Supplementary File S1 for Pedersen et al. (2013), Nature Biotechnology

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This document is the supplementary file for the manuscript entitled "A kinetic model of enzyme recruiting oligonucleotides predicts an optimal affinity and thus explains why shorter and less affine oligonucleotides may be more potent" (2013) and a vignette for the R-package ASOmodel.

The functions and data used to produce the figures in the main manuscript and this supplementary file are available after installing and requiring the ASOmodel package in R

```
> require(devtools)
> install_github('ASOmodel',username='lykkep')
> require(ASOmodels)
```

The ASOmodels package contains the following functions:

1. `Trel`
2. `TrelNO`
3. `Trelstoc`
4. `plot.doseresponse`
5. `IC50`
6. `IC50NO`
7. `IC50stoc`
8. `diffASO`
9. `pretty10expLP`

Contents

S1 The rate-equations of the ASO model

The kinetic ASO model governs eight ODEs for the seven variables: free target (T), free oligonucleotide (O), free RNAse H (E), complex of oligonucleotide and target (OT), complex of oligonucleotide, target and RNAse H (OTE), complex of cleaved target, oligonucleotide and RNase H (OCE), and complex of cleaved target and oligonucleotide (OC). The ASO model is described by the seven equations

$$\frac{\mathrm{d}[T]}{\mathrm{d}t} = v_{\mathrm{prod}} - v_{\mathrm{degrad}}[T] - k_{O+T\to OT}[T][O] + k_{OT\to O+T}[OT] \tag{1}$$

$$\begin{aligned}\frac{\mathrm{d}[OT]}{\mathrm{d}t} &= k_{O+T\to OT}[O][T] - k_{OT\to O+T}[OT] \\ &\quad - k_{OT+E\to OTE}[OT][E] + k_{OTE\to OT+E}[OTE] - v_{\mathrm{degrad}}[OT]\end{aligned} \tag{2}$$

$$\begin{aligned}\frac{\mathrm{d}[OTE]}{\mathrm{d}t} &= k_{OT+E\to OTE}[E][OT] - k_{OTE\to OT+E}[OTE] \\ &\quad - (v_{\mathrm{degrad}} + k_{OTE\to OCE})[OTE]\end{aligned} \tag{3}$$

$$\begin{aligned}\frac{\mathrm{d}[E]}{\mathrm{d}t} &= -k_{OT+E\to OTE}[E][OT] + k_{OTE\to OT+E}([OTE] + [OCE]) \\ &\quad + v_{\mathrm{degrad}}[OTE]\end{aligned} \tag{4}$$

$$\begin{aligned}\frac{\mathrm{d}[O]}{\mathrm{d}t} &= k_{OT\to O+T}[OT] - k_{O+T\to OT}[O][T] \\ &\quad + k_{*C\to *+C}[OC] + v_{\mathrm{degrad}}([OT] + [OTE])\end{aligned} \tag{5}$$

$$\frac{\mathrm{d}[OCE]}{\mathrm{d}t} = k_{OTE\to OCE}[OTE] - k_{OTE\to OT+E}[OCE] - k_{*C\to *+C}[OCE] \quad (6)$$

$$\frac{\mathrm{d}[OC]}{\mathrm{d}t} = k_{OTE\to OT+E}[OCE] - k_{*C\to *+C}[OC] \quad (7)$$

Complex formation and breaking are denoted by rate constants k with subscripts. Target production and degradation rates are denoted by v_{prod} and v_{degrad}, respectively. The default parameter values are listed in Table S1.

Steady-state is reached when the Eqs. (1)-(8) are equated to zero. Using Maple16 the steady-state concentrations are found. They all depend on the roots to a fourth order polynomial with coefficients calculated within the function `Trel()`. The one root that ensures that all concentrations are non-negative and also fullfills that

$$[O] + [OTE] + [OT] + [OCE] + [OC] = O_t \quad \text{and}$$

$$[OTE] + [OCE] + [E] = E_t \ ,$$

is chosen.

