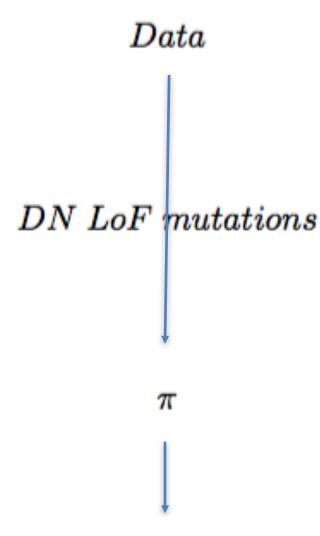**TADA**

$$x_d \sim Pois(2N_d\mu\gamma_{dn})$$
$$x_{ca} \sim Pois(qN_1\gamma_{cc})$$
$$x_{cn} \sim Pois(qN_0)$$
$$\gamma_{dn} \sim Gamma(\bar{\gamma}_{dn}\beta_{dn}, \beta_{dn})$$
$$\gamma_{cc} \sim Gamma(\bar{\gamma}_{cc}\beta_{cc}, \beta_{cc})$$
$$q \sim Gamma(\rho, \nu)$$

Data

↓

DN LoF mutations

↓

π

↓

Mean RRs
(from π and known risk genes
or manually from data)

↓

$$BF_{gene} = \left[\prod_{k=1}^{Cdn} BF_{dn_{hk}}\right]\left[\prod_{b=1}^{Ccc} BF_{cc_{ab}}\right]$$

↓

FDRs

↓

Significant genes

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extTADA

$$x_d \sim Pois(2N_d\mu\gamma_{dn})$$
$$x_{ca} \sim Pois(qN_1\gamma_{cc})$$
$$x_{cn} \sim Pois(qN_0)$$
$$\gamma_{dn} \sim Gamma(\bar{\gamma}_{dn}\beta_{dn}, \beta_{dn})$$
$$\gamma_{cc} \sim Gamma(\bar{\gamma}_{cc}\beta_{cc}, \beta_{cc})$$
$$q \sim Gamma(\rho, \nu)$$

Data from multiple populations

↓

$$\beta = e^{a*\bar{\gamma}^b+c}$$
$$P(x_{ca}, x_{cn}|H_j) = P(x_{ca}|x_{ca}+x_{cn}, H_j)P(x_{ca}+x_{cn}|H_j)$$

↓

Mean RRs + π
(directly from the likelihood function
using MCMC)

↓

$$BF_{gene} = \left[\prod_{h=1}^{Ndn_{pop}}\left(\prod_{k=1}^{Cdn} BF_{dn_{hk}}\right)\right]\left[\left(\prod_{a=1}^{Ncc_{pop}}\prod_{b=1}^{Ccc} BF_{cc_{ab}}\right)\right]$$

↓

FDRs

↓

Significant genes