Pseudo-code for MDLINFER

1 Step 1 of MDLINFER: **Find the $\alpha^*_{\text{reported}}$**

Step 1 Find the $\alpha^*_{\text{reported}}$

Input: Epidemiological model O_M and calibration procedure CALIBRATE, reported infections time sequence D_{reported}.

1: Calibrate baseline parameterization $\mathbf{p} = \text{CALIBRATE}(O_M, \{D_{\text{reported}}, \text{others}\})$
2: Initialize the array to save the MDL cost for α_{reported}: CostArray $= [\ ]$
3: **for** α_{reported} in the linear search space **do**
4:     $D = \frac{D_{\text{reported}}}{\alpha_{\text{reported}}}$
5:     $D_{\text{unreported}} = D - D_{\text{reported}}$
6:     Calibrate candidate parameterization $\mathbf{p'} = \text{CALIBRATE}(O_M, \{D_{\text{reported}}, D_{\text{unreported}}, \text{others}\})$
7:     CostArray$[\alpha_{\text{reported}}] = L(D_{\text{reported}}, D, \mathbf{p'}, \mathbf{p})$
8: **end for**
9: Find the $\alpha^*_{\text{reported}} = \arg\min_{\alpha_{\text{reported}}} \text{CostArray}[\alpha_{\text{reported}}]$
Output: Reported rate $\alpha^*_{\text{reported}}$

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2 Step 2 of MDLINFER: **Find the D^* given $\alpha^*_{\text{reported}}$**

Step 2 Find the D^* given $\alpha^*_{\text{reported}}$

Input: Epidemiological model O_M and calibration procedure CALIBRATE, reported infections time sequence D_{reported}, reported rate $\alpha^*_{\text{reported}}$.

1: Calibrate baseline parameterization $\mathbf{p} = \text{CALIBRATE}(O_M, \{D_{\text{reported}}, \text{others}\})$
2: Find the D^* minimizes $L(D_{\text{reported}}, D, \mathbf{p'}, \mathbf{p})$ using Nelder-Mead.
Output: Total infections D^*