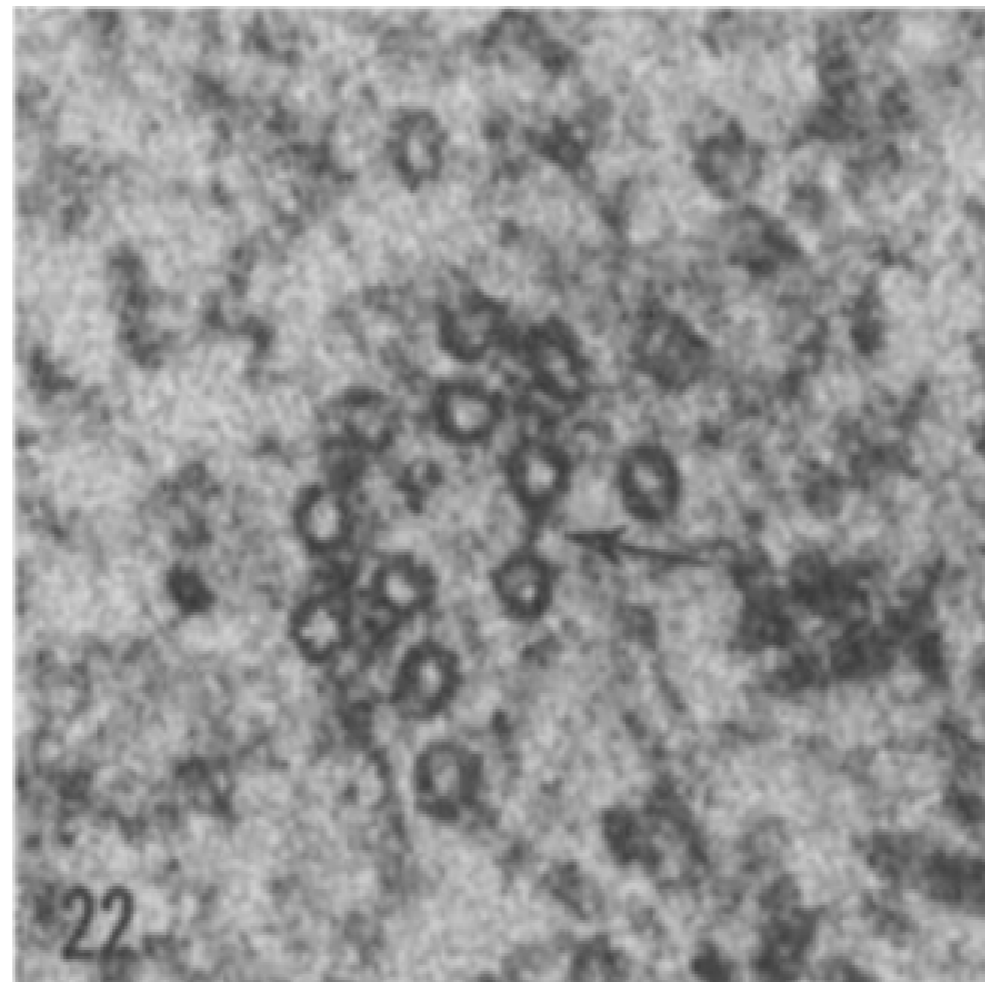
# Microtubules during mitosis (cell division)

Microtubule

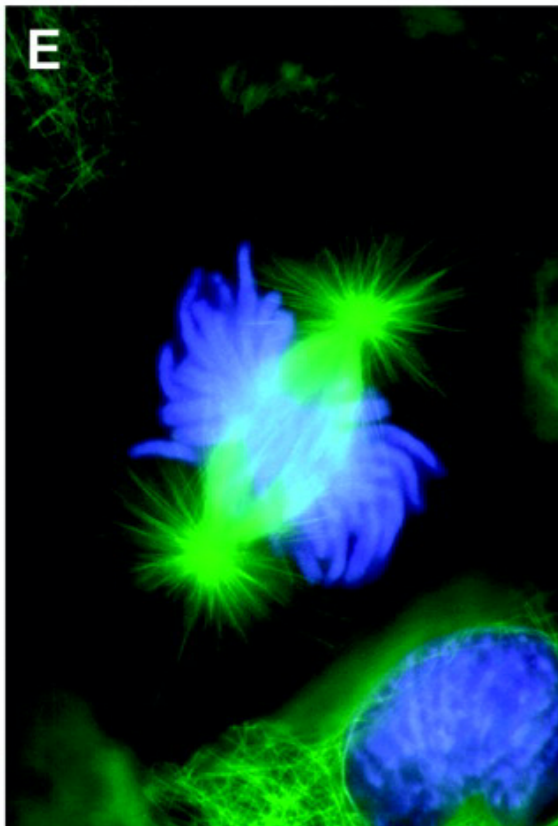
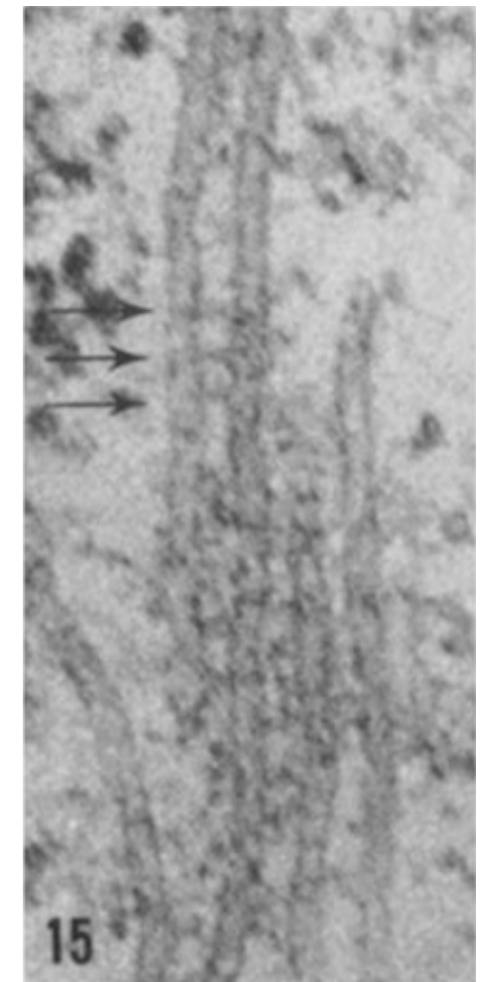


