Adherence to antiretroviral HIV drugs: how many doses can you miss before resistance emerges?

Robert Smith?
The problem

- The emergence of drug resistance is one of the most prevalent reasons for HIV treatment failure

"Clarification of the degree of adherence is the most urgent unanswered question in HIV research today"
- The U.S. Department of Health and Human Services.
Research Questions

1. How can we quantify the relationship between drug levels and resistance?
2. Can we prescribe dosing intervals and dosages to prevent or reduce resistance?
3. For strongly adherent patients, how many doses can be missed before resistance emerges?
Outline

- Biology of HIV and drug resistance
- Mathematical model of resistance
- Impulsive differential equations
- Equilibria, periodic orbits, stability
- Quantify dosages and dosing intervals
- Derive adherence thresholds
- Extend results to combination therapy.
Population with HIV RNA > 500 copies/ml

RTI = Reverse transcriptase inhibitor
NRTI = Nucleoside RTI
NNRTI = Nonnucleoside RTI
PI = Protease inhibitor

Drug resistance detected:
- Any drug: 76%
- NRTI: 71%
- PI: 41%
- NNRTI: 48%
- 2 class: 25%
- 3 class: 13%
This is a timely question

- Drug regimens to be introduced in sub-Saharan Africa will likely only use RTIs, not PIs.
- In the developed world, the introduction of fusion inhibitors and integrase inhibitors suggests that cocktails may consist primarily of drugs that prevent viral infection of a T cell.

**RTI=Reverse transcriptase inhibitor**
**PI=Protease inhibitor**
PI-sparing regimens

- These are drugs that prevent the virus from transcribing its RNA onto host DNA
- Includes RTIs, fusion inhibitors and integrase inhibitors, but not protease inhibitors.

RTI=Reverse transcriptase inhibitor
DNA=deoxyribonucleic acid
RNA=ribonucleic acid
Fusion inhibitors block here

Integrate Inhibitors block here

Reverse Transcriptase Inhibitors block here

Protease Inhibitors block here
The two strains

We assume two strains of the virus:
1. The wild-type strain will dominate in the absence of drugs
2. There is also a mutant strain that is a less efficient competitor, but more resistant to the drugs.
The basic idea

• Resistant mutants are not impervious to the drugs
• Rather, resistance confers a 5-50 fold resistance to the drugs
• Thus, if drug concentrations in the cell were sufficiently high, then even the mutant would be controlled.
Drug dependence

- As drug levels fall, the wild-type strain is controlled, but the mutant may take hold.
- When the drug falls to trough levels, the wild-type strain can regain its advantage.
- Thus the amount of drug will determine how and when one, the other or neither strain gains dominance.
How to model something like this?

We consider three drug regimes:

- Region 1 (low): drugs are not sufficient to inhibit either strain
- Region 2 (medium): drugs will inhibit the wild type, but not the mutant
- Region 3 (high): drugs will inhibit both strains.
The model itself changes

- Within each regime, the model itself will be different
- We have three models, connected by the drug behaviour
- Thus, as the drug levels change, so too does each model.
\[ T_S = \text{Susceptible T cells} \quad T_I = \text{Infected (wild type)} \quad T_Y = \text{Infected (mutant)} \]

\[ T_{RI} = \text{Intermediately inhibited} \quad T_{RY} = \text{Highly inhibited} \]

\[ V_I = \text{wild-type virus} \quad V_Y = \text{mutant virus} \]

\[ m_{RI} = \text{waning rate} \quad m_{RY} = \text{waning rate} \]
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\( m_{RI} = \text{wanning rate} \quad m_{RY} = \text{wanning rate} \quad R = \text{drug} \)
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Impulsive Differential Equations

- Assume drug effects are instantaneous.
- That is, the time-to-peak is assumed to be negligible.
- This results in a system of impulsive differential equations.
Impulsive effect

- According to impulsive theory, we can describe the nature of the impulse at time $r_k$ via the difference equation

\[ \Delta y \equiv y(r_k^+) - y(r_k^-) = f(r_k, y(r_k^-)) \]
Impulsive DEs

- Solutions are continuous for $t \neq r_k$
- Solutions undergo an instantaneous change in state when $t = r_k$. 

