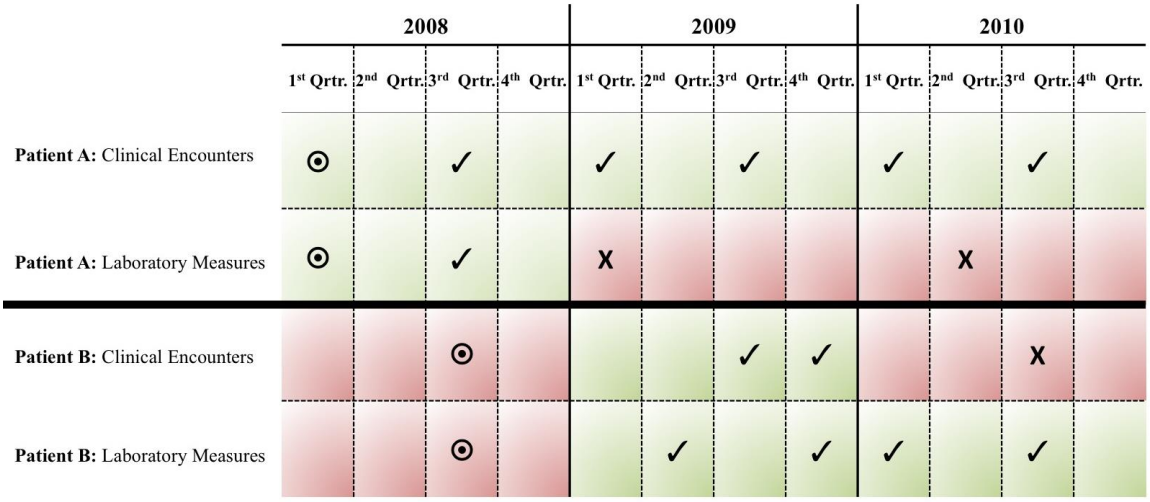
WEB APPENDIX 1

Retention Measures

Whether measured by laboratory collection surrogates or by clinical encounters themselves, retention in clinical care has been defined in the IOM recommendations as 2 visits within a 12-month period (>90 days apart).[1] To assess concordance between definitions of retention based on laboratory measures vs. those based on clinic encounters, one can use elapsed time since patient entry to care (and subsequently anchor to calendar time, a hybrid of assessment on two time axes) to define retention. Using the hybrid method, a patient may fulfill criteria for retention in a calendar period based on clinic encounters alone, based on laboratory measures alone, based on both, or may not qualify as retained in care by either laboratory measure or encounters. Further, a patient may have more laboratory measures than encounters, more encounters than laboratory measures, or the same number of each in a given period (Web Figure 1).

Web Figure 1. Conceptual framework for continuity and retention in clinical care over time by calendar periods, as defined by laboratory measures or clinical encounters, illustrated for two hypothetical patients "A" and "B".



IOM: Institute of Medicine

⊙ : **Initial encounter in clinical care in NA-ACCORD**

✓ : **Encounter or Lab that contributes to retention by IOM indicator (≥2 encounters/labs within 1 year, >90 days apart)**

X : **Encounter or Lab that does *not* contribute to retention by IOM indicator**