When there is no oligonucleotide added to the system, then the steady-state concentration of target is $[T] = \frac{v_{\mathrm{prod}}}{v_{\mathrm{degrad}}}$. When oligonucleotide is added to the system then the total concentration of target at steady-state is the sum of the concentrations $[T]$, $[OT]$ and $[OTE]$. The relative total target concentration at steady-state is then calculated as

$$T_{\mathrm{rel}} = \frac{[T] + [OT] + [OTE]}{\frac{v_{\mathrm{prod}}}{v_{\mathrm{degrad}}}} \ . \quad (8)$$

The half maximal inhibitory concentration (IC_{50}) is the concentration of total nucleotide needed to inhibit the target concentration by half. The IC_{50} is a measure of the potency of an oligonucleotide. A more potent oligonucleotide will have a lower IC_{50} value. In mathematical terms the IC_{50} value is defined as

$$IC_{50} = \left(O_t \,\middle|\, T_{\mathrm{rel}} = \frac{\mathrm{Eff}}{2} + T_{\mathrm{rel,min}} \right) \ , \quad (9)$$

where the efficacy (Eff, the maximum decrease in T_{rel}), and the minimum value of T_{rel} ($T_{\mathrm{rel,min}}$) are defined by

$$\mathrm{Eff} = 1 - \lim_{O_t\to\infty} T_{\mathrm{rel}} = 1 - T_{\mathrm{rel,min}} \ . \quad (10)$$

S2 Supplementary Table S1

Supplementary Table S1: Default values for the parameter-space of the ASO model. Concentrations are measured in nM and time in min.

Parameter	Description	Default value	Ref
E_t	Total RNAse H conc	1 nM	Ref. [1]
O_t	Total oligo concentration	$\mathcal{O}(\mu M)$	
v_{prod}	Production of target	0.2 nM/min	Ref. [5]
v_{degrad}	Degradation of target	0.04 min^{-1}	Ref. [7]
D_{OT}	Dissociation constant of OT	0.3 nM	Ref. [2]
D_{OTE}	Dissociation constant of OTE	70 nM	Ref. [1]
$k_{O+T\to OT}$	Rate of $O + T \to OT$	0.2 $(\text{nM}\,\text{min})^{-1}$	Ref. [2]
$k_{OT+E\to OTE}$	Rate of $OT + E \to OTE$	5 $(\text{nM}\,\text{min})^{-1}$	Ref. [1]
$k_{OTE\to OCE}$	Rate of $OTE \to OCE$	8 min^{-1}	Ref. [1]
α	Ratio of $\frac{k_{OT\to O+T}}{k_{*\text{C}\to *+\text{C}}} \leq 1$	0.1	

S3 Supplementary Figure S1

The R-function `Trel()` calculates T_{rel} and takes O_t and the set of parameters as input

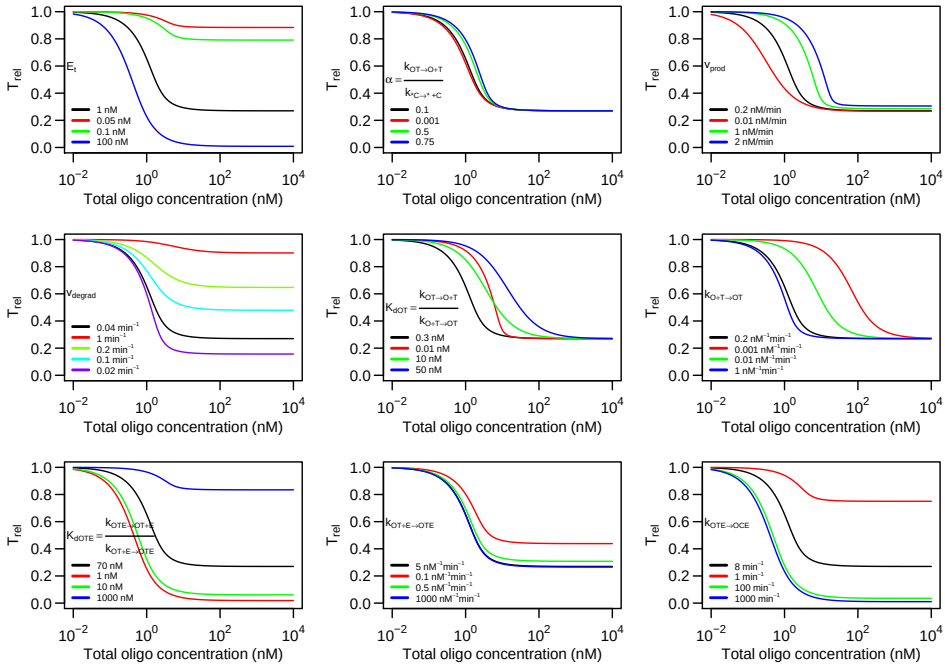
```
> parms <- c(Et = 1,KdOT = 0.3,kOpT = 0.2,KdOTE = 70,kOTpE = 5,
+            vprod = 0.2,vdegrad = 0.04,alpha=0.1,kcleav = 8)
> Trel(otot=1,param=parms)

[1] 0.6538694
```

For a sequence of different oligonucleotide concentrations (O_t), T_{rel} can be calculated for varying parameter values. From this a dose-response curve is obtained. Figure S1 shows the change in the dose-reponse curve as the parameters vary. The plots in Fig. S1 are produced using `plot.doseresponse()`.

