

Evaluation of Rapid and Sustained Population Viral Response Rates Predicted Under Hepatitis C Viral Dynamic Models



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Objectives

The objective of this study was to compare both short- and long-term population-level viral responses predicted under two HCV dynamic models [3, 13] with observed response rates in a meta data set compiled from published clinical reports.

Methods

- HCV dynamic models published by Dahari et. al. [3] and Snoeck et. al. [13] were used to simulate individual-level viral load versus time profiles in *in silico* populations of HCV genotype-1 infected patients (N=5000)
- Viral load profiles simulated in R using the `lsoda()` function in the `deSolve()` library
- Simulation Assumptions:
 - Standard of care regimen:
 - peg-IFN-alfa-2a 180 μ g per week + ribavirin 13 mg/kg/day x 48 weeks
 - Viral load limit of detection: 100 copies/mL
 - $ED_{50_{IFN}}$, $ED_{50_{RBV}}$, all between-subject variability parameters same for Snoeck and Dahari models
 - Individual-level random effects uncorrelated; no residual unexplained variability in observations
- Subjects were dropped out from the study and assigned non-responder status according to virologic response at either 12 weeks (detectable viral load and < 2 -log drop from baseline viral load) or 24 weeks (detectable viral load) [9]
- Response rates (fraction of subjects with undetectable viral load and not dropped out) were calculated at 4, 12, 24, 48, and 72 weeks after starting treatment
- Meta Data Set
 - Simulated viral response rates were compared to response rates previously reported in clinical trials evaluating standard of care (peg-IFN-alfa-2a + ribavirin) therapy [12, 2, 4, 6, 9, 8, 1, 11, 7, 10]
 - Pooled response rates (across studies) were estimated at 4, 12, 24, 48 and 72 weeks using a beta-binomial model in WinBUGS, ignoring within-study correlation
 - Meta data was summarized by the 50, 2.5 and 97.5th percentile of the posterior distribution for time-specific viral response probability

HCV Dynamic Model Differential Equations as Published by Snoeck et. al. [13]

$$\frac{dT}{dt} = s + r \cdot T \cdot \left(1 - \frac{T+I}{T_{max}}\right) - d \cdot T - \beta \cdot V_I \cdot T \quad (1)$$

$$\frac{dI}{dt} = \beta \cdot V_I \cdot T + r \cdot I \cdot \left(1 - \frac{T+I}{T_{max}}\right) - \delta \cdot I \quad (2)$$

$$\frac{dV_I}{dt} = (1 - \rho) \cdot (1 - \varepsilon) \cdot (1 - \mathbf{I}^{I < CB}) \cdot p \cdot I - c \cdot V_I \quad (3)$$

$$\frac{dV_{NI}}{dt} = \rho \cdot (1 - \varepsilon) \cdot (1 - \mathbf{I}^{I < CB}) \cdot p \cdot I - c \cdot V_{NI} \quad (4)$$

$$R_0 = \frac{p \cdot \beta \cdot s}{c \cdot \delta \cdot d}$$

$$\varepsilon = \frac{DOSE_{IFN}}{ED_{50_{IFN}} + DOSE_{IFN}}$$

$$\rho = \frac{DOSE_{RBV}}{ED_{50_{RBV}} + DOSE_{RBV}}$$

Table 1: HCV Dynamic Model Parameters

Parameter	Description	Units	SN	DH	IIV (%)
T_{max}	Maximum hepatocyte number	cells $\cdot$ mL ⁻¹	18.5x10 ⁶	1x10 ⁷	
s	Hepatocyte production rate	cells $\cdot$ day ⁻¹	61.7x10 ³	2.6x10 ³	
d	Hepatocyte death rate constant	day ⁻¹	0.0033	0.0026	
R_0	Basic Reproductive Number	–	7.15	4.18	137
c	Viral elimination rate constant	day ⁻¹	4.53	6	120
δ	Infected cell death rate constant	day ⁻¹	0.139	0.26	58
p	Viral production rate constant	copies $\cdot$ cell ⁻¹ day ⁻¹	25.1	2.9	
r	Hepatocyte regeneration rate constant	day ⁻¹	0.00562	4.2	
IFN ED ₅₀	peg-interferon ED ₅₀	mcg.week ⁻¹	20.9	–	281
RBV ED ₅₀	ribavirin ED ₅₀	mg.kg ⁻¹ .day ⁻¹	14.4	–	
k_{off}	Treatment effect decay	day ⁻¹	0.0238	–	
CB	Cure boundary	cell $\cdot$ mL ⁻¹	1/13500	–	

SN = Snoeck et. al. model [13], DH = Dahari et. al. model [3]