Calendar year in which patient is "Retained" by IOM indicator

Calendar year in which patient is "Not Retained" by IOM indicator

WEB APPENDIX 2

Selection of Toeplitz Correlation Structure in the GEE Context

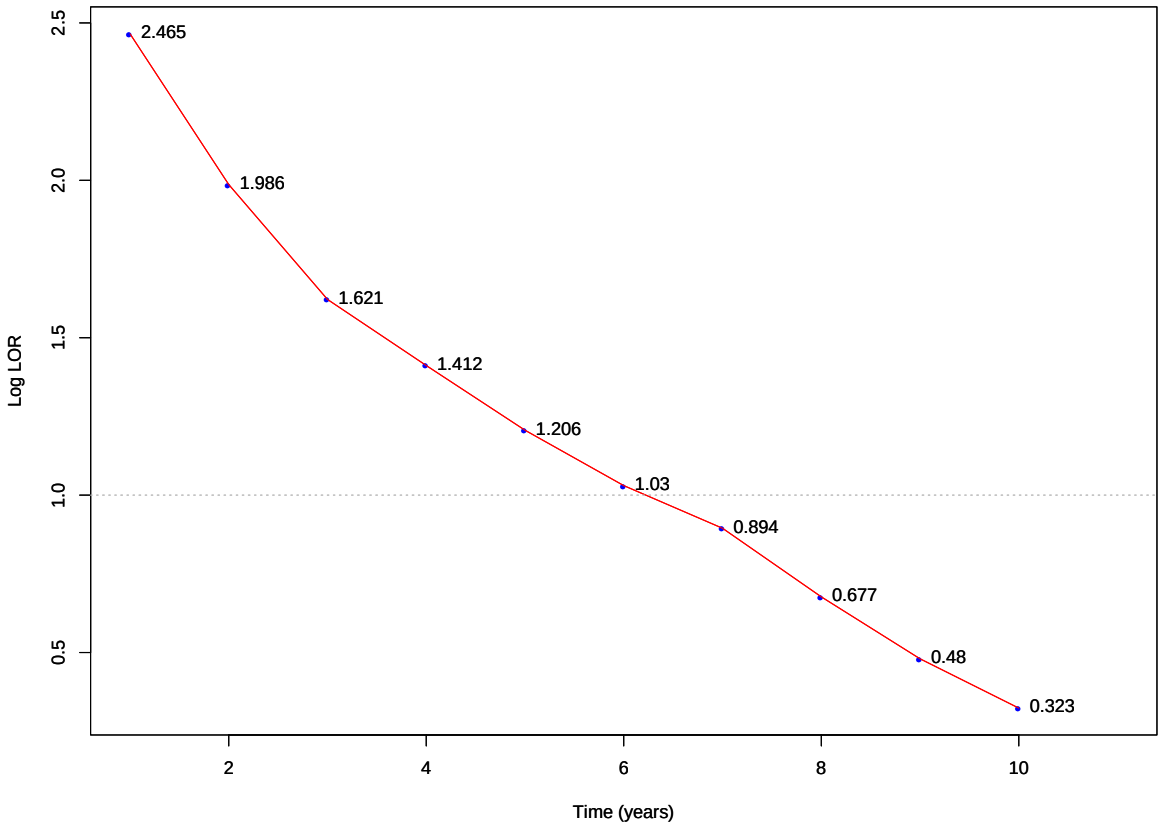
The concordance of two longitudinal binary measures can be modeled as odds ratios using estimating equations that properly account for within-individual clustering of outcomes.[2]

Further, the lorelogram, defined as $\mathrm{LOR}(t_j, t_k) = \log \mathrm{OR}(Y_{ij}, Y_{ik})$ $\mathrm{LOR}(t_j, t_k) = \log \mathrm{OR}(Y_{ij}, Y_{ik}) \mathrm{LOR}(t_j, t_k) = \log \mathrm{OR}(Y_{ij}, Y_{ik})$, can be used to quantify the degree of within-individual clustering, and when applied to the recurrence of R_{EB} over time, it is clear that an independence correlation structure within the GEE is inappropriate (Web Figure 2).[3]

With that understanding, the marginal model diagnostics and associated covariance/correlation structures are explained further below.

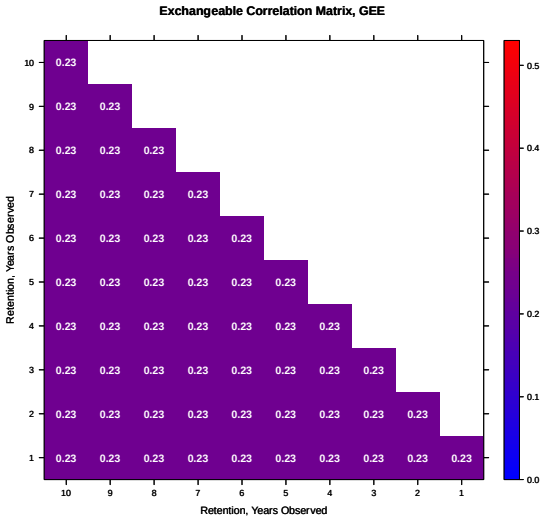
The quasi-likelihood information criterion (QIC), Copula information criterion (CIC), area under the receiver operating characteristic curve (c-statistic), and variance differences between the model-based and sandwich estimators can be used to assess which of the models incorporating the various correlation structures is closest to the true model and which produces the most accurate predictions.[4,5,6,7] These diagnostics, with the exception of the QIC, generally indicated in this analysis that the Toeplitz correlation structure was superior to the independence, exchangeable, AR1, and unstructured structures (Web Figure 3, Web Table 1).