S4 Supplementary Figure S2

Using the R-function `drm()` from the drc package (v2.3-0) a dose-response curve is fitted to T_{rel} as a function of O_t to obtain an IC_{50} value. This is calculated through the function `IC50()` that takes K_{dOT} and the set of parameters as input:



Supplementary Figure S1: Dose-response curves for different values of E_t, α, v_{prod}, v_{degrad}, D_{OT}, $k_{O+T\rightarrow OT}$, D_{OTE}, $k_{OT+E\rightarrow OTE}$, and $k_{OTE\rightarrow OCE}$ (top,left to bottom,right). Black lines correspond to the parameter values listed in Supplementary Table S1.

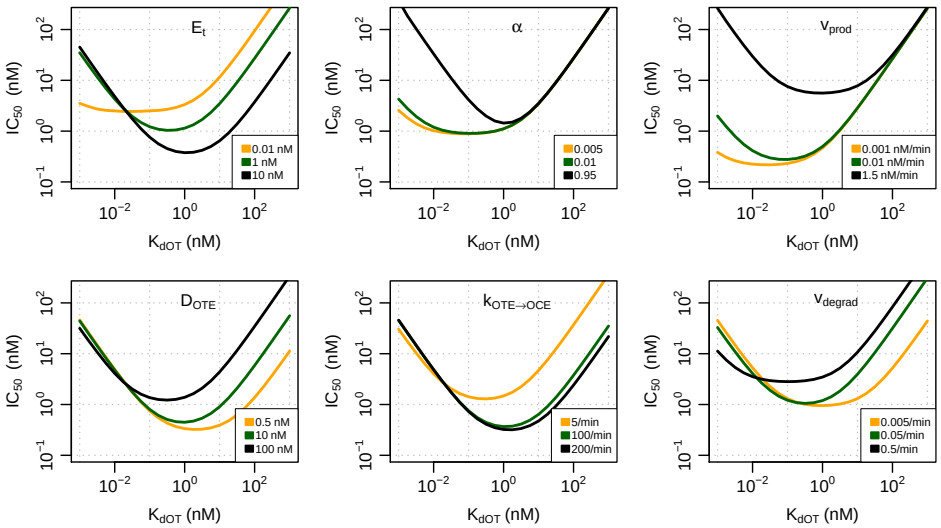
```
> IC50(KdOT=0.1,param=parms)
```

```
    IC50
1.218908
```

For a sequence of K_{dOT} values one can calculate the corresponding IC_{50} values and obtain Fig. 2c from the main manuscript, see Main Figure vignette. Figure S2 shows IC_{50} as a function of K_{dOT} for various parameter values. It can be seen that the optimum affinity, quantified by K_{dOT}, changes as parameters are changed. A larger value of K_{dOT} correponds to a better affinity for the oligonucleotide.

S5 Supplementary Figure S3

The stochastic simulation of the ASOmodel is carried out by use of the `ssa()` function from the GillespieSSA package (v.0.5-4). The inputs of ssa are an initial state vector (x0), which is the initial number of molecules, a propensity vector (a), which denotes the different states of the system, a state-change matrix (nu), which is the change in number of molecule (rows)



Supplementary Figure S2: The optimum affinity is dependent on the parameter settings. In the panels the IC_{50} concentration is plotted against the binding affinity quantified by K_{dOT} for various parameters. From top-left to bottom-right we have varied the total RNAse H concentration (E_t), alpha, the rate of target cleavage ($k_{OTE \rightarrow OCE}$), the target production (v_{prod}) and degradation (v_{degrad}), and the dissociation constant for the OTE complex (D_{OTE}).

