An Extended Random-effects Approach to Analysing Repeated, Overdispersed Count Data

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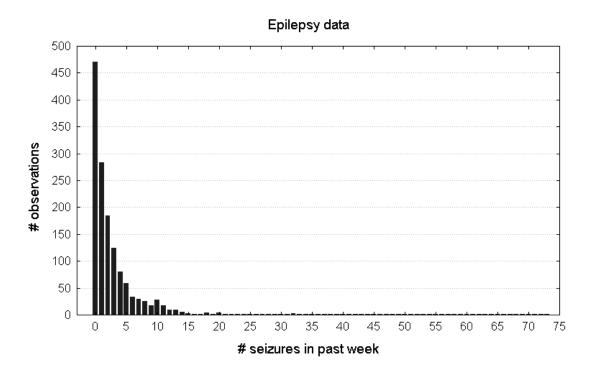
Outline

- Motivating application A Clinical Trial in Epileptic Patients
- Generalized linear models
- Poisson regression models
- Overdispersion in GLM's
- Univariate overdispersed count data
- Longitudinal overdispersed count data
- Estimation
- Discussion of the example
- Final remarks

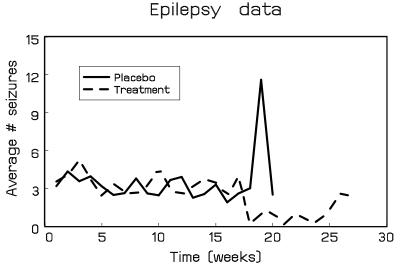
Motivation - A Clinical Trial in Epileptic Patients

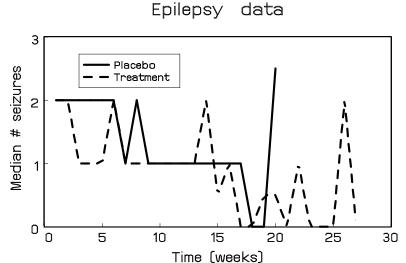
- a randomized, double-blind, parallel group multi-center study for the comparison of placebo with a new anti-epileptic drug (AED)
- after a 12-week baseline period, 45 epilepsy patients were assigned to the placebo group, 44 to the active (new) treatment group
- patients measured weekly during 16 weeks (double-blind) and some up to 27 weeks in a long-term open-extension study
- outcome of interest: the number of epileptic seizures experienced during the last week, i.e., since the last time the outcome was measured
- key research question: whether or not the additional new treatment reduces the number of epileptic seizures

Considerations about the data



• a very skewed distribution, with the largest observed value equal to 73 seizures in week





- unstable behavior explained by:
 - presence of extreme values,
 - very little observations available at some of the time-points, especially past week 20
- longitudinal count data:
 - discrete data
 - possible correlation between measurements for the same individual

	# Observations					
Week	Placebo	Treatment	Total			
1	45	44	89			
5	42	42	84			
10	41	40	81			
15	40	38	78			
16	40	37	77			
17	18	17	35			
20	2	8	10			
27	0	3	3			

• serious drop in number of measurements past the end of the actual double-blind period, i.e., past week 16

Generalized Linear Models (GLM's)

- unifying framework for much statistical modelling (Nelder and Wedderburn, 1972)
- an extension to the standard normal theory linear model
- three components:
 - independent random variables Y_i , $i=1,\ldots,n$, from a linear exponential family distribution with means μ_i and constant scale parameter ϕ ,

$$f(y) \equiv f(y|\theta,\phi) = \exp\left\{\phi^{-1}[y\theta - \psi(\theta)] + c(y,\phi)\right\},$$

where $\mu = \mathsf{E}[Y] = \psi'(\theta)$ and $\mathsf{Var}(Y) = \phi \psi''(\theta)$.

• a linear predictor vector η given by

$$\eta = X\beta$$

where β is a vector of p unknown parameters and $X = [\mathbf{x}_1, \dots, \mathbf{x}_n]^T$, the design matrix;

ullet a link function $g(\cdot)$ relating the mean to the linear predictor, i.e.

$$g(\mu_i) = \eta_i = \mathbf{x}_i^T \boldsymbol{\beta}$$

Poisson regression models

If Y_i , $i=1,\ldots,n$, are counts with means μ_i , the standard Poisson model assumes that $Y_i \sim \mathsf{Pois}(\mu_i)$ with

$$f(y_i) = \frac{e^{-\mu_i} \mu_i^{y_i}}{y_i!}$$

and

$$\mathsf{E}(Y_i) = \mu_i$$
 and $\mathsf{Var}(Y_i) = \mu_i$ (too restrictive!)