Web Figure 2. Lorelogram of encounter-based retention (R_{EB}) for 10,523 individuals with observations present over the entire 11-year study period, showing the within-individual correlation of R_{EB} over time.

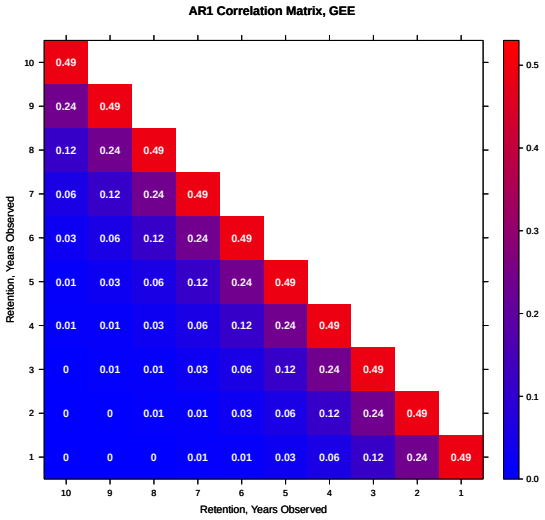


Web Figure 3. Lower diagonals of the empirical **a)** exchangeable, **b)** AR1, **c)** unstructured, and **d)** Toeplitz correlation matrices derived from models of R_{EB} predicted by R_{LB}. The Toeplitz bands are the means of the unstructured matrix.

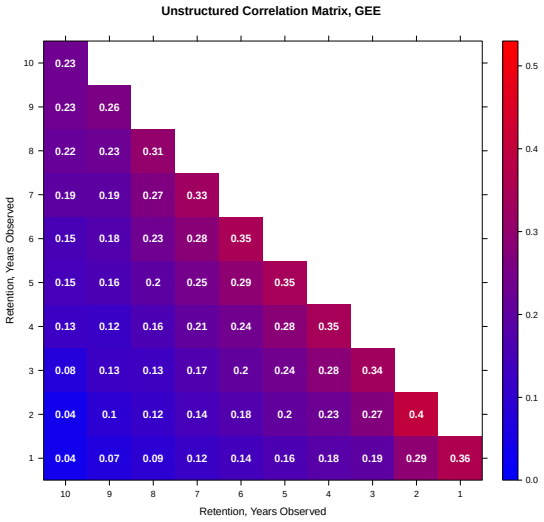
a.



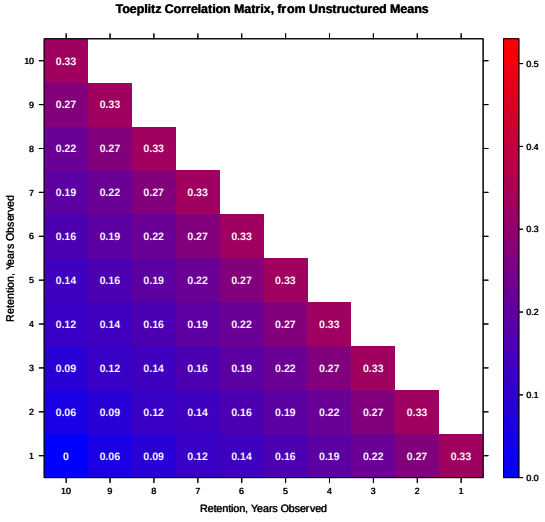
b.



c.



d.



Web Table 1. Model diagnostics for different correlation structures used to model R_{EB} based on R_{LB}. Adjusted models account for age, sex, race, HIV risk factor, and cohort site. QIC is the quasi-likelihood information criterion of Pan. CIC is the Copula Information Criterion. AUC is the area under the receiver operating characteristic curve (*C* statistic).