Thousands of HIV particles emerging from an infected T-cell

$r_k =$ impulse time
Putting it together

- The model thus consists of a system of ODEs (virus and T cells) together with an ODE and a difference equation (drugs).
The model in Region 1 (low drugs)

\[ \frac{dV_I}{dt} = n_I \omega T_I - d_V V_I - r_I T_S V_I \]
\[ \frac{dV_Y}{dt} = n_I \omega T_Y - d_V V_Y - r_Y T_S V_Y - r_Y T_RI V_Y \]
\[ \frac{dV_{NI}}{dt} = n_I (1 - \omega) (T_I + T_Y) - d_V V_{NI} \]
\[ \frac{dT_S}{dt} = \lambda - r_I T_S V_I - r_Y T_S V_Y - d_S T_S + m_RI T_RI \]
\[ \frac{dT_I}{dt} = r_I T_S V_I - d_I T_I \]
\[ \frac{dT_Y}{dt} = r_Y T_S V_Y - d_I T_Y + r_Y T_RI V_Y \]
\[ \frac{dT_{RI}}{dt} = -r_Y T_RI V_Y - (d_S + m_RI) T_{RI} + m_RY T_{RY} \]
\[ \frac{dT_{RY}}{dt} = -(d_S + m_RY) T_{RY} \]

\( T_S \) = Susceptible T cells \quad T_I = Infected (wild type) \quad T_Y = Infected (mutant) \quad V_{NY} = noninfectious
\( T_{RI} = Intermediately \ inhibited \quad T_{RY} = Highly \ inhibited \quad V_I = wild-type \ virus \quad d_j = clearance \ rates \\
V_Y = mutant \ virus \quad m_j = waning \ rates \quad \lambda = lymphic \ source \quad n_I = # \ particles \quad \omega = infectious \ fraction \\
r_I = wild \ type \ infection \ rate \quad r_Y = mutant \ infection \ rate
The model in Region 2 (intermediate drugs)

\[
\begin{align*}
\frac{dV_I}{dt} &= n_I \omega T_I - d_V V_I - r_I T_S V_I \\
\frac{dV_Y}{dt} &= n_I \omega T_Y - d_V V_Y - r_Y T_S V_Y - r_Y T_{RI} V_Y \\
\frac{dV_{NI}}{dt} &= n_I (1 - \omega) (T_I + T_Y) - d_V V_{NI} \\
\frac{dT_S}{dt} &= \lambda - r_I T_S V_I - r_Y T_S V_Y - d_S T_S - r_P T_S R + m_{RI} T_{RI} \\
\frac{dT_I}{dt} &= r_I T_S V_I - d_I T_I \\
\frac{dT_Y}{dt} &= r_Y T_S V_Y - d_I T_Y + r_Y T_{RI} V_Y \\
\frac{dT_{RI}}{dt} &= r_P T_S R - r_Y T_{RI} V_Y - (d_S + m_{RI}) T_{RI} + m_{RY} T_{RY} \\
\frac{dT_{RY}}{dt} &= -(d_S + m_{RY}) T_{RY}
\end{align*}
\]

\( T_S = \) Susceptible \( T \) cells \quad \( T_I = \) Infected (wild type) \quad \( T_Y = \) Infected (mutant) \quad \( \lambda = \) lymphic source \quad \( R = \) drug

\( T_{RI} = \) Intermediately inhibited \quad \( T_{RY} = \) Highly inhibited \quad \( V_I = \) wild-type virus \quad \( d_j = \) clearance rates

\( V_Y = \) mutant virus \quad \( V_{NI} = \) noninfectious \quad \( m_j = \) waning rates \quad \( n_i = \# \) particles \quad \( \omega = \) infectious fraction

\( r_I = \) wild type infection rate \quad \( r_Y = \) mutant infection rate
The model in Region 3 (high drugs)