- Centrosomes = centrioles + microtubules
- Centrioles help the spindle into proper formation
- Spindle microtubules are arranged in K-fibers
- Intertubule bridges formed by mesh

Perpendicular to the microtubule axis



Parallel



# Microtubules locations as point patterns

Stephen Royle's Lab (Centre for Mechanochemical Cell Biology) asks:  
**What is the role of TACC3 protein for the structure of microtubules within K-fibres and mesh?**

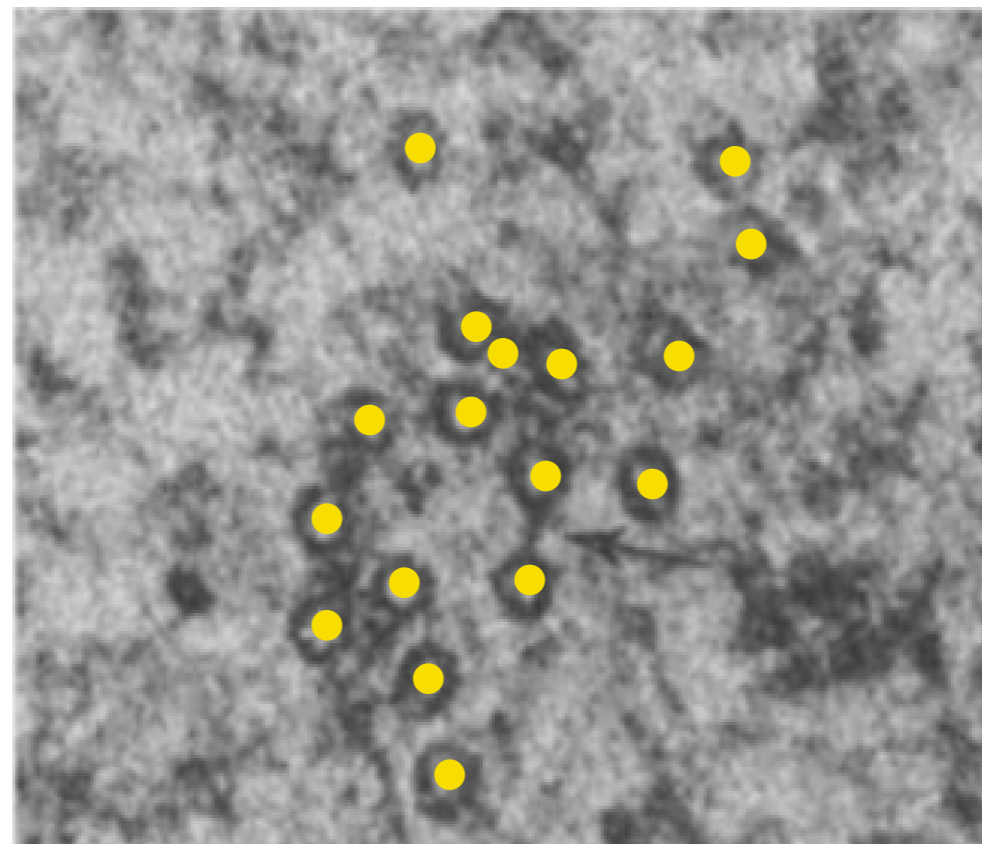
**Experiment:** Overexpression of TACC3 through treatment versus control.

**Data:** Microscopic images collected in planes perpendicular to the fibre axes.



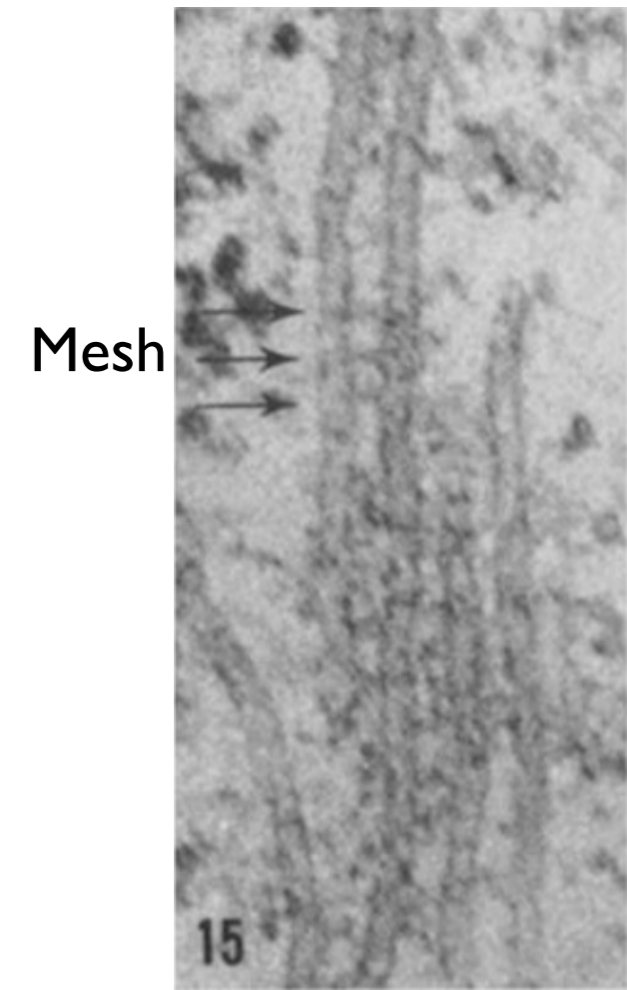
Team:  
Steve Royle  
Tom Honnor (now at UCL)  
Adam Johnson  
Julia Brettschneider

