A diagnostic plot for assessing model fit in count data models

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Introduction

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- Assume that a routine to obtain estimates $\hat{\mu}_i = \hat{E}(Y_i|x_i)$ and $\hat{\theta}_i$ is readily available.
- Denote $N(k)$, for $k = 0, 1, 2, \ldots$, the number of observed counts k in $y_1, \ldots, y_n$.
- Idea: check whether, for each count $k = 0, 1, 2, \ldots$, the number $N(k)$ is 'plausible' under the distribution $F(\hat{\mu}_i, \hat{\theta}_i)$.

Poisson-Binomial distribution

- The random variable $N(k)$ follows a Poisson–Binomial distribution with parameters $p_1(k), \ldots, p_n(k)$, where

$$p_i(k) = P(k|\mu_i, \theta_i)$$

  is the probability of observing the count k under covariate x_i and model F (Chen and Liu, 1997).
- The $p_i(k)$ can be estimated by $\hat{p}_i(k) = P(k|\hat{\mu}_i, \hat{\theta}_i)$ from the fitted model.

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- The $p_i(k)$ can be estimated by $\hat{p}_i(k) = P(k|\hat{\mu}_i, \hat{\theta}_i)$ from the fitted model.
  - For instance, in the special case that $F(\mu_i, \theta_i)$ corresponds to Pois(μ_i), one has $\hat{p}_i(k) = \exp(-\hat{\mu}_i)\hat{\mu}_i^k/k!$.
  - This scenario was discussed in the previous talk with focus on the case $k = 0$.
  - This talk generalizes those ideas to general k and F and proposes a generic diagrammatic tool.

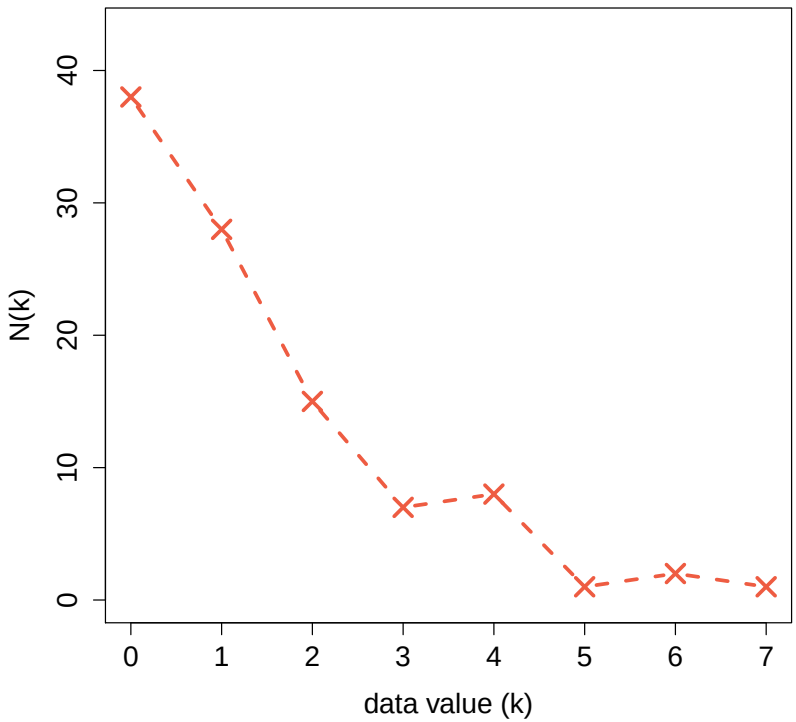
Plausibility intervals for N(k)

- Knowing the distribution of $N(k)$, one can derive intervals of plausible values of $N(k)$ by considering appropriate quantiles from this distribution.
- For fixed k, appropriate lower and upper quantiles, say $q_{\alpha/2}(k)$ and $q_{1-\alpha/2}(k)$ of the Poisson–Binomial distribution can be computed using the R package `poibin` (Hong, 2013).
- Do this for a range of values of k, and plot intervals $(q_{\alpha/2}(k), q_{1-\alpha/2}(k))$ alongside observed values $N(k)$ as a function of k.

Example: simulated data

- $n = 100$ observations $y_1, \ldots, y_n$ simulated from a Zero–inflated Poisson (ZIP) distribution with Poisson parameter $\mu = 1.5$ and zero–inflation parameter $p = 0.2$

k	$N(k)$
0	38
1	28
2	15
3	7
4	8
5	1
6	2
7	1



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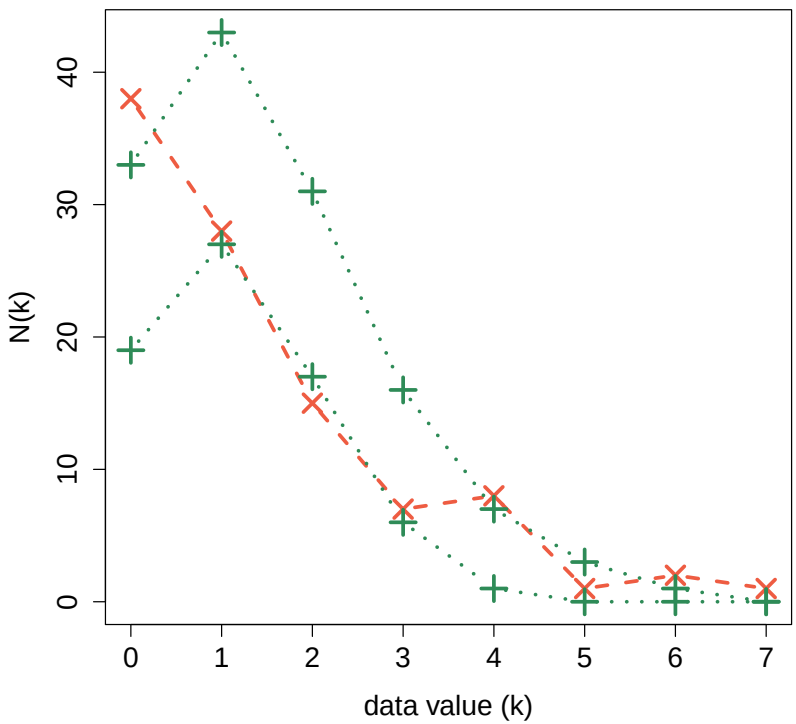
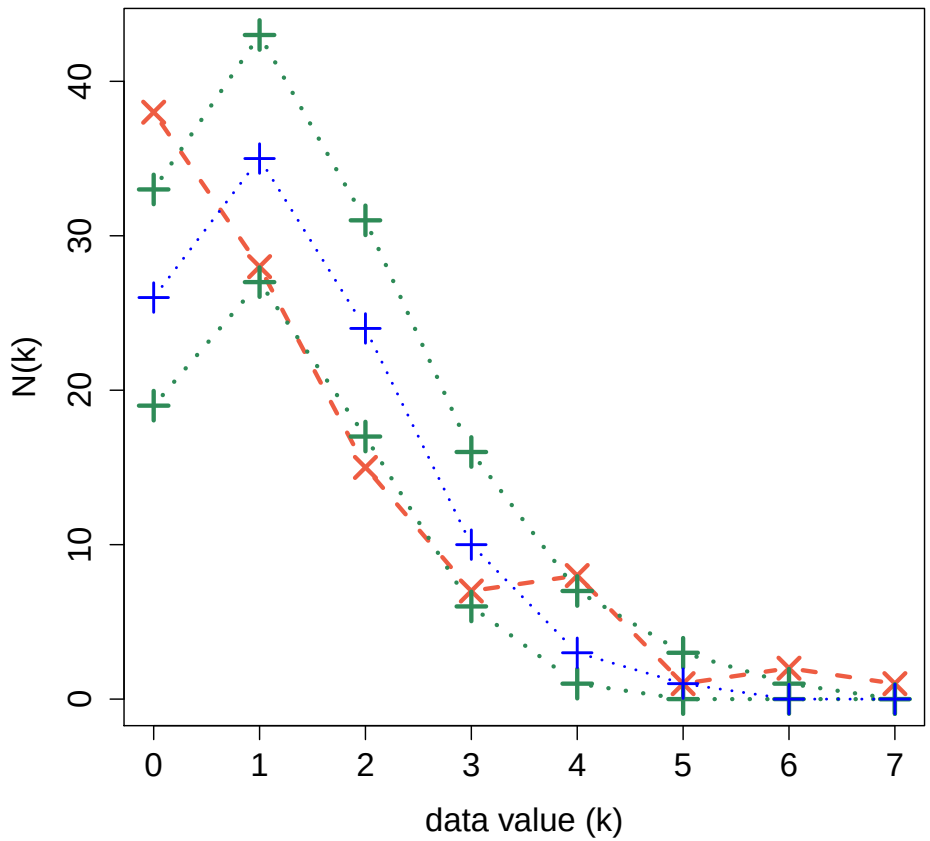
- Consider $F(\mu) \sim \text{Pois}(\mu)$ with $\hat{\mu} = \bar{y}$.

k	$N(k)$	$q_{0.05}(k)$	$q_{0.95}(k)$
0	38	19	33
1	28	27	43
2	15	17	31
3	7	6	16
4	8	1	7
5	1	0	3
6	2	0	1
7	1	0	0



Median-adjustment

- The previous graph can be difficult to read if the sample size is large, and so the bounds get very tight.
- We therefore adjust it by subtracting the medians $M(k) = \text{med}(N(k))$ from all values, where the median is taken wrt to the Poisson-Binomial distribution of $N(k)$.