Results

- 5-10% of simulated subjects had a baseline viral load that was BQL and were excluded from the data set prior to response rate determination.
- Overall dropout rate due to insufficient viral response was:
 - Snoeck: 34.4% (22.5% at 12 weeks and 11.9% at 24 weeks)
 - Dahari: 36.4% (35.2% at 12 weeks and 1.2% at 24 weeks)
- Among subjects with undetectable simulated viral load at 72 weeks, 28.8, 81.6, and 97.5% also had undetectable viral load at 4, 12, and 24 weeks, respectively

Figure 1: Viral Load Versus Time Simulated from Snoeck et. al. Model [13]

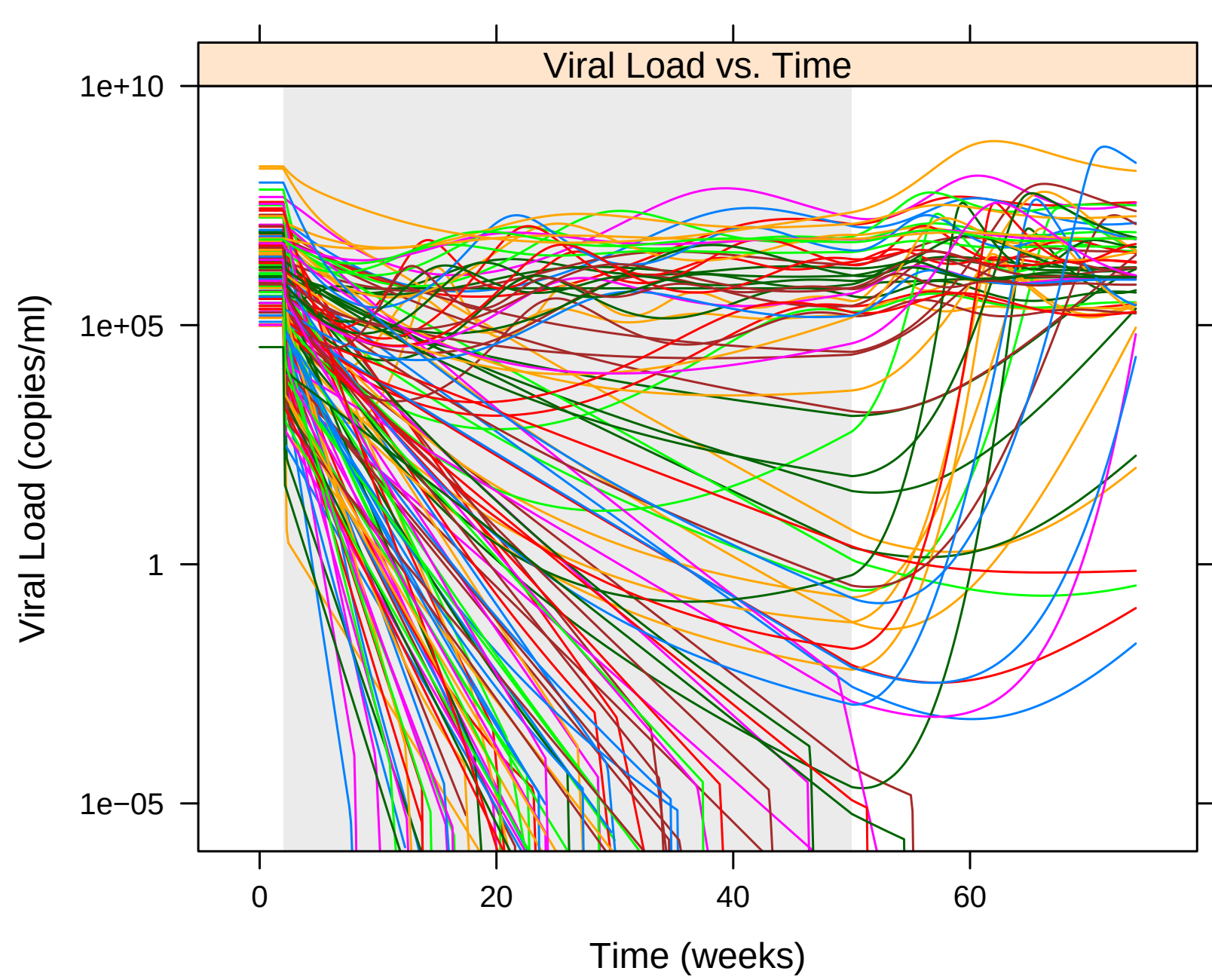
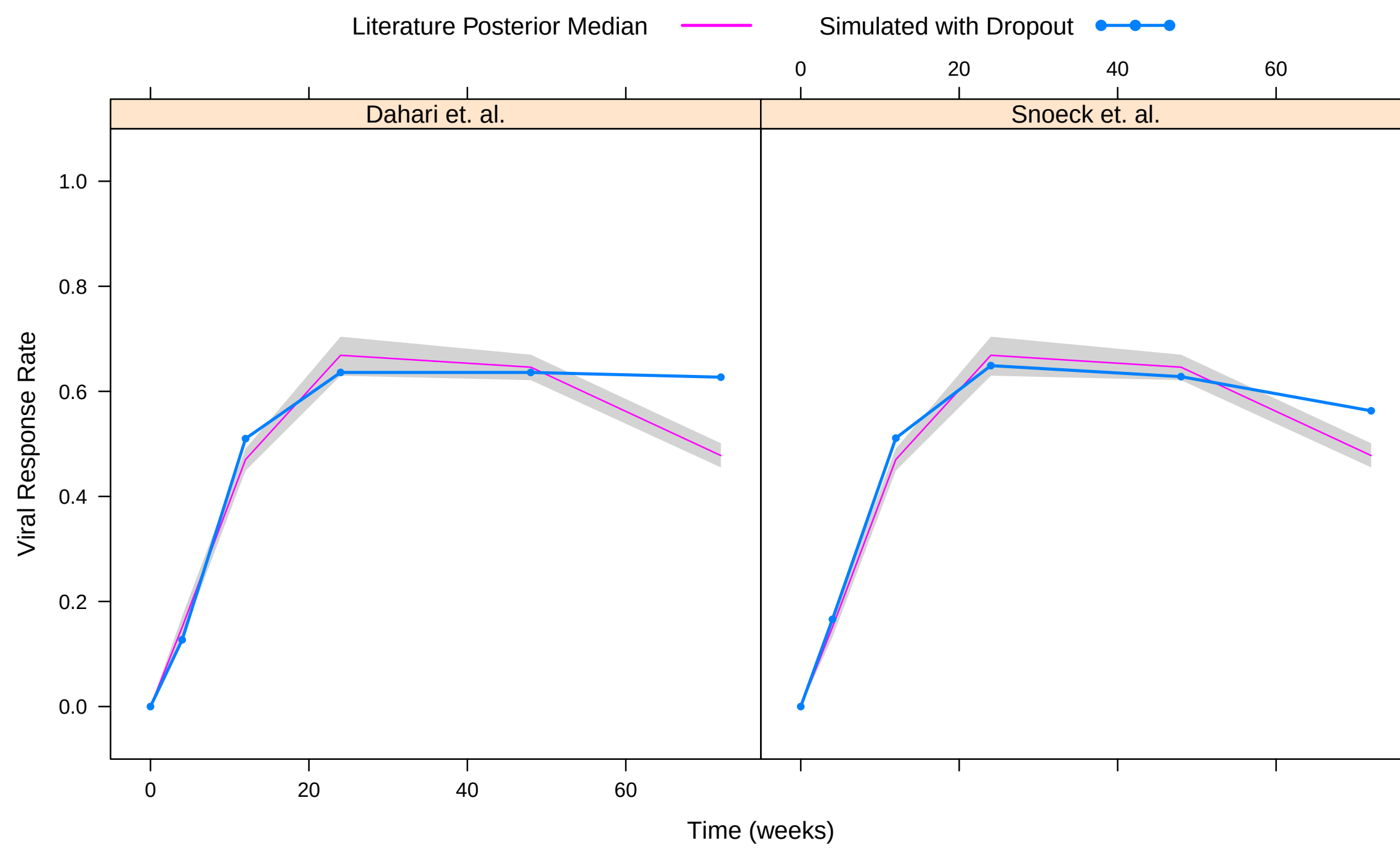