Perpendicular view



Model: locations as point pattern

Parallel

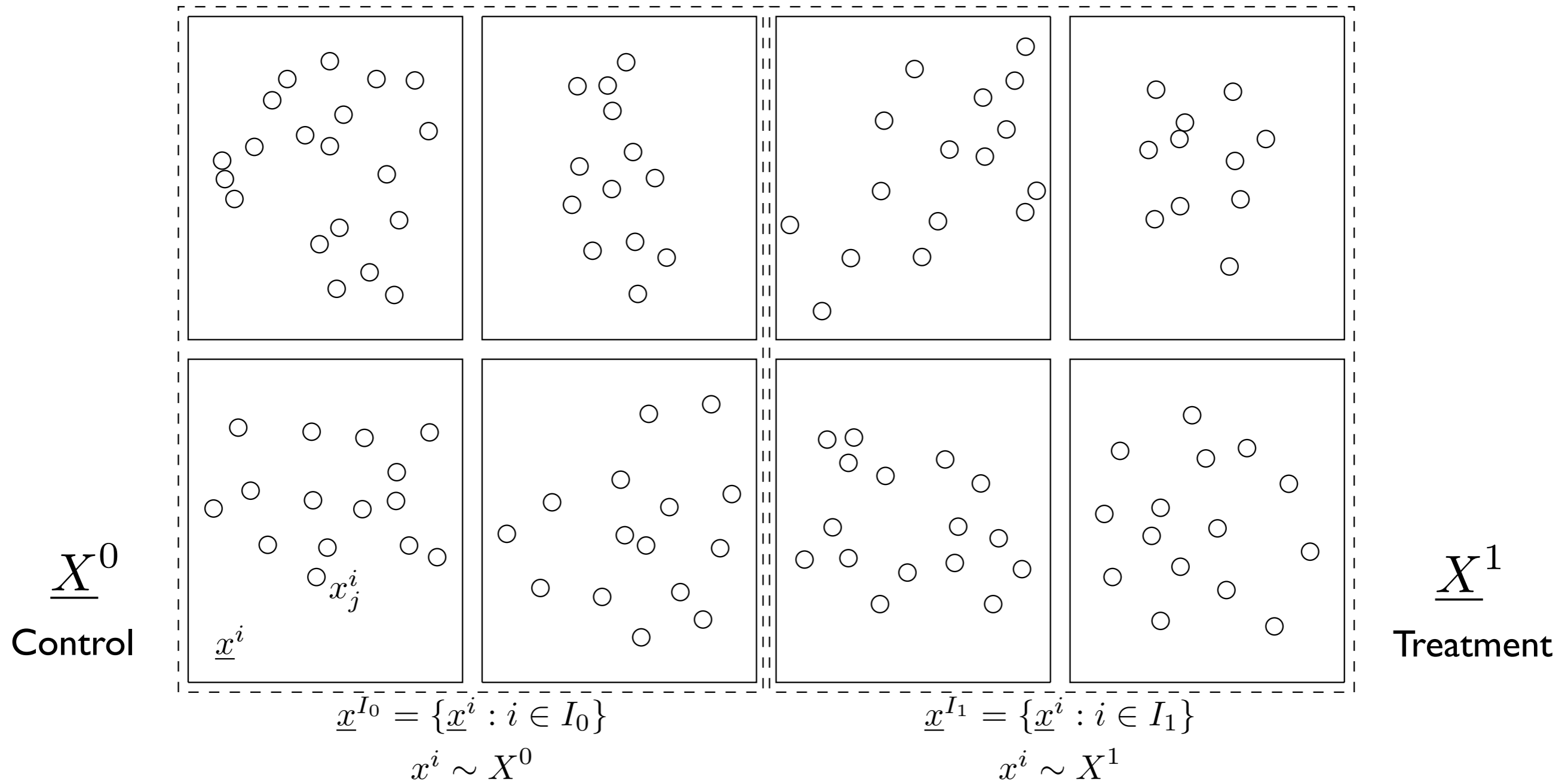


# Study I: Microtubules - mathematical model

## Data:

Microscopic images of treatment (n=37) versus control (n=26)

Observation window surrogate for cross sectional area of K-fibres



# Point patterns models

Set of point patterns:

$$\chi_2 := \{(\underline{x} = x_1, x_2, \dots, x_{n(\underline{x})}) : n(\underline{x}) \in \mathbb{N}, x_i \in \mathbb{R}^2 \text{ for } i = 1, 2, \dots, n\}$$

Model pattern as realisations of a point process:

Random subset  $\underline{X}$  on  $\mathbb{R}^2$ .