\[
\frac{dV_i}{dt} = n_I \omega T_I - d_V V_I - r_I T_S V_I
\]
\[
\frac{dV_y}{dt} = n_I \omega T_Y - d_V V_Y - r_Y T_S V_Y - r_Y T_{RI} V_Y
\]
\[
\frac{dV_{NI}}{dt} = n_I (1 - \omega) (T_I + T_Y) - d_V V_{NI}
\]
\[
\frac{dT_S}{dt} = \lambda - r_I T_S V_I - r_Y T_S V_Y - d_S T_S - r_R T_S R + m_{RI} T_{RI}
\]
\[
\frac{dT_I}{dt} = r_I T_S V_I - d_I T_I
\]
\[
\frac{dT_Y}{dt} = r_Y T_S V_Y - d_I T_Y + r_Y T_{RI} V_Y
\]
\[
\frac{dT_{RI}}{dt} = r_R T_S R - r_Y T_{RI} V_Y - (d_S + m_{RI}) T_{RI} + m_{RY} T_{RY} - r_Q T_{RI} R
\]
\[
\frac{dT_{RY}}{dt} = r_Q T_{RI} R - (d_S + m_{RY}) T_{RY}
\]

\[ T_S = \text{Susceptible T cells} \quad T_i = \text{Infected (wild type)} \quad T_Y = \text{Infected (mutant)} \quad \lambda = \text{lymphic source} \quad R = \text{drug} \]
\[ T_{RI} = \text{Intermediately inhibited} \quad T_{RY} = \text{Highly inhibited} \quad V_I = \text{wild-type virus} \quad d_j = \text{clearance rates} \]
\[ V_Y = \text{mutant virus} \quad V_{NY} = \text{noninfectious} \quad m_j = \text{waning rates} \quad n_i = \# \text{ particles} \quad \omega = \text{infectious fraction} \]
\[ r_I = \text{wild type infection rate} \quad r_Y = \text{mutant infection rate} \]
with the (impulsive) dynamics of the drugs:

\[
\frac{dR}{dt} = -d_R R, \quad t \neq t_k
\]

\[
\Delta R = \begin{cases} 
  R^i & \text{if a dose is to be taken} \\
  0 & \text{if no dose is to be taken}
\end{cases}
\]

- $R =$ drug
- $d_R =$ decay rate
- $R^i =$ dosage
- $t_k =$ impulse time
Limitations of the model

• Approximating the change in drug levels by impulsive differential equations means that results may be less accurate for short dosing intervals

• Dispersal and delay in intracellular dynamics may affect conclusions.
The drugs satisfy a recursion relation

\[ R(t) = R(t_k^+) e^{-d_{R}(t-t_k)} \]

\[ R(t_k^+) = R(t_k^-) + R^i \]

\[ t_k < t \leq t_{k+1} \]

\( R = \text{drug} \)
\( d_R = \text{decay rate} \)
\( R^i = \text{dosage} \)
\( t_k = \text{impulse time} \)
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R(t_k^+) = R(t_k^-) + R^i
\]

\(t_k < t \leq t_{k+1}\)

Hence

\(R=\text{drug}\)  \\
\(d_R=\text{decay rate}\)  \\
\(R^i=\text{dosage}\)  \\
\(t_k=\text{impulse time}\)
The drugs satisfy a recursion relation

\[ R(t) = R(t_k^+) e^{-d_R(t-t_k)} \quad \text{for} \quad t_k < t \leq t_{k+1} \]

\[ R(t_k^+) = R(t_k^-) + R^i \]

Hence

\[ R(t_k^+) \rightarrow \frac{R^i}{1 - e^{-d_R \tau}}. \]

\( R = \text{drug} \)
\( d_R = \text{decay rate} \)
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The drugs satisfy a recursion relation

\[ R(t) = R(t_k^+) e^{-d_R(t-t_k)} \quad \text{for} \quad t_k < t \leq t_{k+1} \]

\[ R(t_k^+) = R(t_k^-) + R^i \]

Hence

\[ R(t_k^+) \to \frac{R^i}{1 - e^{-d_R \tau}} \]

as \( k \to \infty \), where \( \tau = t_{k+1} - t_k \) is the dosing interval.

\[ \begin{align*}
R &= \text{drug} \\
d_R &= \text{decay rate} \\
R^i &= \text{dosage} \\
t_k &= \text{impulse time}
\end{align*} \]
Thus, for the drugs, there is a unique, positive impulsive periodic orbit with one impulse per cycle. It can also be shown that the endpoints of each cycle monotonically approach the endpoints of this periodic orbit.
Region 1: Low drug levels

- Three equilibria: disease-free, wild type only, mutant only
- We can prove that the wild type equilibrium is stable and the others are unstable

(Proof: Smith & Wahl, 2004.)
Region 2: Intermediate levels

- There are no equilibria, due to impulses
- Four impulsive periodic orbits: disease-free, wild type only, mutant only and coexistence
- We can prove that the wild type and mutant coexist