if a reaction occur (column), the model-parameters (parms) and the final time (tf).

```
> library(GillespieSSA)
> parms1 <- c(k1 = 2E-5,k2 =50E-5 ,vt = 150,  kd = 0.04,
+                kE = 2, km1 =0.06, km2=2, k3 = 0.1)
> x0 <- c(Tt=parms1["vt"]/parms1["kd"],
+         OT=0,OTE=0,E=1e3,O=1e5,OCE=0,OC=0)
> names(x0) <- c('Tt','OT','OTE','E','O','OCE','OC')
> a <-  c("vt","k1*O*Tt","kd*Tt","km1*OT","km2*OTE","kd*OT",
+          "k2*OT*E","kd*OTE","kE*OTE","k3*OC","km2*OCE" )
> nu <- matrix(0,7,length(a))
> dimnames(nu) <- list(names(x0),a)
> #T
> nu['Tt',c('vt','km1*OT')] <- 1
> nu['Tt',c('k1*O*Tt','kd*Tt')] <- -1
> #OT
> nu['OT',c('k1*O*Tt','km2*OTE')] <- 1
> nu['OT',c('km1*OT','k2*OT*E','kd*OT')] <- -1
> #OTE
```

```
> nu['OTE',c('k2*OT*E')] <- 1
> nu['OTE',c('km2*OTE','kd*OTE','kE*OTE')] <- -1
> #E
> nu['E',c('km2*OTE','kd*OTE','km2*OCE')] <- 1
> nu['E',c('k2*OT*E')] <- -1
> #O
> nu['O',c('km1*OT','kd*OTE','kd*OTE','kd*OT','k3*OC')] <- 1
> nu['O',c('k1*O*Tt')] <- -1
> #OCE
> nu['OCE',c('kE*OTE')] <- 1
> nu['OCE',c('km2*OCE')] <- -1
> #OC
> nu['OC',c('km2*OCE')] <- 1
> nu['OC',c('k3*OC')] <- -1
> Gillespie <- ssa( x0=x0,# initial state vector
+       a=a, # propensity vector
+       nu=nu, # state-change matrix
+       parms = parms1, # model parameters
+       tf=1E3, # final time
+       method = "ETL" # SSA method
+ )
```

Check that $[O] + [OT] + [OTE] + [OCE] + [OC] = O_t$ at all times:

```
> range(rowSums(Gillespie$data[,c('O','OT','OTE','OCE','OC')])-
+         x0['O'])
```

```
[1] 0 0
```

Check that $[E] + [OTE] + [OCE] = E_t$ at all times:

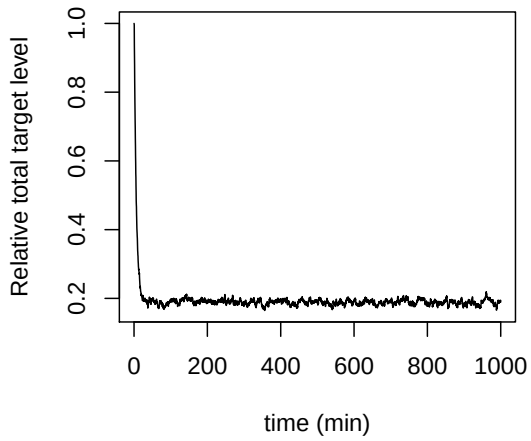
```
> range(rowSums(Gillespie$data[,c('OTE','OCE','E')])-x0['E'])
```

```
[1] 0 0
```

Supplementary Figure S3 shows T_{rel}, from the Gillespie simulation, as a function of time.

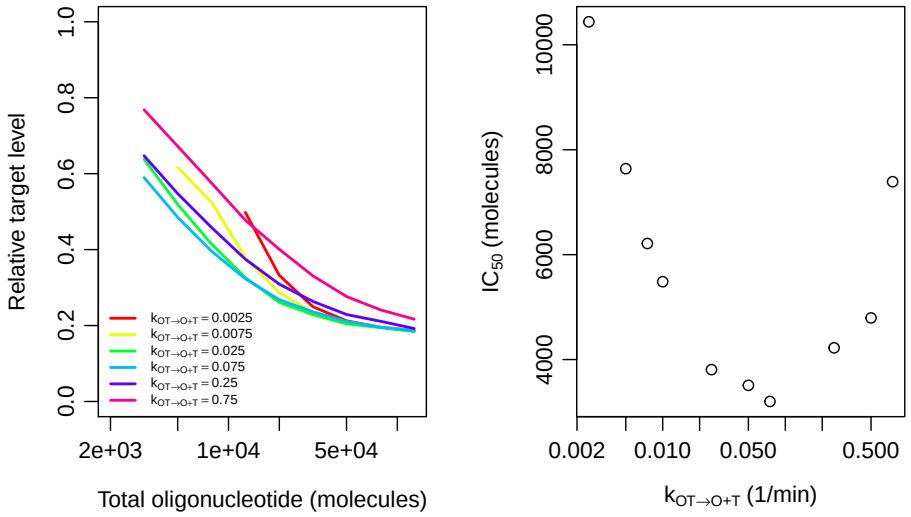
S6 Supplementary Figure S4

After a while the relative target concentration reaches a plateau. In Supplementary Figure S3 the plateu starts around $50min$. The mean of T_{rel} within the plateu is calculated through the function `Trelstoc()`. Using this function we can generate dose-response curves (Supplementary Figure S4,left). From these the IC_{50} values can be calculated using the `IC50stoc()` function and subsequently plotted as a function of $k_{OT\rightarrow O+T}$ (Supplementary Figure S4,right).