For  $B$  in Borel  $\sigma$ -algebra  $\mathcal{B}(\mathbb{R}^2)$  on  $\mathbb{R}^2$  :  $\underline{X}_B = \underline{X} \cap B$

Counts (random variable):  $N(B) = n(\underline{X}_B) =$  number of points of  $\underline{X}$  in  $B$

Intensity measure  $\mu$

$$\mu(B) = \mathbb{E}[N(B)], \quad \forall B \in \mathcal{B}(\mathbb{R}^d).$$

If for some function  $\rho : \mathbb{R}^2 \rightarrow [0, \infty)$

$$\mu(B) = \int_{x \in B} \rho(x) dx, \quad \forall B \in \mathcal{B}(\mathbb{R}^d),$$

then  $\rho$  is referred to as the intensity function of  $\underline{X}$ .

# Summary statistics: basics

---

Let  $\underline{x}$  be a realisation of  $\underline{X}$  on the observation window  $W$ .

Estimator for the **intensity** of  $\underline{X}$  :

$$\hat{\rho} = \frac{n(\underline{x})}{|W|}$$

Let  $\text{nn}(x_j)$  be the (set of) **nearest neighbours** of point  $x_j$ .

$$\text{nn}(x_j) = \{x_k : k = \operatorname{argmin}_l \|x_l - x_j\|\},$$

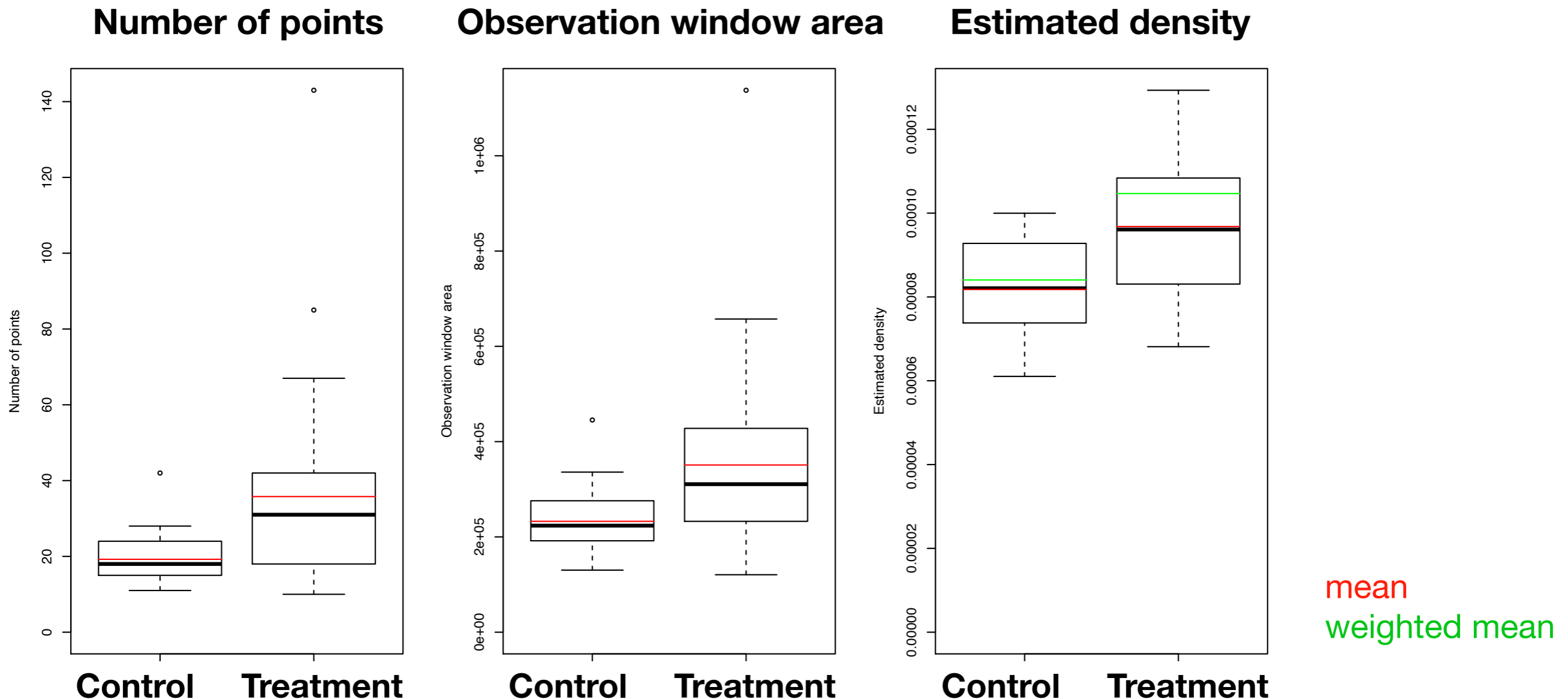
and  $\text{nnd}(x_j)$  its **nearest neighbour distance**

$$\text{nnd}(x_j) = \inf_{x \in \text{nn}(x_j)} \{\|x_j - x\|\}.$$

Estimator for the **mean nearest neighbour distance** for  $\underline{X}$  :

$$\overline{\text{nnd}}(\underline{x}) = \frac{1}{n(\underline{x})} \sum_{j=1}^{n(\underline{x})} \text{nnd}(x_j)$$

# EDA: First order statistics



- All means/medians are greater for treatment
- Treated K-fibers are made up of a greater number of microtubules which are more closely separated within thicker K-fibers
- Weighted mean densities greater than unweighted means densities (i.e. K-fibers with greater numbers of microtubules are more tightly packed)

# Summary statistics: K-function

K-function (Ripley 1977) (scaled neighbourhood count function):

$$K(r) = \frac{1}{\rho} \mathbb{E} \left[ \frac{1}{N(S)} \sum_{x_j \neq x_k \in \underline{X}} 1_{\{\|x_j - x_k\| < r\}} \right]$$

Estimate:

$$\hat{K}(\underline{x}, r) = \frac{|W|}{n(\underline{x})^2} \sum_{j \neq k} e_{j,k} 1_{\{\|x_j - x_k\| \leq r\}}$$

where  $e_{j,k}$  is the proportion of the circumference of the circle with centre  $x_j$  and radius  $\|x_j - x_k\|$  in  $W$  (edge correction).