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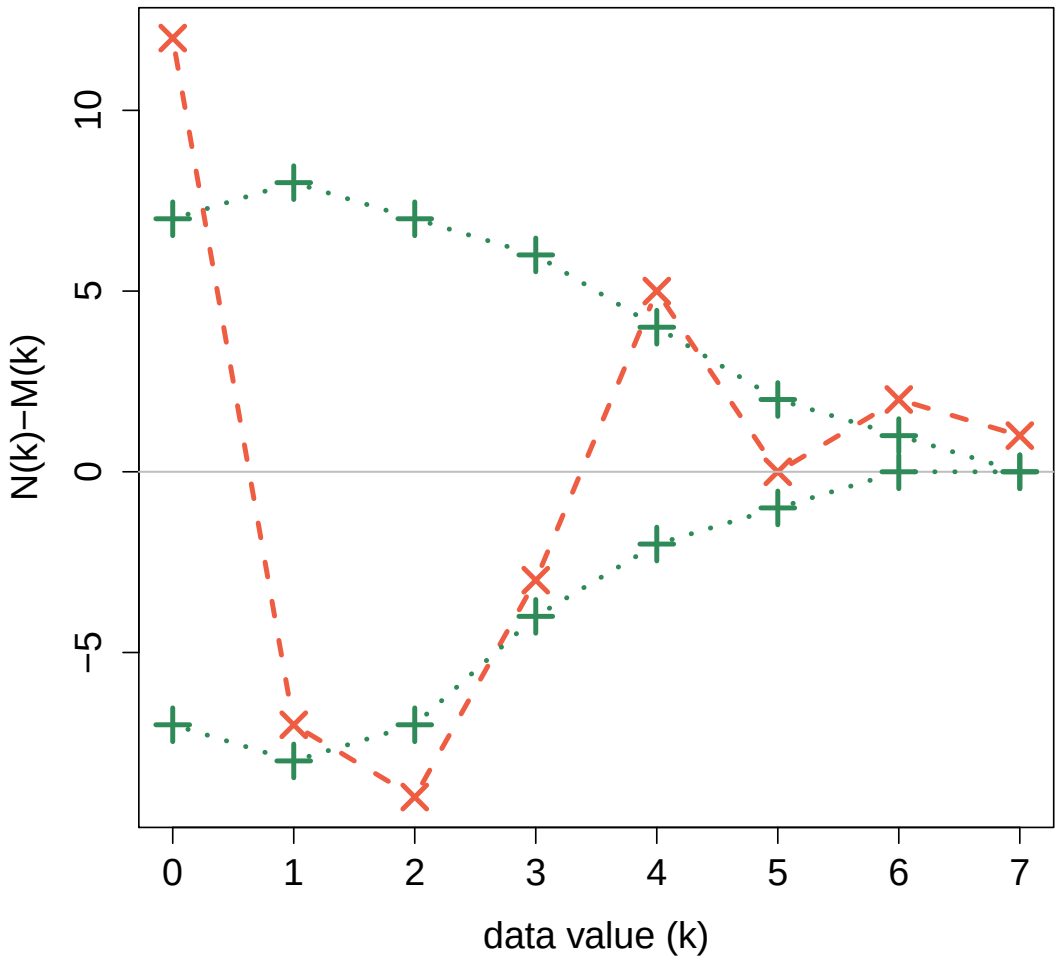
k	$N(k)$	$M(k)$	$N(k)$–$M(k)$	$q_{0.05}(k)$–$M(k)$	$q_{0.95}(k)$– $M(k)$
0	38	26	12	-7	7
1	28	35	-7	-8	8
2	15	24	-9	-7	7
3	7	10	-3	-4	6
4	8	3	5	-2	4
5	1	1	0	-1	2
6	2	0	2	0	1
7	1	0	1	0	0

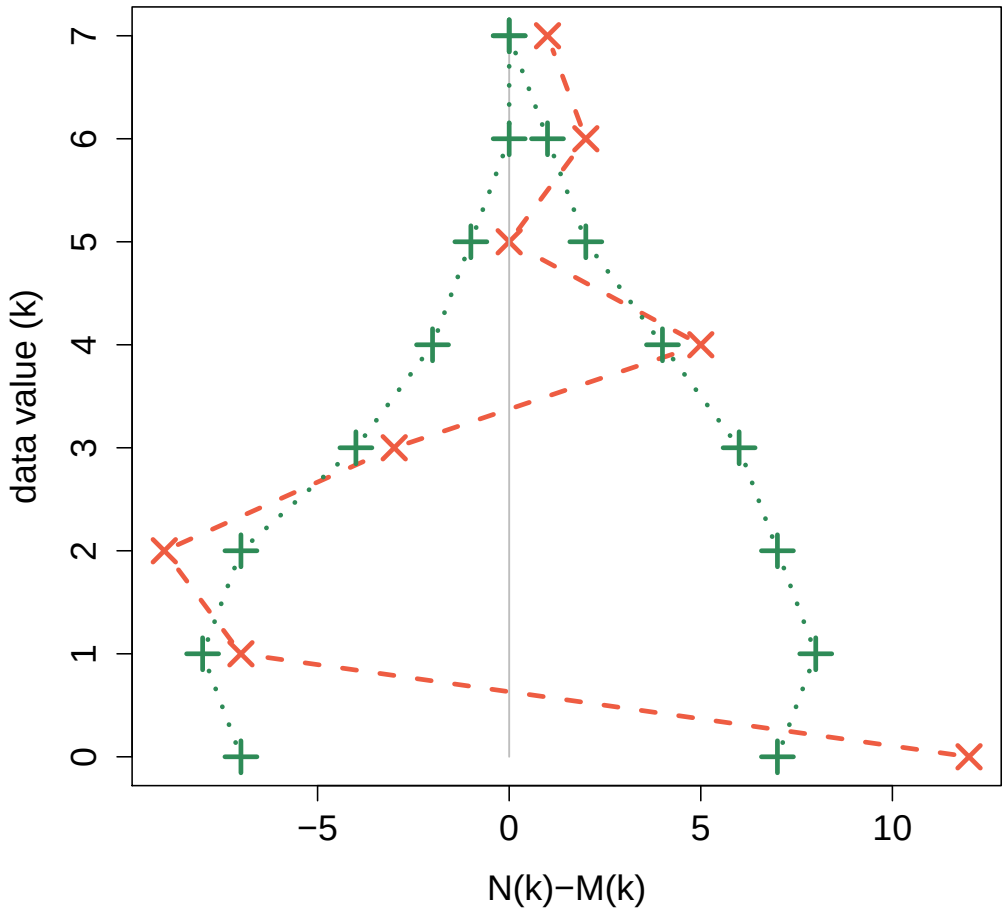
Median–adjusted bounds

- Diagnostic plot for the accuracy of the Poisson assumption.