(Proof: Smith & Wahl, 2004.)
Region 3: High drug levels

- If \( r_R \geq r_Q \), which we expect, then there are no interior orbits
- Three impulsive periodic orbits: disease-free, wild type only, mutant only
- We can prove that the disease-free orbit is unstable if and only if the wild type orbit exists

(Proof: Smith & Wahl, 2004.)
Clearing the virus is possible

• Within Region 3, there is a region of viral elimination where the disease-free orbit is stable
• Otherwise the mutant alone dominates

(Proof: Smith & Wahl, 2004).
Summarizing

• For low drug levels, resistance does not emerge and the wild-type strain dominates.
• For intermediate levels, resistance is guaranteed to emerge.
• For high drug levels, either the mutant strain dominates, or both strains are eliminated.
Equilibrium T cell counts

- Region 1 (low drug levels):

\[ \bar{T}_S + \bar{T}_I = \frac{\lambda}{d_I} + \frac{d_V (d_I - d_S)}{r_I (n_I \omega - d_I)} \ll \frac{\lambda}{d_S} \]

- Region 2 (intermediate levels):

\[ \bar{T}_S + T^*_I + T^*_Y + \bar{T}_{RI} = \frac{\lambda}{d_I} + \frac{d_V (d_I - d_S)}{r_Y (n_I \omega - d_I)} \ll \frac{\lambda}{d_S} \]

$T_S =$ Susceptible T cells  $T_I =$ Infected (wild type)  $T_Y =$ Infected (mutant)  $\lambda =$ lymphic source  $T_{RI} =$ Intermediately inhibited  $d_V =$ viral clearance rate  $d_S =$ uninfected T cell clearance rate  $d_I =$ infected T cell clearance rate  $n_I =$ # particles  $\omega =$ infectious fraction  $r_I =$ wild type infection rate  $r_Y =$ mutant infection rate
Region 3

- What happens as the dosing interval shrinks to zero, or the dosage increases to infinity?
- Eventually we’ll be in the region of viral elimination.
Which T cells dominate?

• We can prove the following:

**Theorem.** As $t \to \infty$ and either $\tau \to 0$, or $R_i \to \infty$, $T_S, T_I, T_Y, T_{RI} \to 0$ and $T_{RY} \to T_{RY}^{(\infty)}$ in region 3, where $T_{RY}^{(\infty)}$ satisfies

$$\frac{\lambda}{d_S + m_{RY}} \leq T_{RY}^{(\infty)} \leq \frac{\lambda}{d_S}$$

(Proof: Smith & Wahl, 2004)

• These T cell levels are close to the levels in the uninfected immune system.
Putting it all together

• In practice, drug trajectories may cross one, two or all three regions

• Therefore, we examine parameter space for dosing intervals and dosages.
Virus may be cleared

Region 3

Regions 1, 2 & 3

Region 2

Regions 1 & 2

Region 1

Dosing interval (hours)

Dosage (μM)
US FDA recommendation

Virus may be cleared

Region 3

Regions 2 & 3

Regions 1, 2 & 3

Dosage (μM)

Dosing interval (hours)
Outcome determined by parameter space

- The choice of dosing interval and dosage will completely determine which region(s) trajectories will ultimately lie in.
Simulations

• Realistic parameters were simulated
• Only the dosing interval and the dosage were varied.
Region 1

```
<table>
<thead>
<tr>
<th></th>
<th>S</th>
<th>R</th>
<th>I</th>
<th>R</th>
<th>Y</th>
<th>I</th>
<th>Y</th>
</tr>
</thead>
</table>
```

- **T cells infected by the mutant virus (per μL)**
- **T cells infected by the wild-type virus (per μL)**
For single regions

Summarizing:

• Region 1 (low drugs): The wild type strain only

• Region 2 (intermediate drugs): The mutant strain mostly, with a small wild-type contribution

• Region 3 (high drugs): Either the mutant strain only, or the virus is eliminated.
Regions 1 & 2

T cells infected by the wild-type virus (per μL)
Regions 1 & 2

discontinuous derivatives

Regions 2 & 3
For multiple regions

Summarizing:

• Regions 1 & 2: Coexistence of both strains, wild type dominates
• Regions 2 & 3: The mutant strain only
• Regions 1, 2 & 3: Coexistence, with high numbers of both types.