$K(r) = \pi r^2$  : CSR (complete spatial randomness)

$K(r) > \pi r^2$  : aggregation at distances less than  $r$

$K(r) < \pi r^2$  : repulsion at distances less than  $r$

# Summary statistics: G-function

Nearest neighbour function (Diggle 2003):

$$G(r) = \frac{1}{\rho|B|} \mathbb{E} \left[ \sum_{x \in \underline{X}_B} 1_{\{\underline{X} \setminus x \cap b(x,r) \neq \emptyset\}} \right]$$

for finite  $B$  in  $\mathbb{R}^2$ , and  $b(x, r)$  the disc centred at  $x$  with radius  $r$ .

(For stationary  $\underline{X}$  it is independent of  $B$ .)

Distribution of distance of randomly selected point to its nearest neighbour.

Estimate:

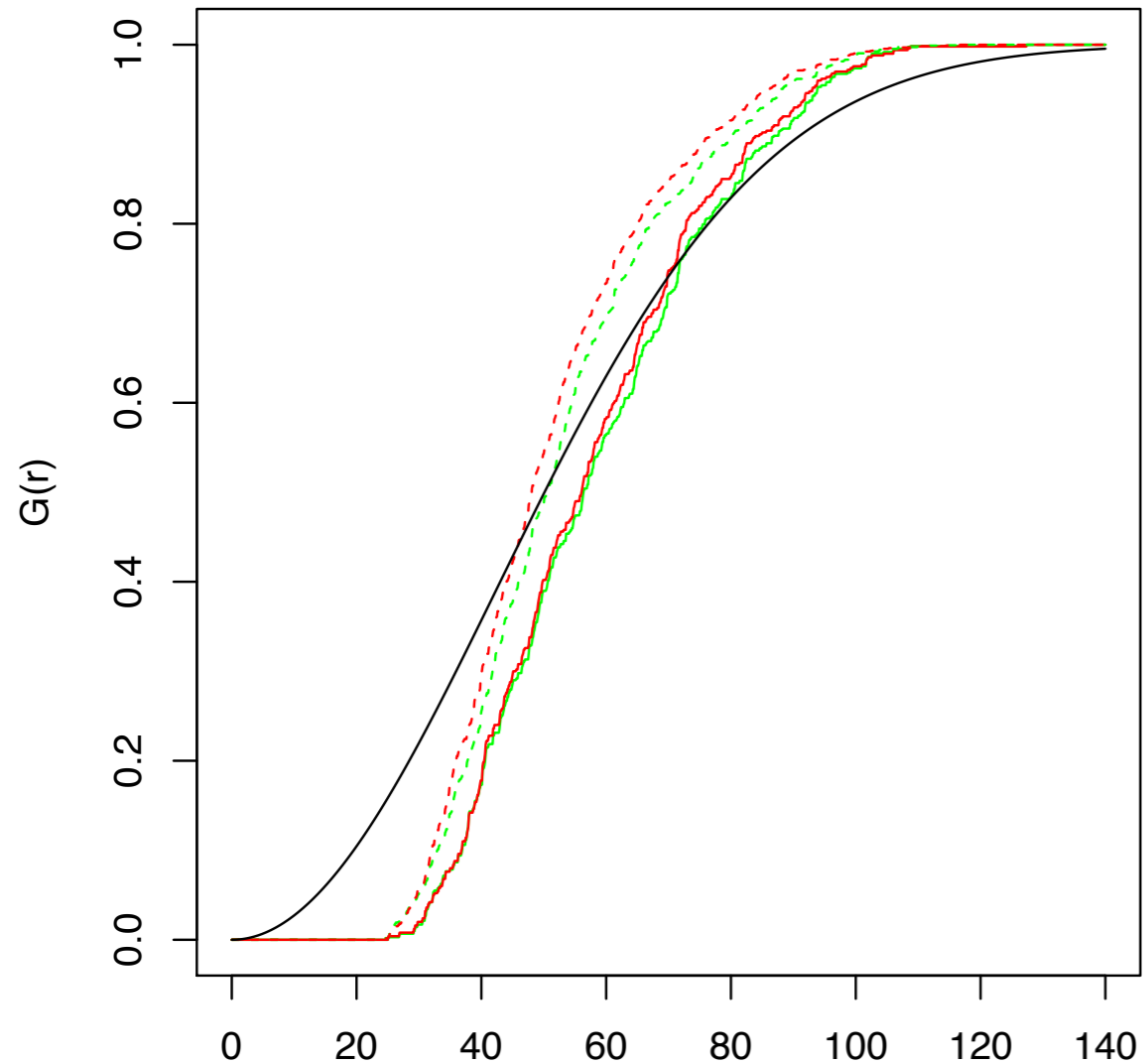
$$\hat{G}(\underline{x}, r) = \frac{1}{n(\underline{x})} \sum_{j=1}^{n(\underline{x})} 1_{\{\text{nnd}(x_j) \leq r\}}$$

If  $\underline{X}$  is completely spatially at random then  $G(r) = 1 - \exp(-\rho\pi r^2)$