The canonical link function is the log

$$g(\mu_i) = \log(\mu_i) = \eta_i$$

and $\eta_i = \mathbf{x}_i^T \boldsymbol{\beta}$.

For a well fitting model (Hinde and Demétrio, 1998a,b):

Residual Deviance ≈ Residual d.f.

Overdispersion in GLM's

What if Residual Deviance ≫ Residual d.f.?

- (i) Badly fitting model
 - omitted terms/variables
 - incorrect relationship (link)
 - outliers
- (ii) variation greater than predicted by model: \Longrightarrow **Overdispersion**
 - count data: $Var(Y) > \mu$
 - counted proportion data: $Var(Y) > m\pi(1-\pi)$

Univariate Overdispersed Count Data

 Y_i - counts with means λ_i (Hinde and Demétrio, 1998a,b)

Negative Binomial Type Variance

$$Y_i | \lambda_i \sim \mathsf{Pois}(\lambda_i) \quad \mathsf{with} \quad \log \lambda_i = \mathbf{x}_i^T oldsymbol{eta}$$
 $\mathsf{E}(Y_i | \lambda_i) = \lambda_i \quad \mathsf{Var}(Y_i | \lambda_i) = \lambda_i$

• no particular distributional form: $\mathsf{E}(\lambda_i) = \mu_i$ and $\mathsf{Var}(\lambda_i) = \sigma_i^2$

$$\mathsf{E}(Y_i) = \mu_i \quad \mathsf{Var}(Y_i) = \mu_i + \sigma_i^2$$

• $\lambda_i \sim \Gamma(\alpha, \beta_i)$

$$\mathsf{E}[Y_i] = \mu_i = \alpha \beta_i \quad \mathsf{Var}(Y_i) = \alpha \beta_i (1 + \beta_i) = \mu_i + \frac{\mu_i^2}{\alpha} \ (NegBinII)$$

• $\lambda_i \sim \Gamma(\alpha_i, \beta)$

$$\mathsf{E}[Y_i] = \mu_i = \alpha_i \beta \quad \mathsf{Var}(Y_i) = \mu_i (1 + \beta) = \phi \mu_i \quad (NegBinI)$$

Poisson-normal model

Individual level random effect in the linear predictor

$$Y_i|b_i \sim \mathsf{Pois}(\lambda_i) \quad \mathsf{with} \quad \log \lambda_i = \mathbf{x}_i^T \boldsymbol{\beta} + b_i$$

where $b_i \sim N(0, d)$, which gives

$$\mathsf{E}[Y_i] = e^{\mathbf{x}_i^T \boldsymbol{\beta} + \frac{1}{2}d} := \mu_i$$

$$Var(Y_i) = e^{\mathbf{x}_i^T \boldsymbol{\beta} + \frac{1}{2}d} + e^{2\mathbf{x}_i^T \boldsymbol{\beta} + d}(e^d - 1) = \mu_i + \mu_i(e^d - 1)\mu_i$$

i.e. a variance function of the form

$$\mathsf{Var}(Y_i) = \mu_i + k\mu_i^2$$

Longitudinal Overdispersed Count Data

 Y_{ij} : the jth outcome for subject i, $i=1,\ldots,N$, $j=1,\ldots,n_i$

 $\mathbf{Y}_i = (Y_{i1}, \dots, Y_{in_i})'$: the vector of measurements for subject i

Negative Binomial Type Variance extension

$$Y_{ij}|\lambda_{ij} \sim \mathsf{Poi}(\lambda_{ij}),$$

 $m{\lambda}_i=(\lambda_{i1},\ldots,\lambda_{in_i})'$, with $\mathsf{E}(m{\lambda}_i)=m{\mu}_i$ and $\mathsf{Var}(m{\lambda}_i)=m{\Sigma}_i$ Unconditionally,

$$\mathsf{E}(\mathbf{Y}_i) = \boldsymbol{\mu}_i, \quad \mathsf{and} \quad \mathsf{Var}(\mathbf{Y}_i) = M_i + \Sigma_i$$

where M_i is a diagonal matrix with the vector $oldsymbol{\mu}_i$ along the diagonal