Region 1=low drug levels
Region 2=intermediate levels
Region 3=high drug levels
In summary

- If the drug levels are low, resistance will not emerge, but T cell counts are low.
- For intermediate drug levels, resistance is guaranteed to emerge. T cell counts are similar to low drug levels.
- For high drug levels, either the resistant strain will dominate, or the virus will be eliminated.
The question of adherence

• Thus, for perfect adherence, the virus is likely to be cleared

• What happens as adherence lapses?

"Clarification of the degree of adherence is the most urgent unanswered question in HIV research today"
- The U.S. Department of Health and Human Services.
"Drug holidays" are extended breaks from the drugs. They may occur due to:

- lifestyle factors
- relief from side effects
- economic implications (especially in the developing world).
YOU HAVE HIV.
YOU HAVE HIV.
PEOPLE SAY TAKE YOUR MEDICATION.
YOU HAVE HIV. PEOPLE SAY TAKE YOUR MEDICATION. THEY HAVE NO IDEA.
Missing $h$ doses

- Assuming perfect adherence, after the $n$th dose, drug levels satisfy

$$R(t^n_+) = \frac{R^i}{1 - e^{-d_R \tau}}$$

- To avoid Region 2 after $h$ doses have been missed, we require

$$\frac{R^i e^{-hd_R \tau}}{1 - e^{-d_R \tau}} > R_2.$$
Avoiding resistance

• Thus the maximum number of missable doses satisfies

\[ h < \frac{1}{d_R \tau} \log \frac{R^i}{R_2(1 - e^{-d_R \tau})}. \]

\( R^i = \) dosage, \( d_R = \) drug decay rate, \( \tau = \) dosing interval,
\( R_2 = \) Region 2 threshold, \( h = \# \) doses missed
How many doses to take subsequently?

- Suppose $k$ subsequent doses are taken in succession.
- To return to drug levels approximating pre-interruption levels, we require

$$R(t_{n+h+k}) > \frac{R^i e^{-d_R \tau}}{1 - e^{-d_R \tau}} - \epsilon,$$

for some required level of tolerance $\epsilon$.

$R^i =$ dosage $\quad d_R =$ drug decay rate $\quad \tau =$ dosing interval $\quad n =$ # doses previously taken $\quad h =$ # doses missed
$R(t^-_{n+h+k})$. 
E.g. Didanosine

- The nucleoside reverse transcriptase inhibitor Didanosine was simulated
- First the maximal number of missable doses were skipped
- Then the drug was allowed to enter Region 2 for 24 hours (equivalent to missing two further doses).

Region 2=intermediate levels
Huge spike of resistance 24 hours inside Region 2 35 days of adherence. 24 hours inside Region 2
A resistant spike

- Thus, entering Region 2 for 24 hours produced a spike of 60,000 $\mu$mol/L.
- The resistant strain takes ~ 35 days to be eliminated, assuming perfect adherence subsequently.
Missable doses for approved drugs

- Similar methods were used to calculate the number of missable and subsequent doses for all PI-sparing drugs approved by the US FDA.

- These levels all assumed 50-fold resistance.

*PI*=protease inhibitors
The number of missable and subsequent doses for all US FDA approved PI-sparing drugs (Smith, 2005)