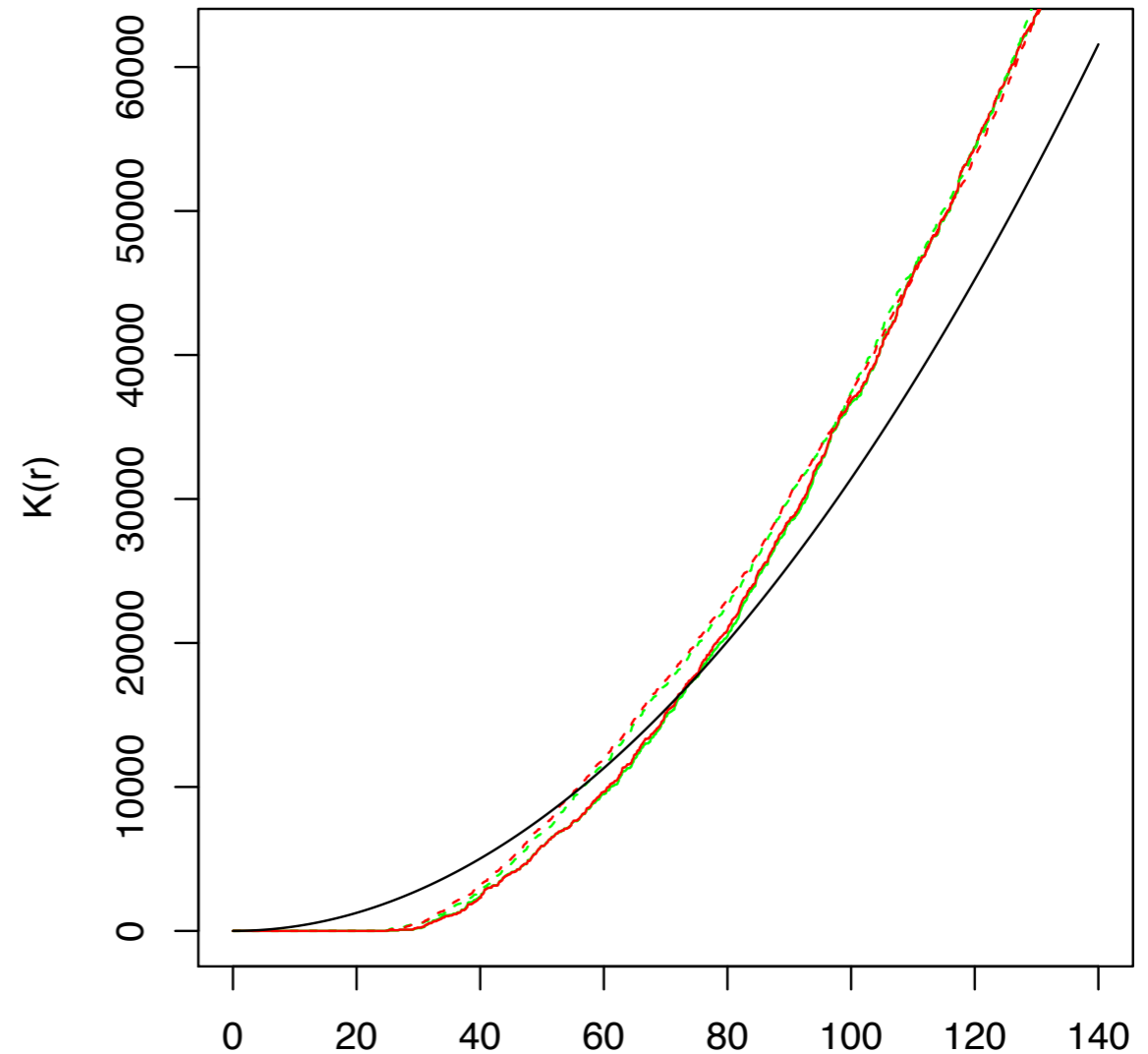


# EDA: Spatial functions

average G functions



average K functions



— control, mean  $r$       — control, weighted mean  
- - - - treatment, mean  $r$       - - - - treatment, weighted mean      — Homogeneous Poisson

- Some evidence of clustering at larger length scales
- Effect of limitation of nnd in [25,105]
- Difference between weighted mean and unweighted mean negligible

# Test statistics based on basic observations

Pattern size test statistic:

$$\delta_N(I) = \frac{1}{|I_0|} \sum_{i \in I_0} n(\underline{x}^i) - \frac{1}{|I_1|} \sum_{i \in I_1} n(\underline{x}^i)$$

Observation window statistic:

$$\delta_W(I) = \frac{1}{|I_0|} \sum_{i \in I_0} |W^i| - \frac{1}{|I_1|} \sum_{i \in I_1} |W^i|$$

Intensity test statistic:

$$\sum_{i \in I_0} \omega_0(\underline{x}^i) \hat{\rho}(\underline{x}^i) - \sum_{i \in I_1} \omega_1(\underline{x}^i) \hat{\rho}(\underline{x}^i)$$

where  $\delta_\rho(I)$  denotes unweighted case using  $\omega_k(\underline{x}^i) = 1/|I_k|$  ( $k = 0, 1$ )

$\delta_{\rho,\omega}(I)$  denotes weighted case using  $\omega_k(\underline{x}^i) = n(\underline{x}^i) / \sum_{j \in I_k} n(\underline{x}^j)$  ( $k = 0, 1$ )

# Test statistics based on G-functions

Estimated nearest neighbour functions averaged over the collection of point patterns  $\underline{x}^J$  with weights  $\omega_J$  as above:

$$\hat{G}(\underline{x}^J, r) = \sum_{i \in J} \omega_J(\underline{x}^i) \hat{G}(\underline{x}^i, r)$$

Nearest neighbour distribution test statistic statistics:

$$\delta_{G,1}(I) = \|\hat{G}(\underline{x}^{I_0}, r) - \hat{G}(\underline{x}^{I_1}, r)\|_1 = \int_0^\infty |\hat{G}(\underline{x}^{I_0}, r) - \hat{G}(\underline{x}^{I_1}, r)| dr$$

$$\delta_{G,\infty}(I) = \|\hat{G}(\underline{x}^{I_0}, r) - \hat{G}(\underline{x}^{I_1}, r)\|_\infty = \sup_r |\hat{G}(\underline{x}^{I_0}, r) - \hat{G}(\underline{x}^{I_1}, r)|$$

For comparison of  $\hat{G}(\underline{x}^{I_0}, r)$  and  $\hat{G}(\underline{x}^{I_1}, r)$  across the range of distances  $r > 0$ .