Median–adjusted bounds: Variant

- Exchange horizontal and vertical axis:



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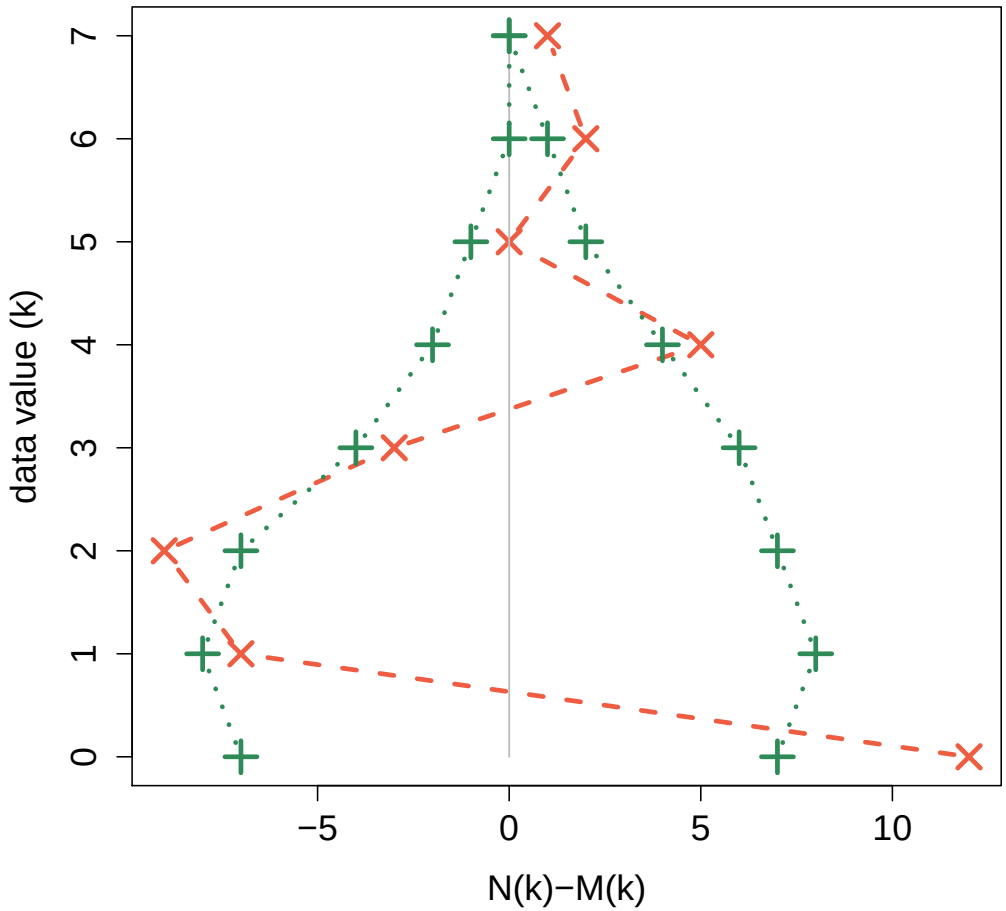

- ‘Christmas tree diagram’.

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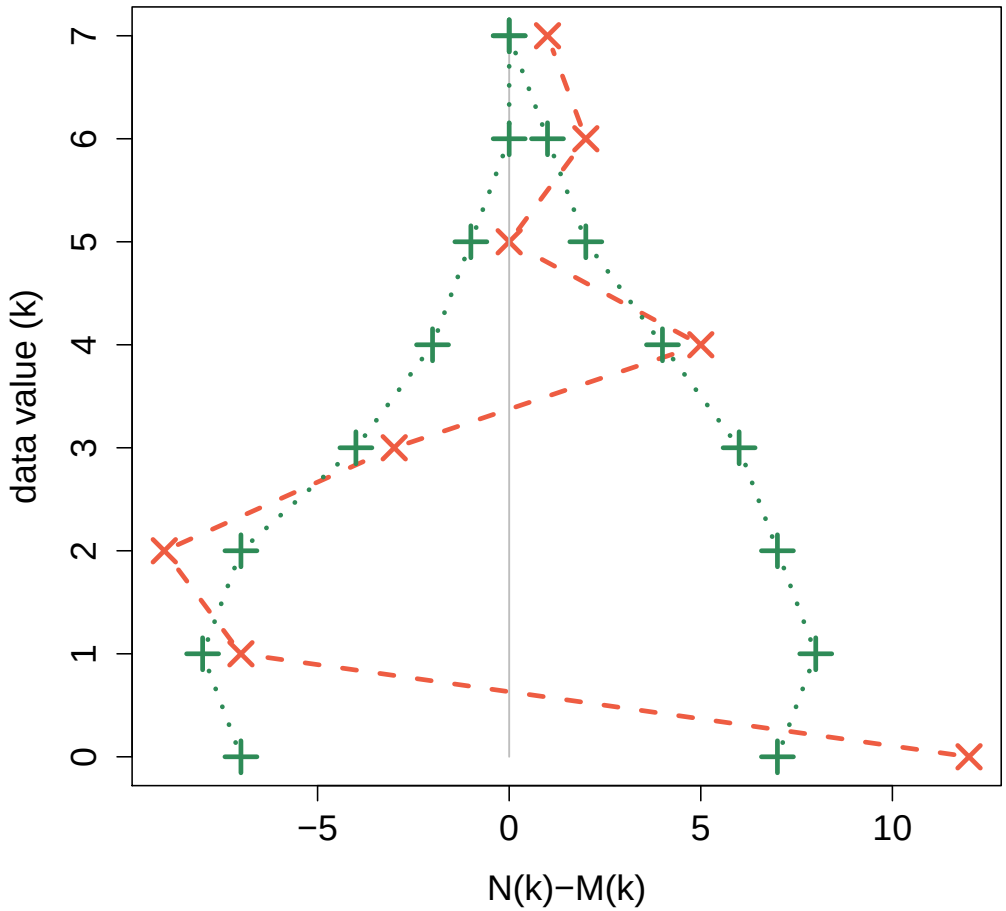
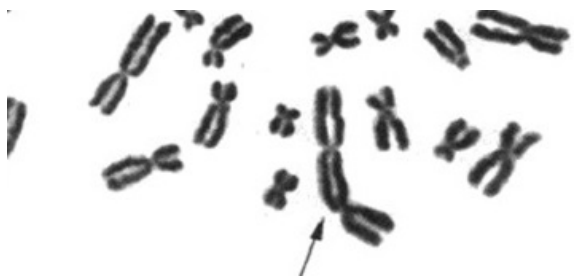


- 'Christmas tree diagram'.
- Adequate models have the 'decoration' inside the tree.

Example: Biodosimetry data

- Frequency of dicentric chromosomes in human lymphocytes after *in vitro* exposure to doses between 1 and 5Gy of 200kV X–rays. The irradiated blood was mixed with non–irradiated blood in a proportion 1:3 in order to mirror a partial body exposure scenario.

	Frequency of counts								
dose	0	1	2	3	4	5	6	7	8
1	2713	78	8	0	1	0	0	0	0
2	1302	71	22	5	0	0	0	0	0
3	1116	46	28	7	2	1	0	0	0
4	929	18	14	22	13	2	0	1	1
5	726	17	18	12	9	13	1	4	0



Modelling of biodosimetry data

- These are $n = 7200$ observations of the type (dose_i, y_i), with y_i being a count in $0, \ldots, 8$.
- X–rays are sparsely ionizing — the literature suggests a quadratic dose model in this case.