- ullet the diagonal structure of M_i reflects the conditional independence assumption
 - all dependence between measurements on the same unit stem from the random effects
- ullet components of $oldsymbol{\lambda}_i$ independent pure overdispersion model, without correlation between the repeated measures
- $\lambda_{ij} = \lambda_i \Rightarrow \text{Var}(\mathbf{Y}_i) = M_i + \sigma_i^2 J_{n_i}$
 - a Poisson version of compound symmetry
- ullet also possible to combine general correlation structures between the components of $oldsymbol{\lambda}_i$

Poisson-normal model extension – a GLMM

$$Y_{ij}|\mathbf{b}_i \sim \mathsf{Poi}(\lambda_{ij}),$$
 $\ln(\lambda_{ij}) = \mathbf{x}'_{ij}\boldsymbol{\beta} + \mathbf{z}'_{ij}\mathbf{b}_i,$
 $\mathbf{b}_i \sim N(\mathbf{0}, D)$

 \mathbf{x}_{ij} and \mathbf{z}_{ij} : p- and q-dimensional vectors of known covariate values $\boldsymbol{\beta}$: a p-dimensional vector of unknown fixed regression coefficients

Then, unconditionally,

 $\boldsymbol{\mu}_i = \mathsf{E}(\mathbf{Y}_i)$ has components:

$$\mu_{ij} = \exp\left(\mathbf{x}'_{ij}\boldsymbol{\beta} + \frac{1}{2}\mathbf{z}'_{ij}D\mathbf{z}_{ij}\right)$$

and the variance-covariance matrix is

$$Var(\mathbf{Y}_i) = M_i + M_i \left(e^{Z_i D Z_i'} - J_{n_i} \right) M_i$$

Models Combining Overdispersion With Normal Random Effects

$$Y_{ij}|\theta_{ij}, \mathbf{b}_i \sim \operatorname{Poi}(\lambda_{ij})$$

$$\lambda_{ij} = \theta_{ij} \exp\left(\mathbf{x}'_{ij}\boldsymbol{\beta} + \mathbf{z}'_{ij}\mathbf{b}_i\right)$$

$$\mathbf{b}_i \sim N(\mathbf{0}, D)$$

$$\mathsf{E}(\boldsymbol{\theta}_i) = \mathsf{E}[(\theta_{i1}, \dots, \theta_{in_i})'] = \Phi_i$$

$$\operatorname{Var}(\boldsymbol{\theta}_i) = \Sigma_i$$

Then, $\mu_i = \mathsf{E}(\mathbf{Y}_i)$ has components:

$$\mu_{ij} = \phi_{ij} \exp\left(\mathbf{x}'_{ij}\boldsymbol{\beta} + \frac{1}{2}\mathbf{z}'_{ij}D\mathbf{z}_{ij}\right)$$

The variance-covariance matrix is

$$Var(\mathbf{Y}_i) = M_i + M_i (P_i - J_{n_i}) M_i$$

where the $(j,k)^{th}$ element of P_i is

$$p_{i,jk} = \exp\left(\frac{1}{2}\mathbf{z}'_{ij}D\mathbf{z}_{ik}\right)\frac{\sigma_{i,jk} + \phi_{ij}\phi_{ik}}{\phi_{ij}\phi_{ik}}\exp\left(\frac{1}{2}\mathbf{z}'_{ik}D\mathbf{z}_{ij}\right)$$

Estimation for the Poisson-normal and Combined Models

- random-effects models fitted by maximization of the marginal likelihood, by integrating out the random effects from conditional densities
- likelihood contribution of subject *i* is from:

$$f_i(\mathbf{y}_i|\boldsymbol{\beta}, D, \phi) = \int \prod_{j=1}^{n_i} f_{ij}(y_{ij}|\mathbf{b}_i, \boldsymbol{\beta}, \phi) f(\mathbf{b}_i|D) d\mathbf{b}_i$$

• likelihood for β , D, and ϕ :

$$L(\boldsymbol{\beta}, D, \phi) = \prod_{i=1}^{N} \int \prod_{j=1}^{n_i} f_{ij}(y_{ij}|\mathbf{b}_i, \boldsymbol{\beta}, \phi) f(\mathbf{b}_i|D) d\mathbf{b}_i.$$