Also, scaled neighbourhood count test statistic (Diggle 2000).

# Significance quantification

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- Based on permutation tests (nonparametric)
- Need exchangeability under the Null under suitable set of operations
- Statistics under permutations are identically distributed
- p-values are uniformly distributed (test e.g. with KS)
- Exact or approximate (subset of operations)
- Evaluated in simulations studies

# Test statistics

Observations of exploratory analysis can be confirmed by formal testing.  
All proposed test statistics show significant results:

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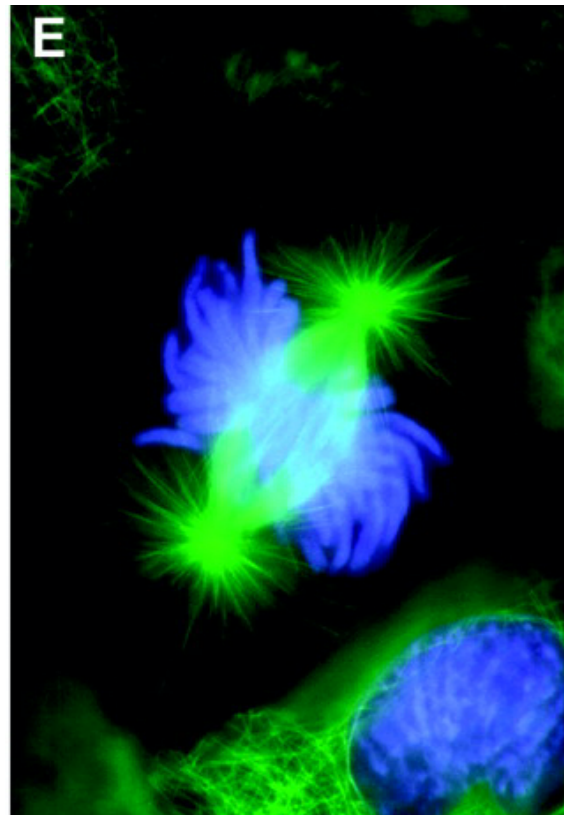
$\delta_N$	0.0005	$\delta_{\text{nnd}}$	0.0057	$\delta_K$	0.1092	$\delta_{EFT}$	0.0011
$\delta_W$	0.0018	$\delta_{\text{nnd},\omega}$	0.0005	$\delta_{G,1}$	0.0061	$\delta_{EFT,\omega}$	0.0005
$\delta_\rho$	0.0001	$\delta_{\text{msd}}$	0.0019	$\delta_{G,1,\omega}$	0.0005		
$\delta_{\rho,\omega}$	0.0002	$\delta_{\text{msd},\omega}$	0.0005	$\delta_{G,\infty}$	0.0087		
				$\delta_{G,\infty,\omega}$	0.0013		

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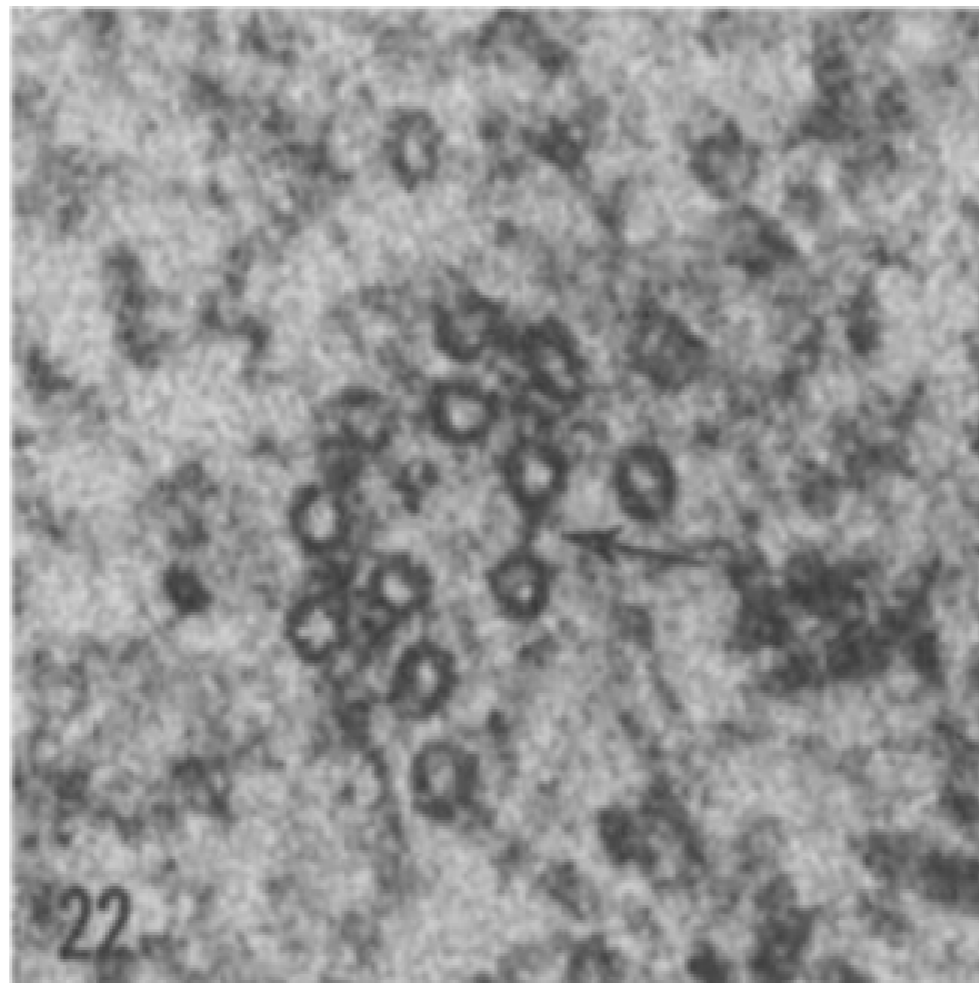
Results remain significant after multiple testing adjustment of critical p-value (using Bonferroni).