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- Link function:
  - Cytogenists prefer identity link.
  - Being among Statisticians, I will use the log link.
- Response (count) distribution:
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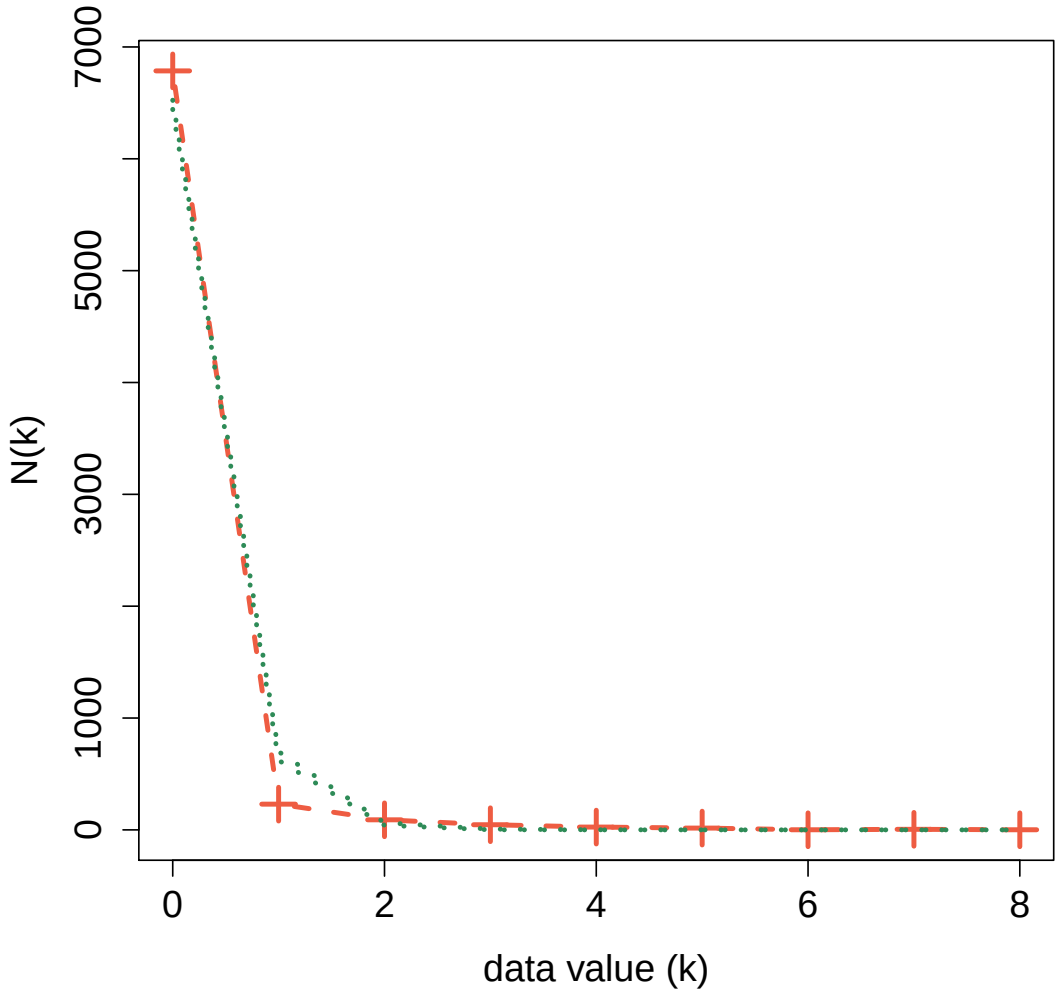
  - However, under a partial body exposure scenario, we would expect a deviation from the Poisson assumption, towards zero–inflation.
- Consider the initial model $y_i|\text{dose}_i \approx \text{Pois}(\mu_i)$ with

$$\mu_i \equiv E(y_i|\text{dose}_i) = \exp\left(\beta_0 + \beta_1 \text{dose}_i + \beta_2 \text{dose}_i^2\right)$$

Diagnostics for biodosimetry data

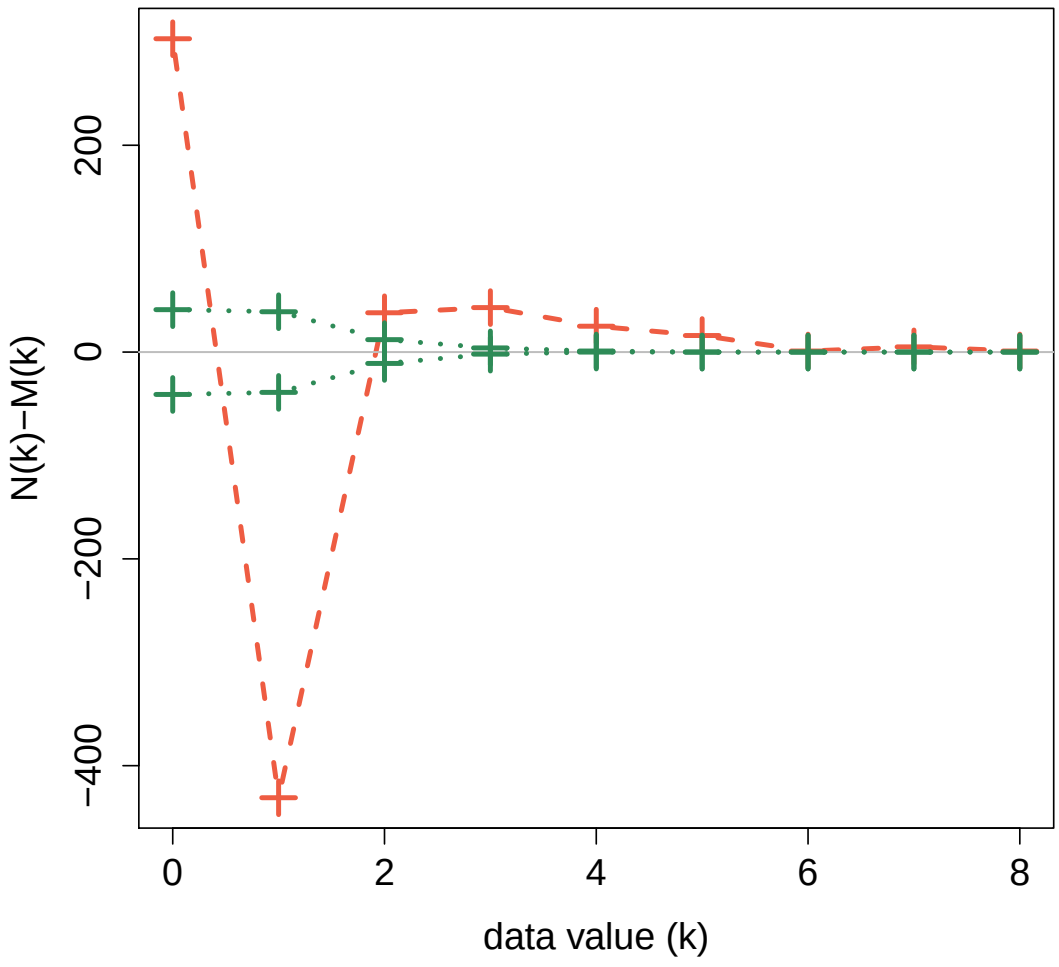
- ...without median– adjustment:



- hard to see anything!

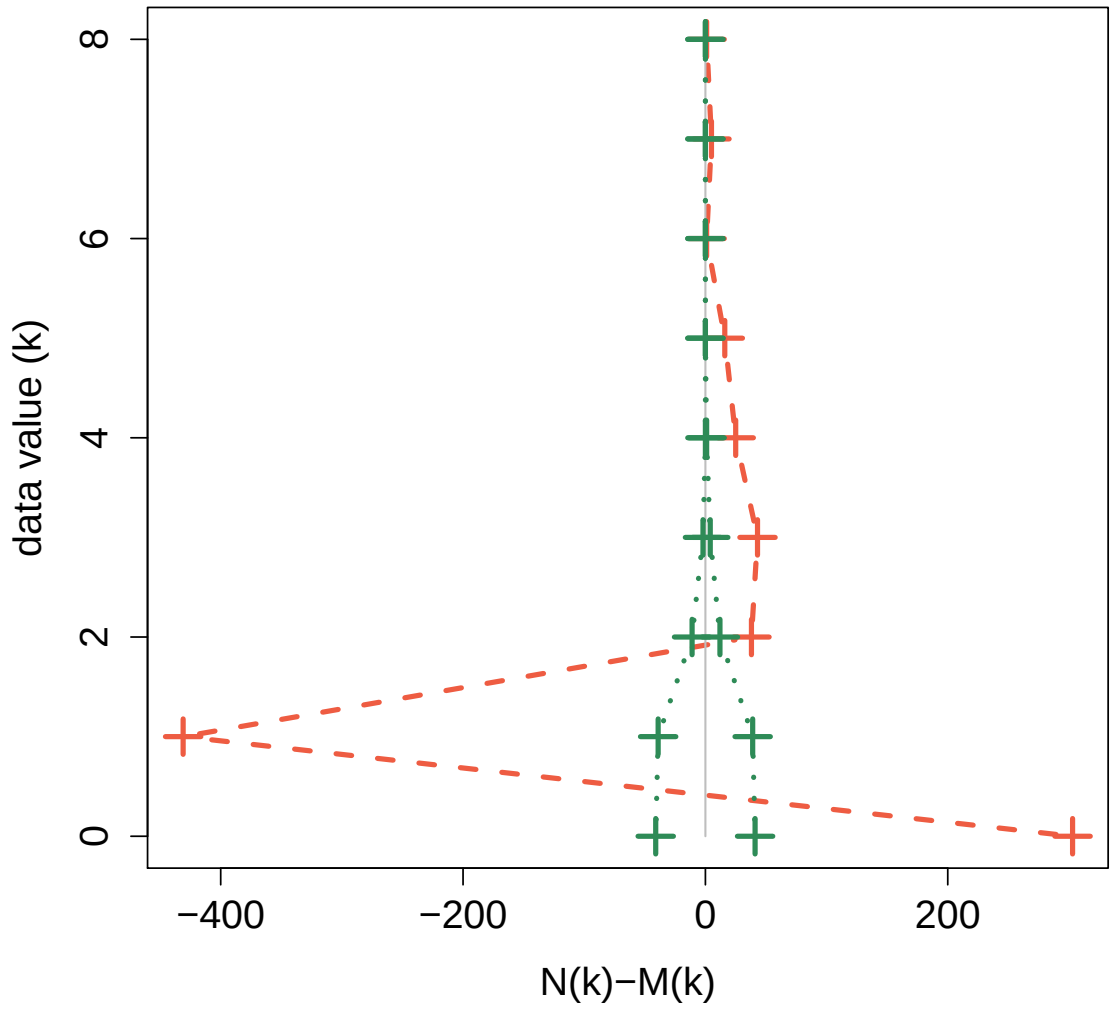
Diagnostics for biodosimetry data

- ...with median– adjustment:



- much better!