- key problem: presence of N integrals in general no closed-form solution exists (Verbeke and Molenberghs, 2000; Molenberghs and Verbeke, 2005). To solve the problem, use of
 - numerical integration SAS procedure NLMIXED
 - series expansion methods (penalized quasi-likelihood, marginal quasi-likelihood), Laplace approximation, etc – SAS procedure GLIMMIX
 - hybrid between analytic and numerical integration
- in some special cases (linear mixed effects model, Poisson-normal model), these integrals can be worked out analytically also true for the combined model
- Fully Bayesian inferences

Full Marginal Density for the Combined Model

The joint probability of Y_i takes the form:

$$P(\mathbf{Y}_i = \mathbf{y}_i) = \sum_{\mathbf{t}} \left[\prod_{j=1}^{n_i} \begin{pmatrix} y_{ij} + t_j \\ y_{ij} \end{pmatrix} \begin{pmatrix} \alpha_j + y_{ij} + t_j - 1 \\ \alpha_j - 1 \end{pmatrix} (-1)^{t_j} \beta_j^{y_{ij} + t_j} \right]$$

$$\times \exp\left(\sum_{j=1}^{n_i} (y_{ij} + t_j) \mathbf{x}'_{ij} \boldsymbol{\beta}\right)$$

$$\times \exp \left\{ \frac{1}{2} \left[\sum_{j=1}^{n_i} (y_{ij} + t_j) \mathbf{z}'_{ij} \right] D \left[\sum_{j=1}^{n_i} (y_{ij} + t_j) \mathbf{z}_{ij} \right] \right\}$$

where $\mathbf{t} = (t_1, \dots, t_{n_i})$ ranges over all non-negative integer vectors

- special cases can be obtained very easily
- usefully used to implement maximum likelihood estimation, with numerical accuracy governed by the number of terms included in the series

Partial marginalization

 integrate over the gamma random effects only, leaving the normal random effects untouched

The corresponding probability is:

$$P(Y_{ij} = y_{ij} | \mathbf{b}_i) = \begin{pmatrix} \alpha_j + y_{ij} - 1 \\ \alpha_j - 1 \end{pmatrix} \left(\frac{\beta_j}{1 + \kappa_{ij} \beta_j} \right)^{y_{ij}} \left(\frac{1}{1 + \kappa_{ij} \beta_j} \right)^{\alpha_j} \kappa_{ij}^{y_{ij}}$$

where
$$\kappa_{ij} = \exp[\mathbf{x}'_{ij}\boldsymbol{\beta} + \mathbf{z}'_{ij}\mathbf{b}_i]$$

- we assume that the gamma random effects are independent within a subject – the correlation is induced by the normal random effects
- easy to obtain the fully marginalized probability by numerically integration the normal random effects out of $P(Y_{ij}=y_{ij}|\mathbf{b}_i)$, using SAS procedure NLMIXED

Analysis of the Epilepsy Data

 Y_{ij} : the number of epileptic seizures patient i experiences during week j of the follow-up period

 t_{ij} : the time-point at which Y_{ij} has been measured, $t_{ij}=1,2,\ldots,27$

models with random intercept

$$\ln(\lambda_{ij}) = \begin{cases} (\beta_{00} + b_i) + \beta_{01}t_{ij} & \text{if placebo} \\ (\beta_{10} + b_i) + \beta_{11}t_{ij} & \text{if treated} \end{cases}$$

where $b_i \sim N(0, d)$

or random intercept and random slope

$$\ln(\lambda_{ij}) = \begin{cases} (\beta_{00} + b_{1i}) + (\beta_{01} + b_{2i})t_{ij} & \text{if placebo} \\ (\beta_{10} + b_{1i}) + (\beta_{11} + b_{2i})t_{ij} & \text{if treated} \end{cases}$$

where $\mathbf{b}_i \sim N(0, D)$

- Formally comparing the models with random intercepts and random slopes in time with their counterparts with random intercepts only, produces likelihood ratio test statistics of
 - 205.5 in the Poisson-normal case and
 - 19.0 in the combined-model case.
- Thus, at the same time, the combined model strongly reduces the need for random slopes, but does not remove it.
- Indeed, when comparing the test statistics against their reference distribution, a 50:50 mixture of a χ^2_1 and χ^2_2 distribution, p < 0.0001 was obtained in both cases.
- Estimates of the parameters in the models with random effects versus those without random effects are rather different (random effects of a non-conjugate type).