# What did we find?

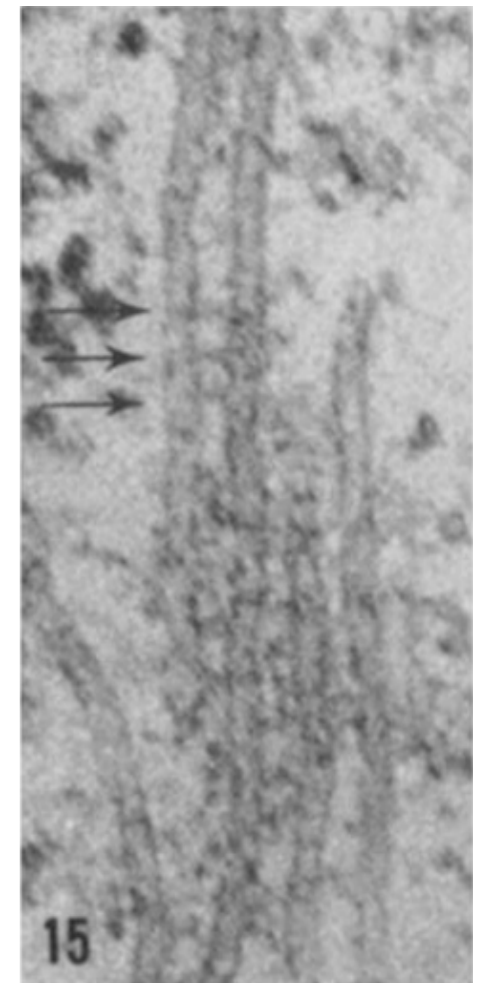
- Microtubules are **bound together** (in K-fibers, by mesh-like structure)
- TACC3 **overexpression** is **associated with an impact** on the mesh
- Detection of treatment effects not visible by eye



Perpendicular to the microtubule axis



Parallel view



# References

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**The (ongoing) work on modelling Covid with Hawkes process is joint with Adam Davison and Marianna Mavroleftherou (integrated Masters students at Warwick Statistics)**

**Dead pixels and other work related to digital X-ray imaging:**

JA Brettschneider, OT Giles, WS Kendall, T Lazauskas

***DetectorChecker: analyzing patterns of defects in detector screens***

[Journal of Open Source Software, 2020, 5\(56\), 2474](#)

JA Brettschneider, JW Warnett, TE Nichols, WS Kendall

***Higher level spatial analysis of dead pixels on detectors based on local grid geometry***

[CRiSM Working Paper Series No. 17-02, 2017](#)

Kueh A, Warnett JM, Gibbons GJ, Brettschneider J, Nichols TE, Williams MA, & Kendall WS

***Modelling the Penumbra in Computed Tomography***

[Journal of X-ray science and technology, 24 \(4\), 2016, 583-97 \(Gold Access\)](#)

Brettschneider J, Thornby J, Nichols TE and Kendall WS

***Spatial analysis of dead pixels***

[CRiSM Working Paper Series No. 14-24, 2014](#)

## Software

[DetectorCheckerWebApp](#) is an interactive WebApp for analysing pixel damage in CT scanners using the associated R-package [DetectorChecker](#). Both have been developed jointly with The Alan Turing Institute and Prof Wilfrid Kendall.

The project emerged as a spin off from our EPSRC [inside-out blog](#). Initial versions of the software were issued on 29.3.2019 and new versions were released on 30.6.2020.

# References

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**Modelling for microscopic images is joint work with Tom Honnor (Warwick Statistics, now UCL), Adam Johnson (Warwick Statistics), Steve Royle (Warwick Medical School)**

*Thomas R. Honnor, Julia A. Brettschneider, Adam M. Johansen (2017),*  
***Differences in spatial point patterns with application to subcellular biological structures***

<https://warwick.ac.uk/fac/sci/statistics/crism/research/17-01/>

*Honor TR, Johansen AM and Brettschneider JA. (2017)*

***A nonparametric test for dependency between estimated local bulk movement patterns***

<https://warwick.ac.uk/fac/sci/statistics/crism/research/17-03/>

*Nixon\*, F.M., Honnor\*, T.R., Starling, G.P., Beckett, A.J., Johansen, A.M., Brettschneider, J.A., Prior, I.A. & Royle, S.J.*

*J Cell Science, April 2017*

***Microtubule organization within mitotic spindles revealed by serial block face scanning EM and image analysis***