Christmas tree diagram: Poisson hypothesis



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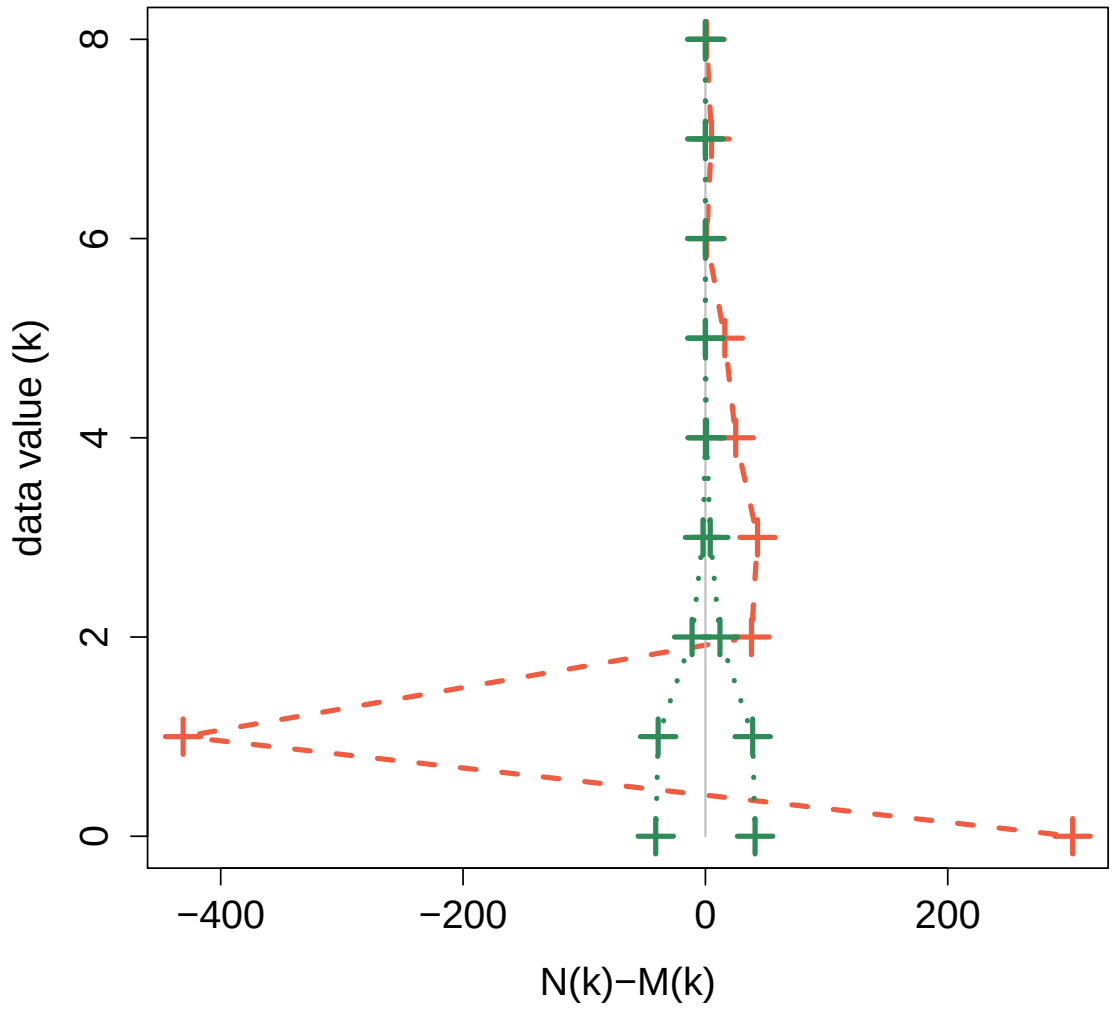

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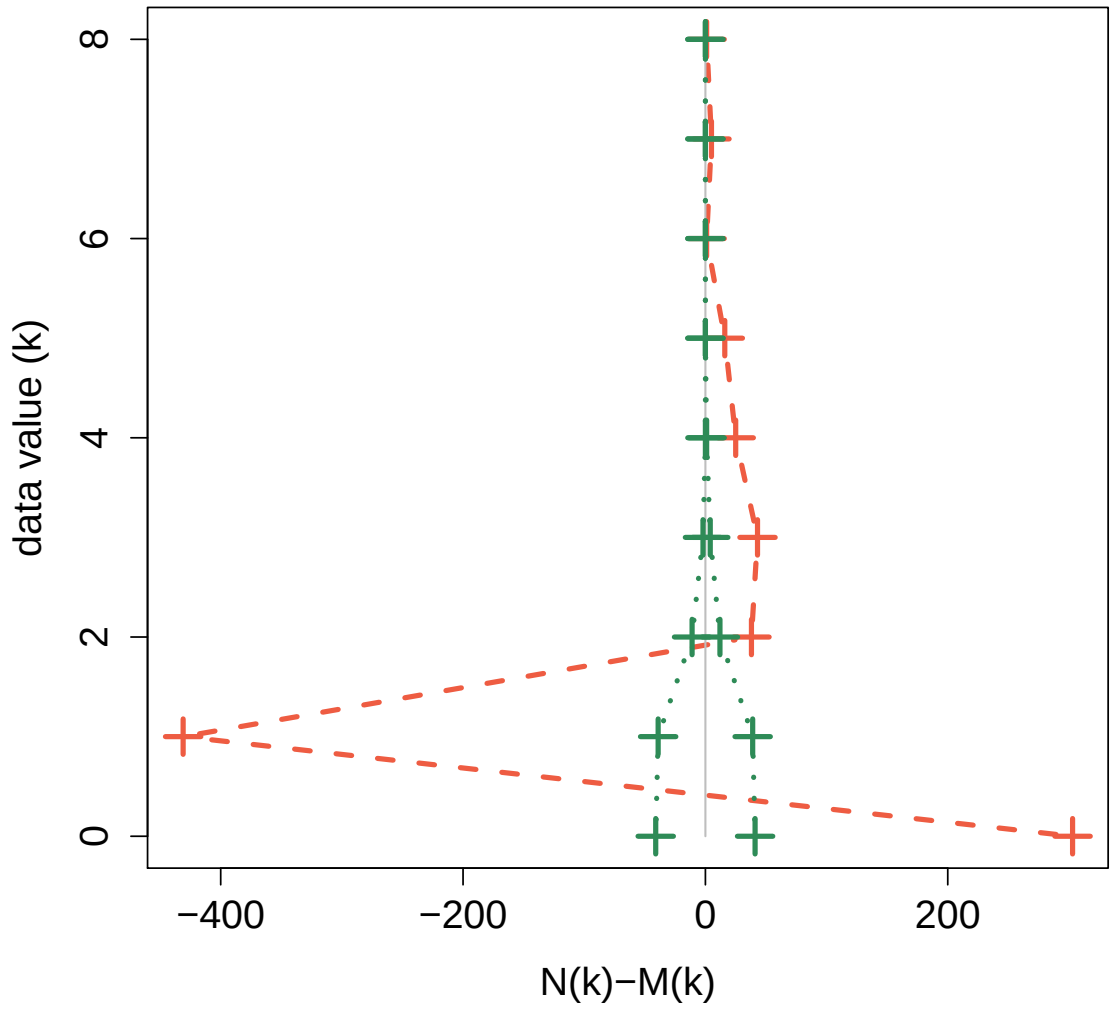