		Poisson	Negative-binomial	
Effect	Parameter ⁻	Estimate (s.e.)	Estimate (s.e.)	
Intercept placebo	β_{00}	1.2662 (0.0424)	1.2594 (0.1119)	
Slope placebo	eta_{01}	-0.0134 (0.0043)	-0.0126 (0.0111)	
Intercept treatment	β_{10}^{51}	1.4531 (0.0383)	1.4750 (0.1093	
Slope treatment	eta_{11}^{20}	-0.0328(0.0038)	-0.0352 (0.010)	
Negative-binomial par.	α_1		0.5274 (0.0255	
Negative-binomial par.	$\alpha_2 = 1/\alpha_1$		1.8961 (0.0918	
Var. of random int.	d		 ,	
Difference in slopes	$\beta_{11} - \beta_{01}$	-0.0195 (0.0058; p = 0.0008)	-0.0227 (0.0150; p = 0.1310)	
Ratio of slopes	β_{11}/β_{01}	2.4576 (0.8481; p = 0.0038)	2.8085 (2.6070; p = 0.2815)	
		Poisson-normal (RI)	Combined (RI)	
Effect	Parameter ⁻	Estimate (s.e.)	Estimate (s.e.)	
Intercept placebo	β_{00}	0.8179 (0.1677)	0.9112 (0.1755	
Slope placebo	β_{01}	-0.0143(0.0044)	-0.0248 (0.0077	
Intercept treatment	β_{10}	0.6475 (0.1701)	0.6555 (0.1782	
Slope treatment	eta_{11}^{10}	-0.0120 (0.0043)	-0.0118 (0.0074	
Negative-binomial par.	α_1	<u> </u>	2.4640 (0.2113	
Negative-binomial par.	$\alpha_2 = 1/\alpha_1$		0.4059 (0.0348	
Var. of random int.	d	1.1568 (0.1844)	1.1289 (0.1850	
Difference in slopes	$\beta_{11} - \beta_{01}$	0.0023 (0.0062; p = 0.7107)	0.0130 (0.0107; p = 0.2260)	
Ratio of slopes	β_{11}/β_{01}	0.8398 (0.3979; p = 0.0376)	0.4751 (0.3445; p = 0.1591	
		Poisson-normal (RI+RS)	Combined (RI+RS)	
Effect	Parameter ⁻	Estimate (s.e.)	Estimate (s.e.)	
Intercept placebo	β_0	0.8943 (0.1789)	0.9233 (0.1795	
Slope placebo	eta_1°	-0.0272 (0.0099)	-0.0286 (0.0102	
Intercept treatment	β_0^-	0.6498 (0.1835)	0.6679 (0.1835	
Slope treatment	$eta_{f 2}^{\circ}$	-0.0165 (0.0102)	-0.0161 (0.0103)	
Negative-binomial par.	α_1^-		2.7913 (0.2604	
Negative-binomial par.	$\alpha_2 = 1/\alpha_1$	_	0.3583 (0.3343	
Var. of random int.	d_{00}	1.2752 (0.2208)	1.1799 (0.2212	
Corr. random int. and slop	es ρ_{01}^{00}	-0.3341 (0.1312)	-0.2480 (0.1786	
Var. of random slopes	d_{11}	0.0024 (0.0006)	0.0016 (0.0006	
Difference in slopes	$\beta_{11} - \beta_{01}$	0.0107 (0.0140; p = 0.4460)	0.0125 (0.0142; p = 0.3834)	
Ratio of slopes	β_{11}/β_{01}	0.6065 (0.4286; p = 0.1607)	0.5645 (0.4054; p = 0.1673)	