<table>
<thead>
<tr>
<th>drug</th>
<th>$R^i$ (µM)</th>
<th>$\tau$ (days)</th>
<th>$T_{1/2}$ (h)</th>
<th>$R_1$ (µM)</th>
<th>$R^{(10)}_2$ (µM)</th>
<th>$R^{(50)}_2$ (µM)</th>
<th>missable</th>
<th>subsequent</th>
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</thead>
<tbody>
<tr>
<td>Abacavir (ABC)</td>
<td>12</td>
<td>1/2</td>
<td>15</td>
<td>$e^{-8}$</td>
<td>$e^{-6}$</td>
<td>$e^{-4}$</td>
<td>13</td>
<td>9</td>
</tr>
<tr>
<td>Didanosine (ddI)</td>
<td>4.65</td>
<td>1/2</td>
<td>25</td>
<td>$e^{-5}$</td>
<td>$e^{-3}$</td>
<td>$e^{-1}$</td>
<td>11</td>
<td>14</td>
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<td>Emtricitabine (FTC)</td>
<td>7.2</td>
<td>1</td>
<td>39</td>
<td>$e^{-8}$</td>
<td>$e^{-6}$</td>
<td>$e^{-4}$</td>
<td>16</td>
<td>11</td>
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<tr>
<td>Lamivudine (3TC)</td>
<td>6</td>
<td>1/2</td>
<td>17</td>
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<td>$e^{-2}$</td>
<td>$e^{-1}$</td>
<td>7</td>
<td>10</td>
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<tr>
<td>Stavudine (d4T)</td>
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<td>1/2</td>
<td>7</td>
<td>$e^{-6}$</td>
<td>$e^{-4}$</td>
<td>$e^{-2}$</td>
<td>2</td>
<td>4</td>
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<tr>
<td>Tenofovir (TDF)</td>
<td>1.184</td>
<td>1</td>
<td>17</td>
<td>$e^{-5}$</td>
<td>$e^{-3}$</td>
<td>$e^{-2}$</td>
<td>1</td>
<td>4</td>
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<td>Zalcitabine (ddC)</td>
<td>0.1008</td>
<td>1/3</td>
<td>3</td>
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<td>$e^{-6}$</td>
<td>$e^{-4}$</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Zidovudine (ZDV)</td>
<td>4.24</td>
<td>1/3</td>
<td>3</td>
<td>$e^{-12}$</td>
<td>$e^{-10}$</td>
<td>$e^{-8}$</td>
<td>5</td>
<td>3</td>
</tr>
<tr>
<td>Delavirdine (DLV)</td>
<td>35</td>
<td>1/3</td>
<td>5.8</td>
<td>$e^{-7}$</td>
<td>$e^{-5}$</td>
<td>$e^{-3}$</td>
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<td>5</td>
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<td>Efavirenz (EFV)</td>
<td>12.9</td>
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<td>$e^{-6}$</td>
<td>$e^{-4}$</td>
<td>20</td>
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<tr>
<td>Nevirapine (NVP)</td>
<td>7.5</td>
<td>1/2</td>
<td>35</td>
<td>$e^{-10}$</td>
<td>$e^{-7}$</td>
<td>$e^{-6}$</td>
<td>40</td>
<td>20</td>
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<tr>
<td>Enfuvirtide (T20)</td>
<td>18.36</td>
<td>1/2</td>
<td>3.8</td>
<td>$e^{-9}$</td>
<td>$e^{-7}$</td>
<td>$e^{-5}$</td>
<td>3</td>
<td>3</td>
</tr>
</tbody>
</table>
Multiple resistance

- If a drug has multiple resistant strains, calculate the Region 2 threshold for the highest strain.
- E.g. if there are 10- and 50-fold resistant strains to Abacavir, use $R_{2}^{(50)}=e^{-4}$, rather than $R_{2}^{(10)}=e^{-6}$.

Region 2=intermediate levels  $R_2=$Region 2 threshold
Combination therapy

For combination therapy, the results can be applied concurrently:

E.g. Trizivir consists of
• Abacavir (6.5 days of missable doses),
• Lamivudine (3.5 days) and
• Zidovudine (1.67 days).
Emerging resistance

- Resistance emerges to Zidovudine after 1.67 days
- After a further 3.5 days, resistance to Lamivudine emerges
- After 6.5 more days, resistance to Abacavir emerges

Therefore, this cocktail could be skipped for 11.67 days
(Probably an underestimate.)
Experimental validation

- Results were compared to experiments in structured treatment interruptions (STIs)
- Patients interrupt therapy at fixed intervals only
- STIs have a delaying effect on the emergence of resistance

Nevertheless, results were broadly consistent with the timeframe.
A small "drug holiday" may be acceptable, so long as sufficient doses are taken subsequently.

However, even 24 hours past the threshold of missable doses leads to extremely high resistance levels.
A general method

1. Identify the Region 2 threshold for the appropriate resistant strain
2. Calculate the number of missable doses
3. Calculate the number of subsequent doses

This method can be applied to any PI-sparing drug (including future drugs) for any level of resistance detected.
Future work

• A model that includes protease inhibitors
• Further investigation of the complicating effects of combination therapy
• Model resistance to the body's immune system response.
Key references


A global view of HIV infection

40 million adults living with HIV/AIDS as of end 2001