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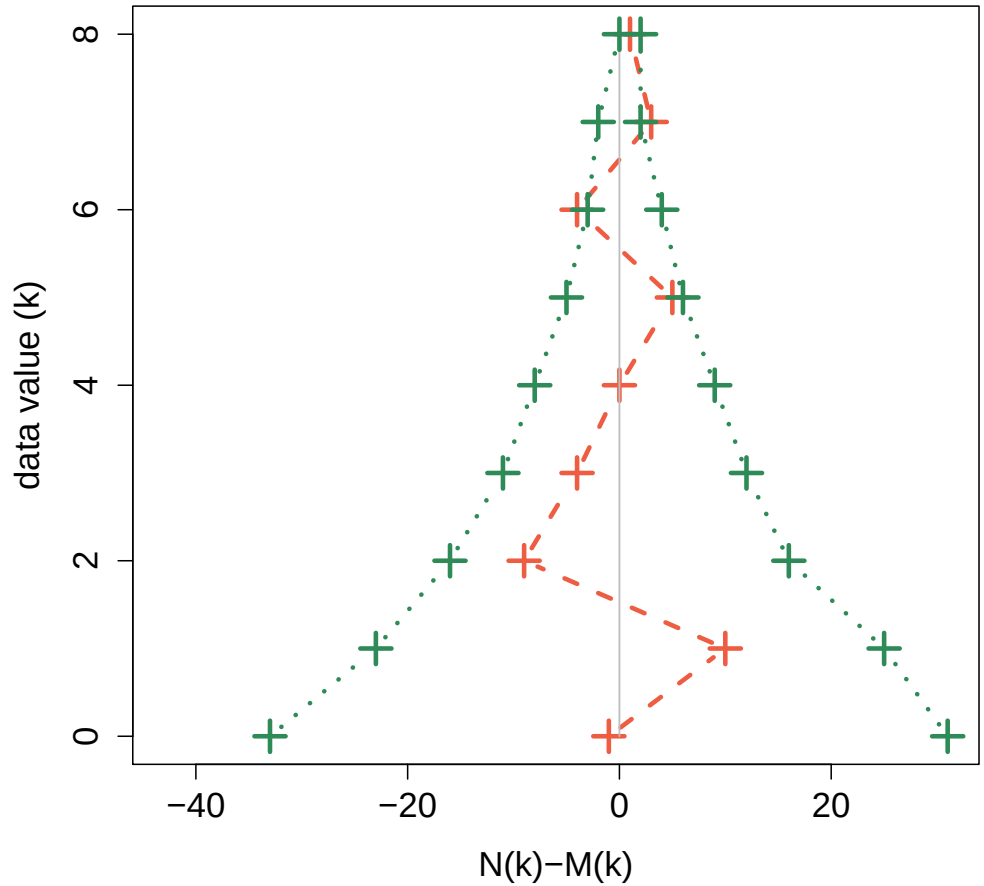
Christmas tree diagram: ZIP hypothesis

- Do all the same as before, but now compute $\hat{\mu}_i$, $\hat{\theta}_i$, and $\hat{p}_i(k)$, using the zero–inflated Poisson (ZIP) model as the hypothesized model.



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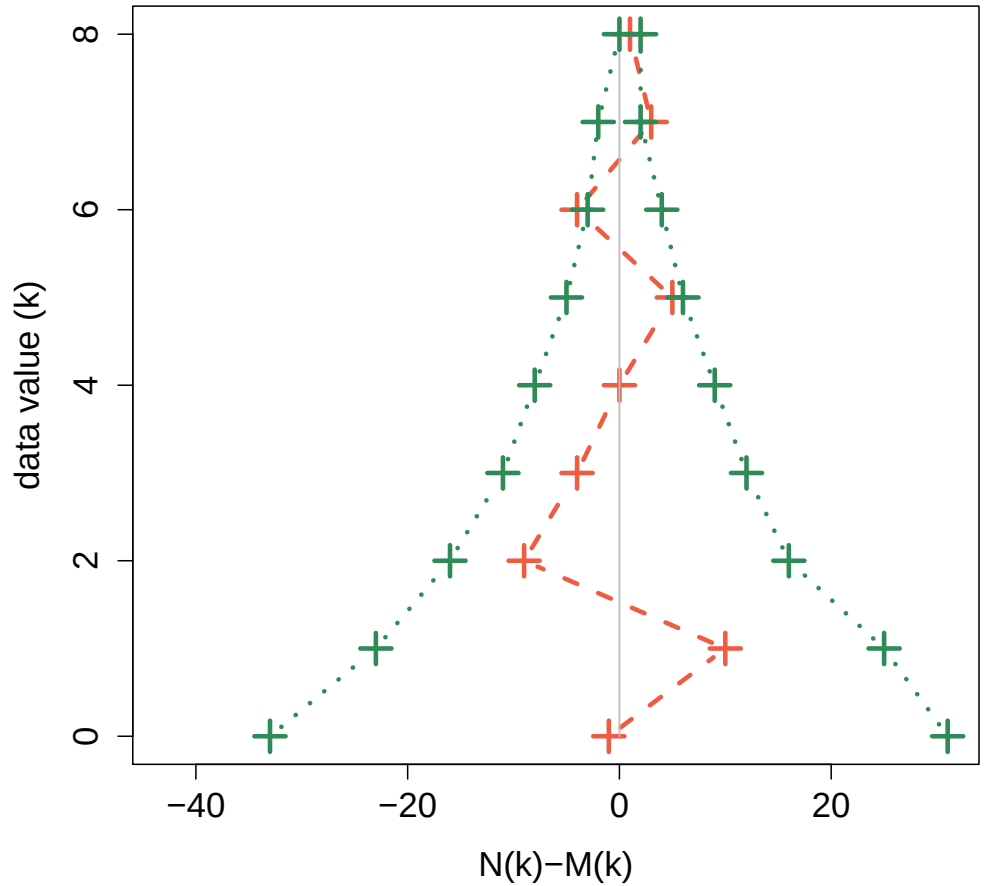
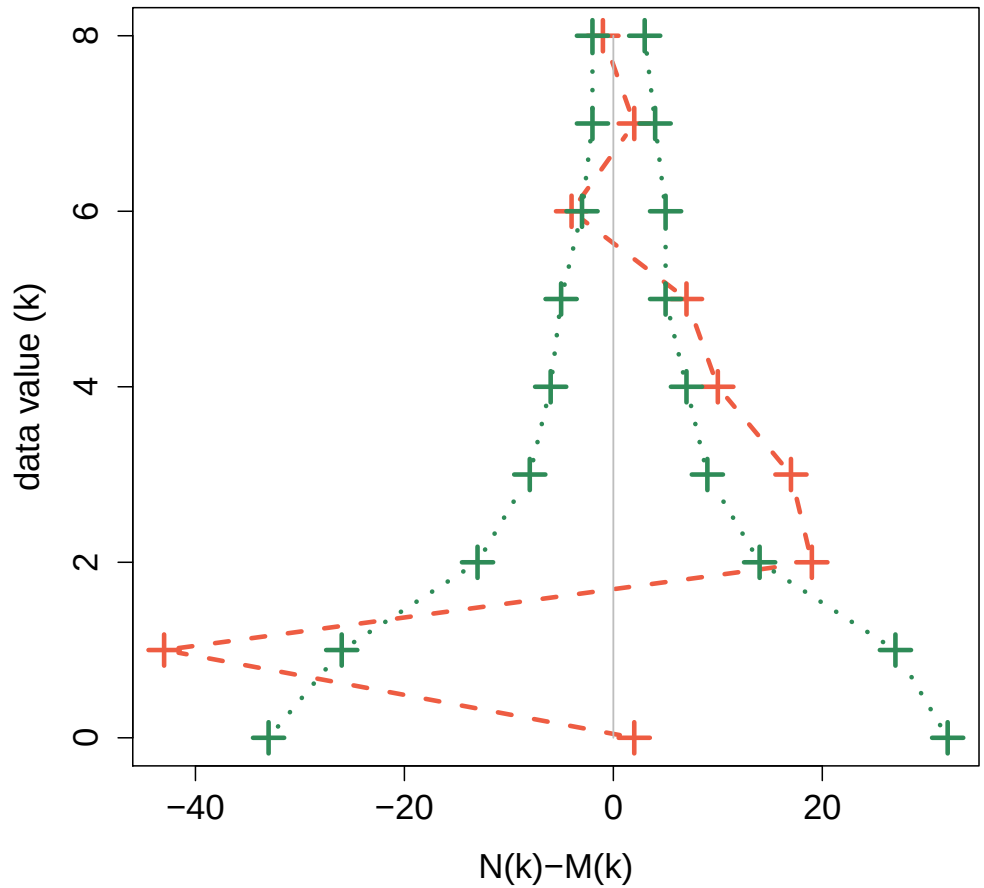


- indicates a good fit.