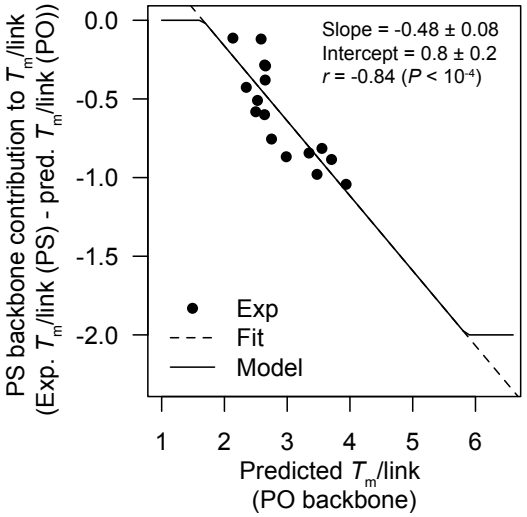
Supplementary Figure S3: The time-trace for the relative total target level.

```
> lseq <- c(1,2.5,5,7.5)
> #### Sequence of k(OT -> O+T) values
> KM <- c(1E-3*lseq[-1],1E-2*lseq,1E-1*lseq)
> #### Generation of dose-response curves
> DRcurve <- lapply(KM,function(kmi){
+             sapply(10^seq(2.5,6,by=0.2),
+                    function(i) Trelstoc(i,km1=kmi)$Tstat)})
> DRc <- lapply(DRcurve,function(x) x[,!is.na(x[3,])] )
> #### Calculation of IC50
> IC50_KM <- sapply(1:length(DRc),
+               function(x){IC50stoc(DRc[[x]][2,],DRc[[x]][1,])})
```



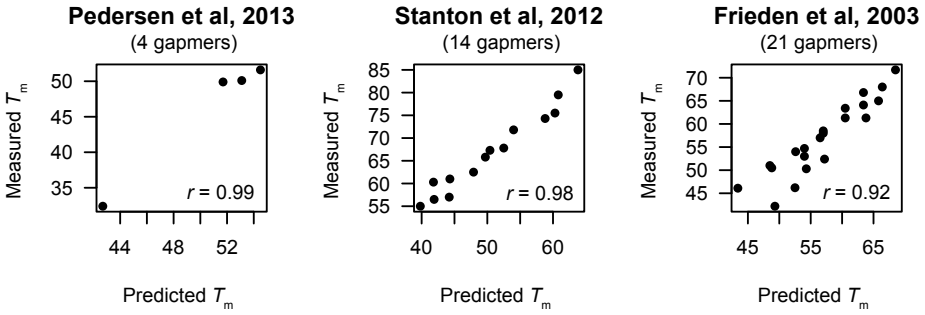
Supplementary Figure S4: Left: Dose-response curves for various values of $k_{OT\rightarrow O+T}$. Right: The IC_{50}-value as a function of $k_{OT\rightarrow O+T}$.

S7 Supplementary Figure S5



Supplementary Figure S5: The effect on T_m of a phosphorothioate backbone was estimated using published data from Ref. [4].

S8 Supplementary Figure S6



Supplementary Figure S6: Measured melting temperature vs predicted melting temperatur. There are clear correlations (r $>$ 0.92, P $<$ 0.01, Pearson's correlation) between predicted and measured T_m. Pedersen et al: 4 LNA-modified oligonucleotides targeting apolipoprotein B (this work), Stanton et al: 14 LNA-modified oligonucleotides targeting the glucocorticoid receptor [6]. Frieden et al: 21 LNA-modified oligonucleotides targeting the luciferase firefly gene [3].

References

[1] N. V. Amirkhanov and P. I. Pradeepkumar. Kinetic analysis of the RNA cleavage of the conformationally-constrained oxetane-modified antisense-RNA hybrid duplex by RNase H. *J Chem Soc*, 2002.

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