Criterion	Exchangeable Correlation Structure	AR1 Correlation Structure	Unstructured Correlation Structure	Toeplitz Correlation Structure
Difference between sandwich and model-based variance (unadjusted)	0.000096	0.000125	0.0000888	0.0000886
Difference between sandwich and model-based variance (adjusted)	0.000189	0.000198	0.000170	0.000170
QIC (unadjusted)	406,961	408,526	407,546	407,579
QIC (adjusted)	406,812	407,748	407,177	407,206
CIC (unadjusted)	3.6	3.55	3.45	3.44
CIC (adjusted)	4.43	4.25	4.15	4.15
AUC for ROC of unadjusted models	0.805	0.805	0.805	0.805
AUC unadjusted model, 2000-2003				0.800
AUC unadjusted model, 2004-2007				0.805
AUC unadjusted model, 2008-2010				0.808

Factor	Exchangeable Correlation Structure	AR1 Correlation Structure	Unstructured Correlation Structure	Toeplitz Correlation Structure
Retention by lab	15.43	13.27	14.38	14.34
Year of care	1.04	1.04	1.04	1.04
Interaction of lab with year	1.03	1.02	1.03	1.03

WEB APPENDIX 3

Distribution of Stabilized Inverse Probability of Selection Weights Over Time

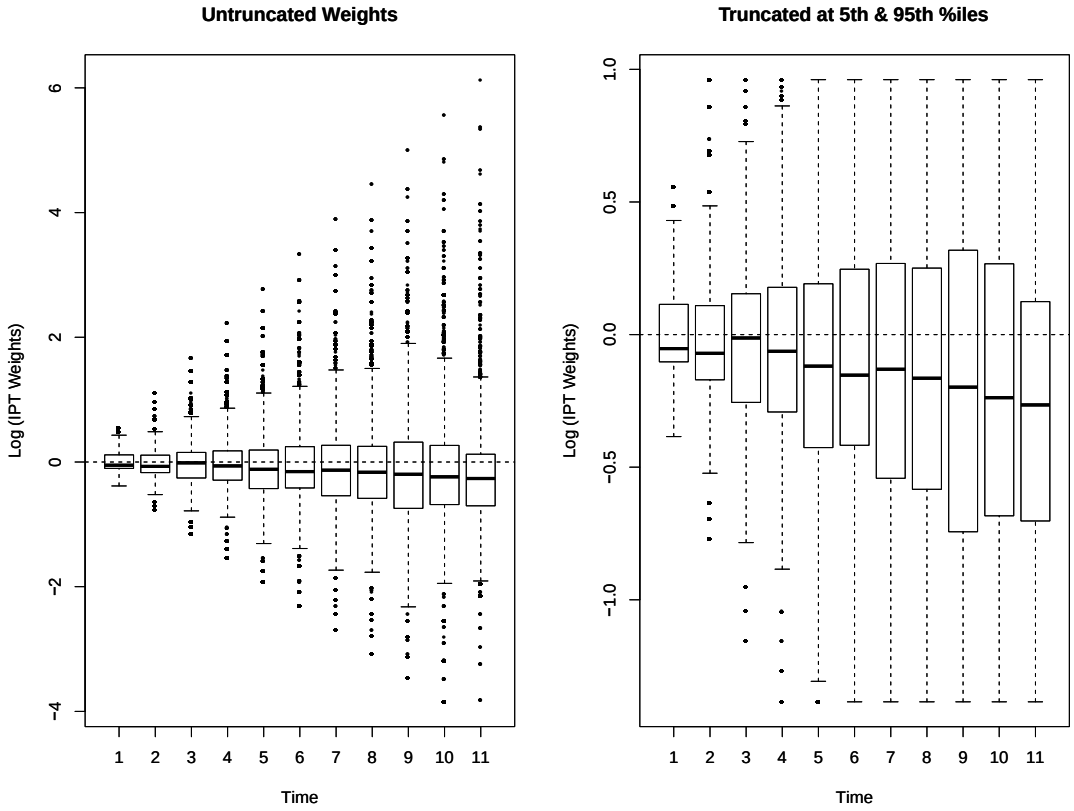
The untruncated and truncated distribution of weights over the study period accounting for site alone and for all available confounders are illustrated below (Web Figure 4).