Christmas tree diagram: NB hypothesis

- Repeat the procedure using the negative Binomial model as the hypothesized model.



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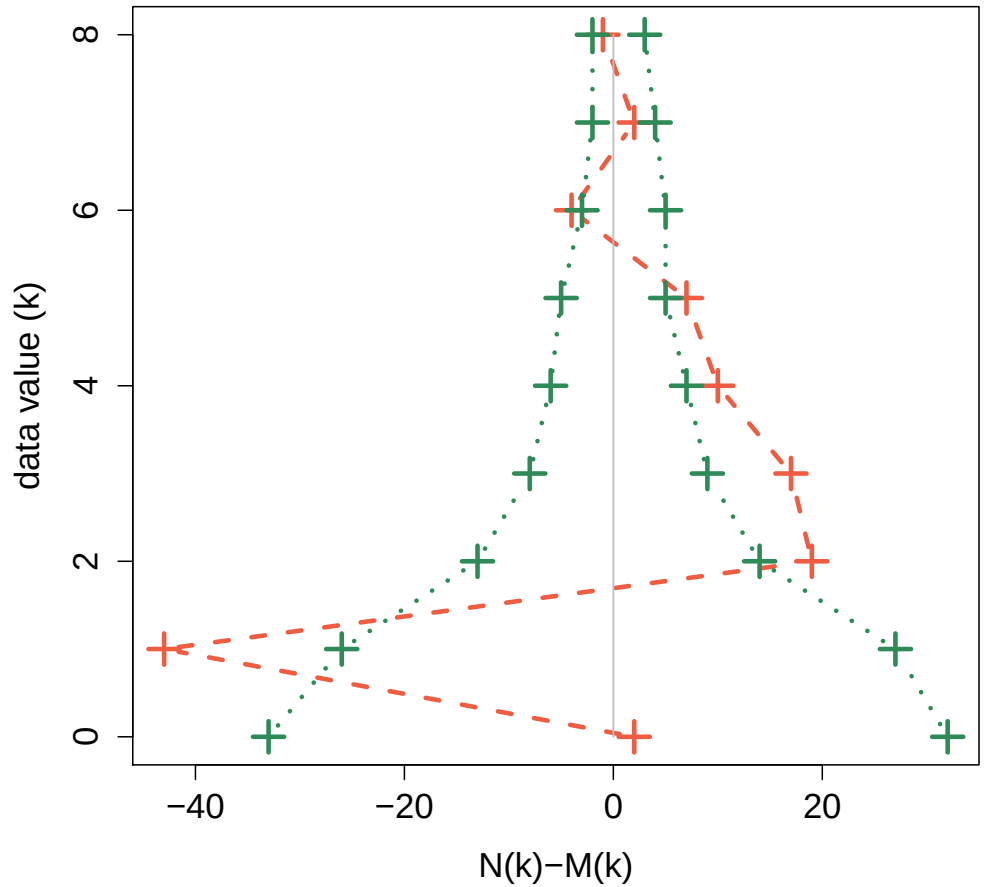

- indicates that the NB model does not capture the data well.

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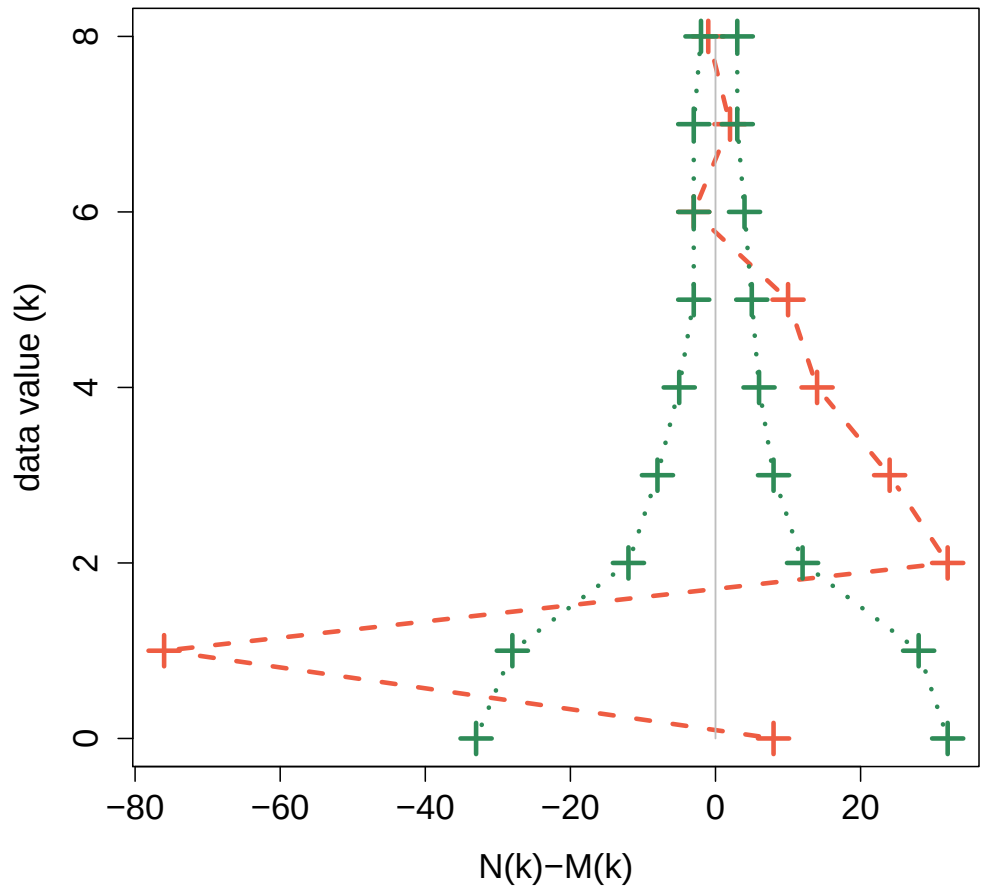

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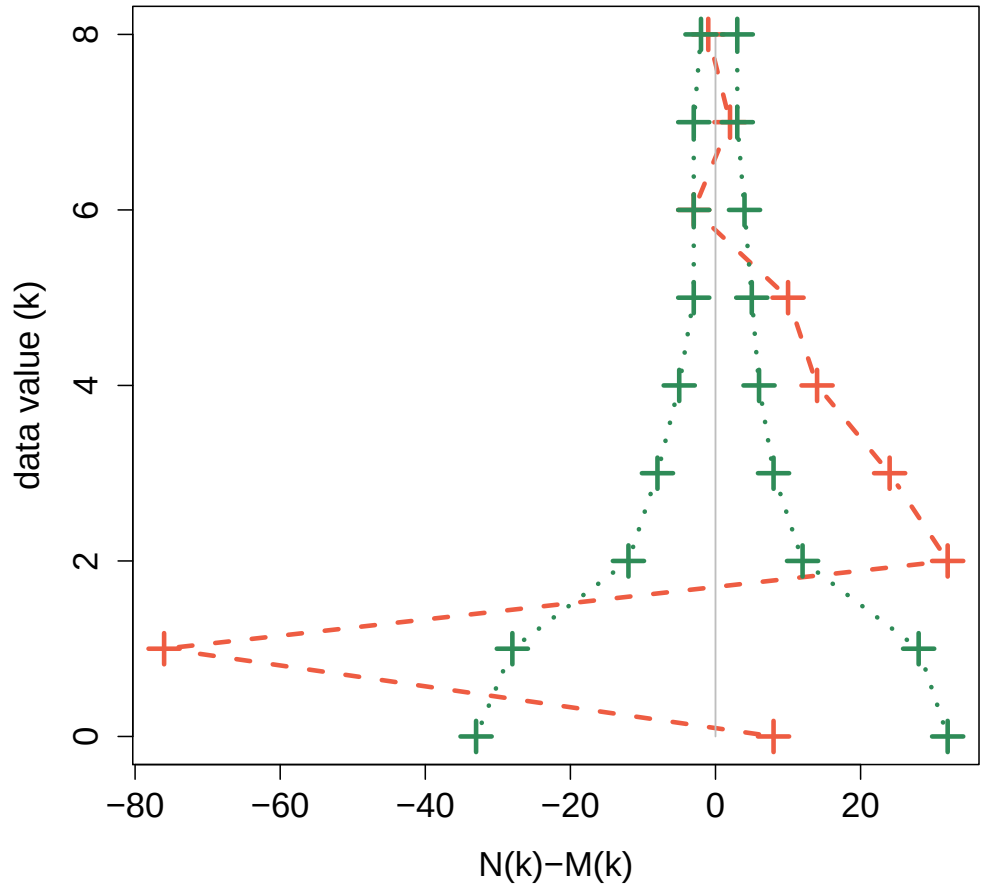

- the PIG model does not capture the data well either.