- negative-binomial improvement over standard Poisson
- Poisson-normal improvement over standard Poisson
- combined model further improvement
- impact on point and precision estimates as the slope difference and the slope ratio
- ullet Poisson: p < 0.01 for the slope difference, p < 0.01 for the slope ratio
- ullet negative-binomial: p=0.13 for the slope difference, p=0.28 for the slope ratio
- \bullet Poisson-normal: p=0.71 (RI) and p=0.44 (RI +RS) for the slope difference, p=0.04 (RI) and p=0.16 (RI +RS) for the slope ratio
- combined model: p=0.22 (RI) and p=0.38 (RI +RS) for the difference, p=0.16 (RI) and p=0.17 (RI +RS) for the slope ratio

Correlation functions (Vangeneugden et al, 2011)

- Gamma random effects are assumed independent, need to consider the Poisson-normal and combined cases
- The fixed-effects structure is not constant, depends on time, need for the general correlation function
- For the Poisson-normal case, and for the placebo group

$$\mathsf{Corr}(Y(t),Y(s)) = \frac{35.58 \cdot 0.99^{t+s}}{\sqrt{(4.04 \cdot 0.99^t + 35.58 \cdot 0.97^t) \cdot (4.04 \cdot 0.99^s + 35.58 \cdot 0.97^s)}}$$

where Y(t) represents the outcome for an arbitrary subject at time t

		Smallest value		Largest value	
Model	Arm	$\overline{\rho}$	time pair	ρ	time pair
Poisson-normal, RI	placebo	0.8577	26 & 27	0.8960	1 & 2
Poisson-normal, RI	treatment	0.8438	26 & 27	0.8794	1 & 2
Combined, RI	placebo	0.8259	26 & 27	0.8981	1 & 2
Combined, RI	treatment	0.8383	26 & 27	0.8744	1 & 2
Poisson-normal, RI+RS	placebo	0.2966	1 & 27	0.9512	26 & 27
Poisson-normal, RI+RS	treatment	0.2936	1 & 27	0.9530	26 & 27
Combined, RI+RS	placebo	0.4268	1 & 27	0.9281	26 & 27
Combined, RI+RS	treatment	0.4225	1 & 27	0.9329	26 & 27

- For models with only random intercepts, the correlations range over a narrow interval; they are rather high and there is little difference between the Poisson-normal and combined models.
- For models with random intercepts and random slopes, several differences become apparent.
 - the values exhibit a much broader range between their smallest and largest values.
 - the range is somewhat over-estimated by the Poisson-normal model, which then narrows for the combined model, incorporating overdispersion effects, random intercepts, and random slopes.
- The random slope allows for the correlation to range over a considerable interval, while the overdispersion effect avoids the range to be overly wide.

- The Poisson-normal model forces the correlation and overdispersion effects to stem from a single additional parameter, the random-intercept variance d. Thus, considerable overdispersion also forces the correlation to increase, arguably beyond what is consistent with the data.
- In the combined model, there are *two* additional parameters, giving proper justice to both correlation and overdispersion effects.
- Half the subjects have missing measurements after the 16th week.
 This provides an additional motivation for the proposed model and its likelihood-based estimation, because, under the assumption of missingness at random inferences are valid.
- A corresponding analysis for a fully marginal model poses complex challenges (Molenberghs and Verbeke 2005).

Concluding Remarks

- normal random effects, to induce association between repeated Poisson data, and gamma random effects in the log-linear predictor for the overdispersion, integrated in the combined model
- special cases: standard negative-binomial and Poisson-normal models for repeated measures and univariate outcomes
- explicit expressions for means, variances, covariances and corelations of the combined model were derived
- closed form solutions obtained for the joint marginal probability of the outcome vector

- maximum likelihood estimation by integrating over the random effects, analytically, implemented in SAS procedure NLMIXED, or by combining analytic and numeric techniques
- epileptic seizures data analysis
 - impact on the conclusions about key scientific parameters
 - the correlations derived from the more conventional but also more restricted Poisson-normal model can be highly misleading – suggests a high within-patient correlation among any two time points within any of the two treatment arms
 - the correlations from the combined model are small to moderate
- general framework, encompassing the binary and Poisson types, in Molenberghs et al (2010)

Why to use a mixed-model approach when marginal correlation is of interest?

- non-likelihood based methods such as GEE treat correlation as nuisance parameters, they cannot be used for inferential purposes
- full likelihood methods may be highly prohibitive in terms of computational requirements
- the correlation ranges attainable in marginal models may be highly restricted,
- in a number of special but important cases, such as exchangeable clustered data, the entire range of positive correlations can be reached

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