The truncated weights based on site alone (excluding age, sex, race, and risk factor as potential confounders) had a median of 0.93 (interquartile range of 0.71-1.17) and a range of 0.25-2.62 (indicating a lack of extreme values which might lead to unstable effect estimates). The truncated weights based on all potential confounding factors available had a median of 0.93 (interquartile range of 0.66-1.16) and a range of 0.21-2.72.

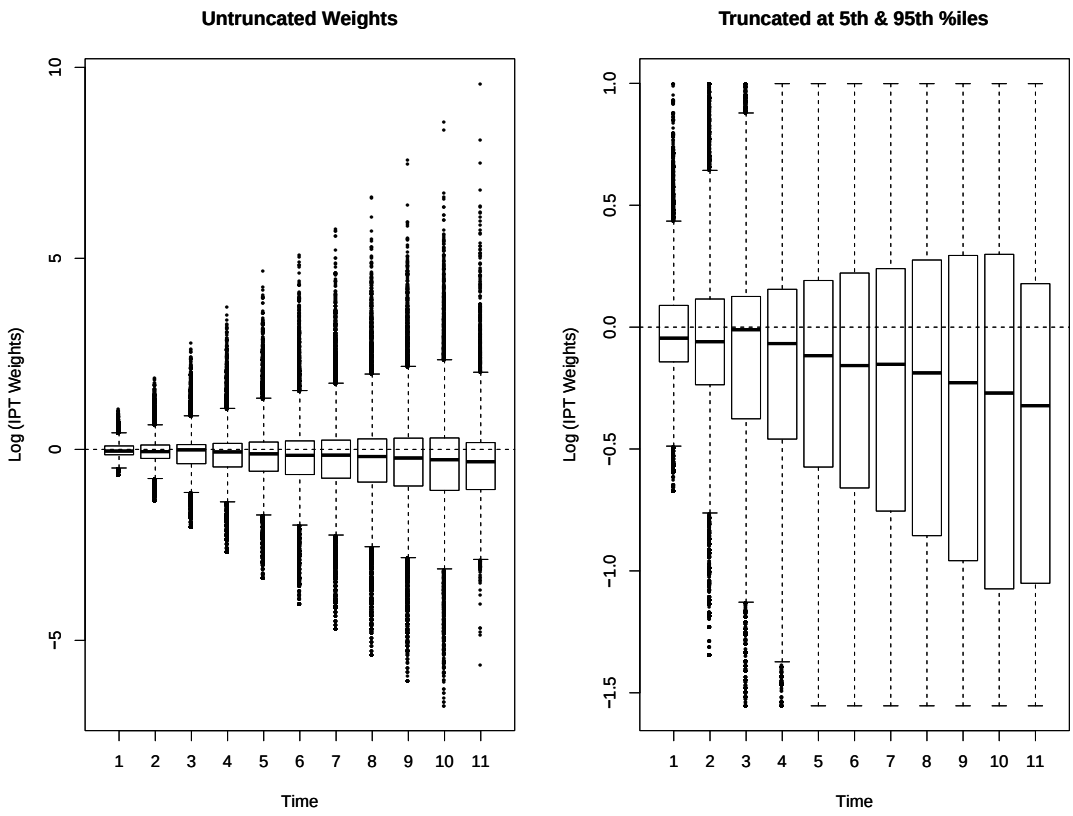
Using these weights, the regression of R_{EB} on R_{LB} with GEE was conducted (as outlined above) to adjust for the potential confounding factors and account for clustering of outcomes within individuals.

Web Figure 4. Distribution of constructed IPW for the probability of R_{LB}, both untruncated and truncated at the 5th and 95th percentiles, **a)** based on clinic site alone and **b)** based on clinic site, age, sex, race/ethnicity, and HIV risk factor.

a.



b.


Untruncated Weights
Log (IPT Weights)
10
5
0
−5
1
2
3
4
5
6
7
8
9
10
11
Time
Truncated at 5th & 95th %iles
Log (IPT Weights)
1.0
0.5
0.0
−0.5
−1.0
−1.5
1
2
3
4
5
6
7
8
9
10
11
Time

Web References

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7. Pan W. Akaike's Information Criterion in generalized estimating equations. *Biometrics*. 2001;57(1):120–125.