Alternative data set: Whole body exposure

- Counts of dicentric chromosomes in 4400 blood cells after *in vitro* 'whole body' exposure with 200kV X-rays from 0 to 4.5Gy.

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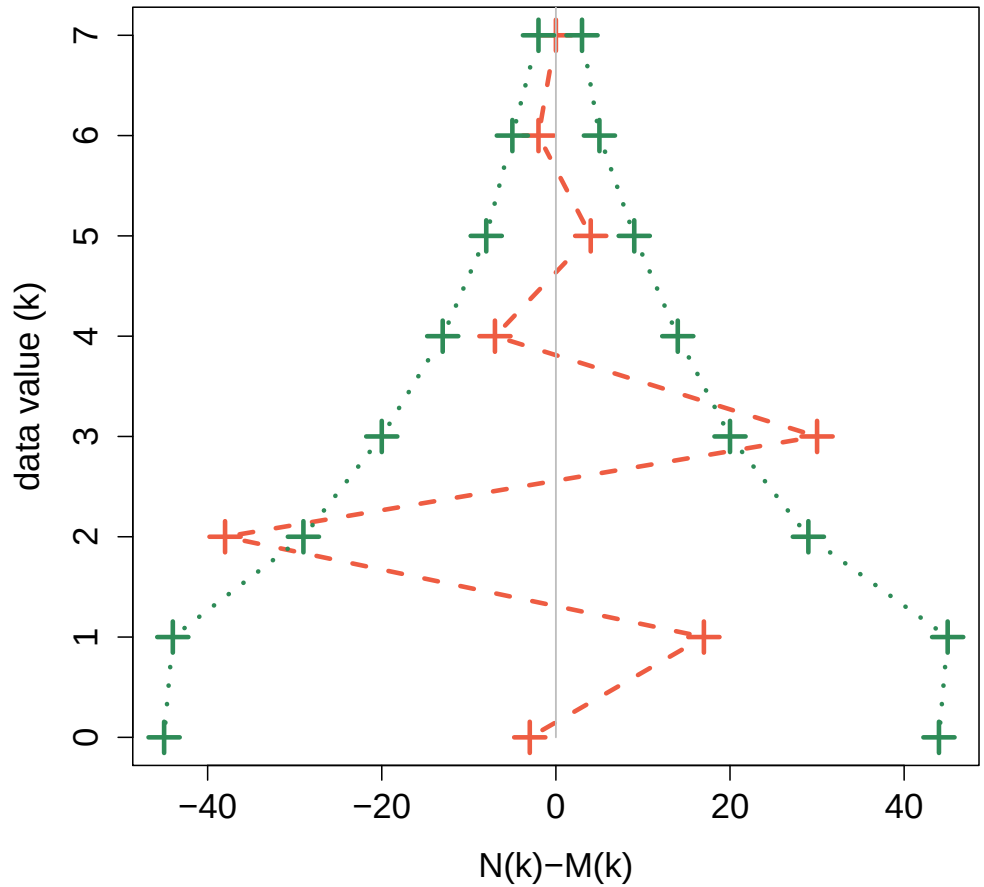

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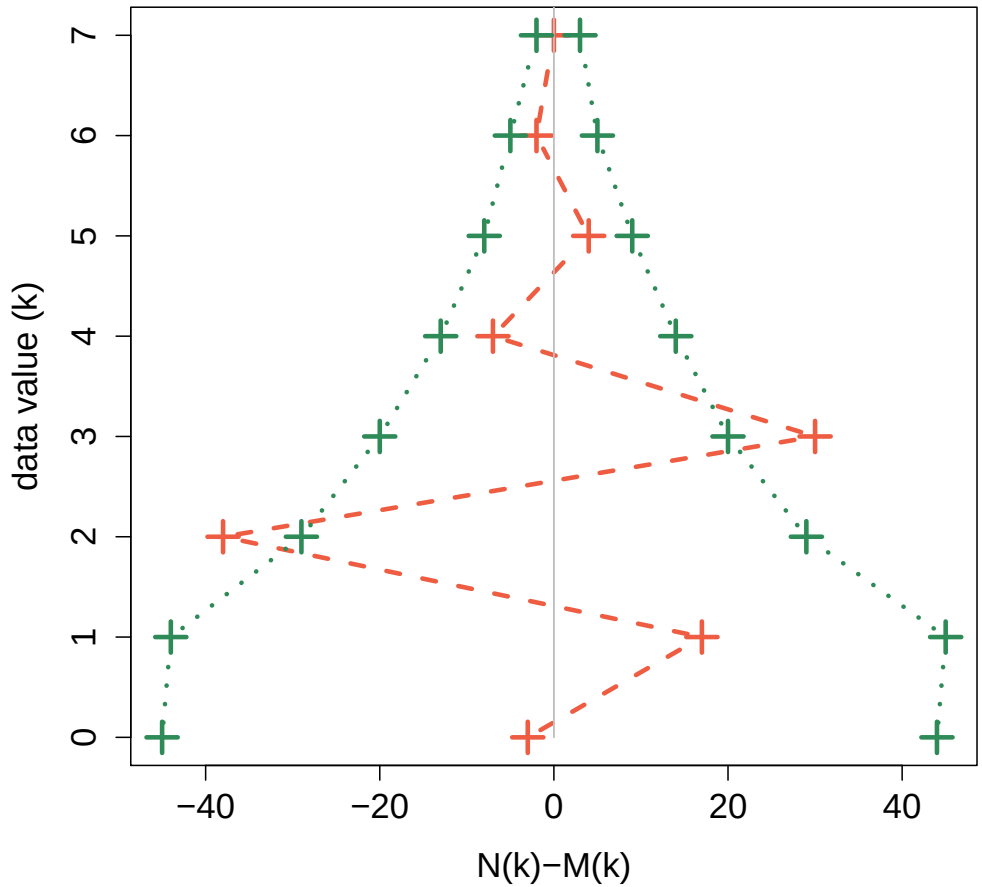

- indicates that Poisson model is fairly reasonable.

Multiple testing ?

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- For instance, if the tree covers ten possible counts, at a significance level of 0.1 one would expect one piece of decoration to fall outside the tree purely by chance.

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- Hence, we do not make such a correction, but explicitly do not advocate this procedure as a testing procedure.
- It should rather be seen as a diagnostic device, similar as a residual plot or a QQ-plot.
- That is, exceeding the boundary limits once or twice should not necessarily be interpreted as rejection of the hypothesized count distribution, as long as the 'decoration' is reasonably consistent with the tree.

Comparison with score tests

- Alternatively, one can carry out traditional score tests.
- For instance, consider H_0: Poisson versus H_1: ZIP or H_1: NB.
- Score test statistic $T = S^T J^{-1} S$, where S and J are the score function and Fisher Information matrix (resp.) evaluated under the Poisson model. Asymptotically, $T \sim \chi^2(1)$.
- Resulting values of T, to be compared with $\chi^2_{1,0.95} = 3.84$ (Oliveira et al, 2016):

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- ...but the score test does not tells us whether it's at all the zero's which cause the problem, nor whether the data are zero–inflated or –deflated!

Conclusion

- We have provided a simple diagrammatic tool to assess the adequacy of any given count data model.
- Essentially, it is verified whether the frequency, $N(k)$, of each count, k, is plausible given the hyptothesized model.
- Can be used for with or without covariates.
- Only requires computation of fitted values, and the resulting plausibility intervals via the Poisson–Binomial distribution.
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  - More work required for the more general case of an arbitrary count/distribution.
- Be aware of multiple testing: It is a diagram, not a test.

References

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