Table 2: Comparison of Viral Response Rates for Simulated and Literature Data

Week	Simulated Data		Meta Data Set	
	Model Source	Response Rate	Weighted Rate	N Subjects
4	DH	12.7	15.1	1888
	SN	17.0		
12	DH	50.1	47.1	2223
	SN	51.6		
24	DH	63.6	66.9	598
	SN	65.5		
48	DH	63.6	64.6	1506
	SN	63.5		
72	DH	62.7	47.8	1801
	SN	56.4		

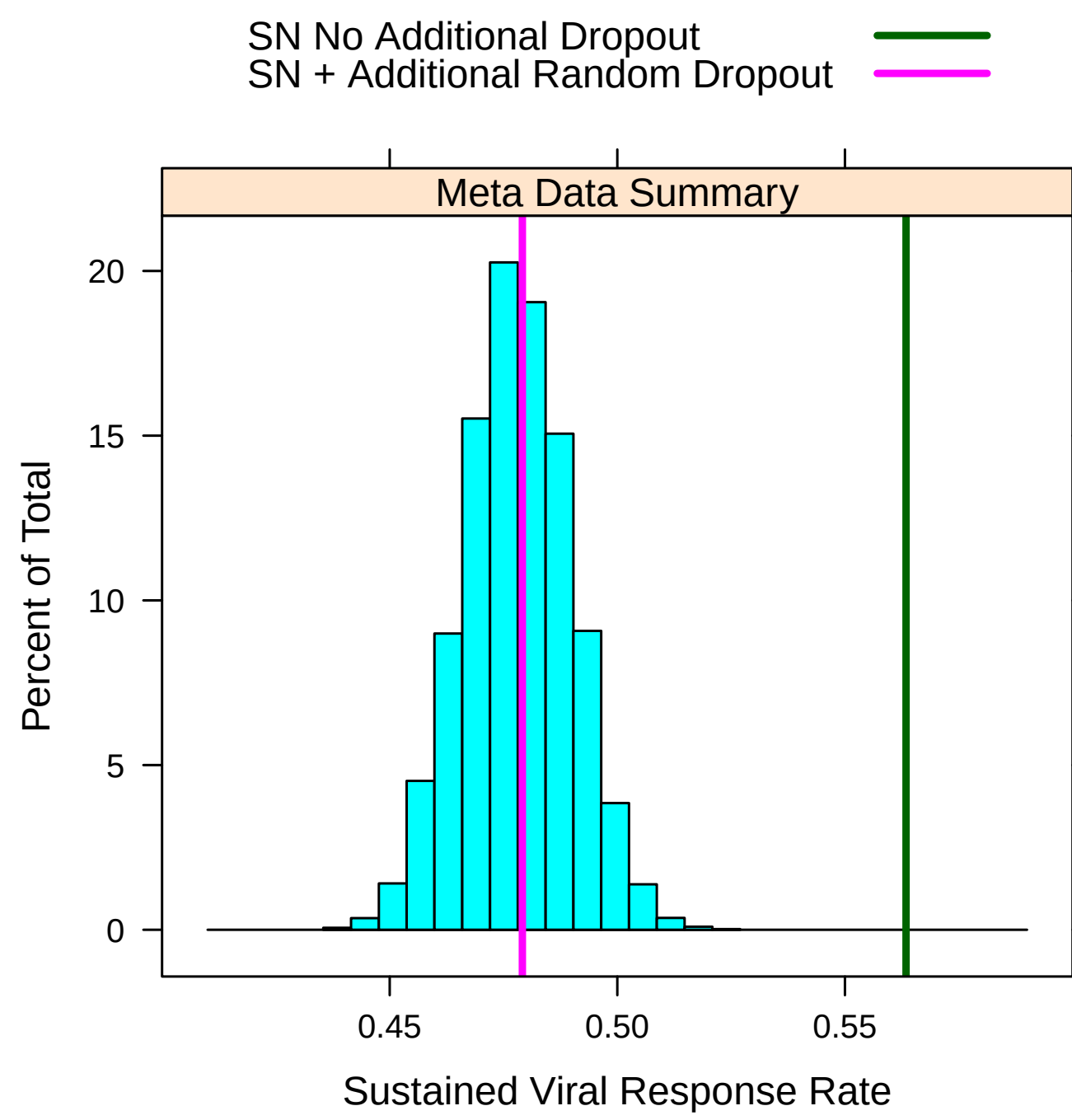
SN = Snoeck et. al. model [13], DH = Dahari et. al. model [3]

Figure 2: Model-predicted and Literature Response Rates Versus Time



Shaded area marks 95% credible interval for time-specific response probability.

Figure 3: Additional Random Dropout Helps SVR Prediction



A 9.8% random dropout (15% of those not already dropped out at end of treatment) was applied after week 48 and helped to match simulated and observed sustained viral response rates.

Conclusion

- Model-predicted viral response rates were similar for both models
- Simulated dropout rates due to insufficient viral response may be higher than observed rates [9, 5]
- SVR predictions were somewhat over-optimistic when dropout was based only on insufficient viral response at 12 and 24 weeks
- An additional ~10% adjustment to responder rate was required after week 48 to match simulated and observed SVR rates
- Further development of an appropriate time-to-event dropout model is needed to forecast viral response rate time-course appropriately under standard of care therapy
- Viral dynamic models need further exploration before they can be used as decision making tools in drug development

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