# **Identification of inflections in T-cell counts among HIV-1-infected individuals and relationship with progression to clinical AIDS**

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**ABSTRACT Studies of circulating T (CD3**1**) lymphocytes have shown that on a population basis T-cell numbers remain stable for many years after HIV-1 infection (blind T-cell homeostasis), but decline rapidly beginning approximately 1.5–2.5 years before the onset of clinical AIDS. We derived a general method for defining the loss of homeostasis on the individual level and for determining the prevalence of homeostasis loss according to HIV status and the occurrence of AIDS in more than 5,000 men enrolled in the Multicenter AIDS Cohort Study.** We used a segmented regression model for  $log_{10}$  CD3<sup>+</sup> cell counts **that included separate T-cell trajectories before and after a time (the T-cell inflection point) where the loss of T-cell homeostasis** was most likely to have occurred. The average slope of CD3<sup>+</sup> **lymphocyte counts before the inflection point was close to zero** for HIV – and HIV + men, consistent with blind T-cell homeostasis. After the inflection point, the HIV+ individuals who devel**oped AIDS** generally showed a dramatic decline in CD3<sup>+</sup> cell **counts relative to HIV- men and HIV+ men not developing AIDS. A CD3**<sup>1</sup> **cell decline of greater than 10 percent per year was present in 77% of HIV+ men developing AIDS but in only 23% of HIV**1 **men with no onset of AIDS. Our findings at the individual level support the blind T-cell homeostasis hypothesis and provide strong evidence that the loss of homeostasis is an important mechanism in the pathogenesis of the severe immunodeficiency that characterizes the late stages of HIV infection.**

Cell-mediated immunity from circulating  $(CD3<sup>+</sup>)$  T lymphocytes is one of the primary defenses against viral infections. Two mechanisms of this antiviral immunity are the destruction of infected cells by  $CD8<sup>+</sup>$  cytotoxic T lymphocytes and the immunestimulating activity of  $CD4<sup>+</sup>$  helper T cells. These latter cells are the primary target of HIV-1 infection, and the depletion of  $CD4^+$ cells has long been recognized as a characteristic feature of HIV-1 disease (1). The pattern of  $CD8^+$  cell counts is more complicated, with increases early in HIV-1 infection followed by a decline before the onset of AIDS  $(2)$ . These increases in CD8<sup>+</sup> cells occurring concomitantly with a decrease in  $CD4^+$  cells suggest that a compensatory mechanism for total T lymphocytes exists in the earlier stages of HIV infection. This compensatory mechanism cannot continue throughout the entire course of HIV infection, however, because people with AIDS have lower numbers of circulating lymphocytes than people with earlier stages of the infection (1).

Longitudinal analyses of T-cell counts from several cohort studies have shown that T-cell numbers in fact remain stable near pre-seroconversion levels without regard to phenotype  $(CD4<sup>+</sup>$  or  $CD8<sup>+</sup>$  expression) for many years after HIV-1 infection. Furthermore, this phenomenon, referred to as blind T-cell homeostasis (2, 3), appears to break down an average of 1.5–2.5 years before the onset of clinically defined AIDS. At this time, an inflection occurs in the trajectory of the number of circulating T cells, changing from little or no decline to an average decline of about 30% per year (2, 4). In populations of people with known times of HIV-1 seroconversion and AIDS onset, varying incubation periods of HIV-1 were largely, if not entirely, accounted for by variations in the time from seroconversion to the time of rapid T-cell loss (2). In other words, the interval from the time at which T-cell loss accelerates to the time of AIDS onset was relatively constant, suggesting that a failure of T-cell homeostasis initiated a common final pathway, resulting in opportunistic illnesses after an average of 1.5–2.5 years.

These previous studies of HIV-1 infection addressed the characteristics and failure of T-cell homeostasis at the population level with primary emphasis on the changes in groups of individuals developing AIDS. The present study was undertaken to extend these studies to the level of the individual and to develop a statistical method that could provide, for any longitudinal series of T-cell counts, the best estimate of the time point at which T-cell inflection occurred. We then developed criteria for determining the prevalence of the loss of T-cell homeostasis among well-characterized groups, based on the T-cell slopes before and after the putative inflection points (IPs). For these analyses, we used the extensive longitudinal data from the Multicenter AIDS Cohort Study (MACS) that has followed approximately 5,500 homosexual and bisexual men since 1984.

The utility of our methods for developing IPs on the individual level is to promote targeted retrospective laboratory studies that characterize the factors occurring around the time of T-cell inflection, as specimens can be classified into those before and after T-cell inflection. More generally, however, this paper describes an important integration of laboratory, statistical, and clinical sciences. The methods developed are appropriate for general problems of investigating changes in trajectories. The phenomenon under study, loss of T-cell homeostasis, is one that is naturally defined by the statistical model, and the immunologic changes defined by statistical parameters are related to important clinical outcomes.

### **METHODS**

**Study Participants.** The MACS was initiated in 1983 to study the natural history of HIV-1 infection among homosexual and bisexual men in the United States. The study design has

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This paper was submitted directly (Track II) to the *Proceedings* office. Abbreviations: MACS, Multicenter AIDS Cohort Study; IP, inflection point; ROC, receiver operating characteristic; IQR, inter-quartile range; SP, seroprevalent; SC, seroconverter; SN, seronegative.

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been previously described (5), and only aspects pertinent to this analysis are presented here. In 1984–1985, 4,954 men were enrolled in Baltimore/Washington, Chicago, Los Angeles, and Pittsburgh. From 1987 to 1991, recruitment was reopened, and an additional 625 men, mostly nonwhite, were enrolled. Men with pre-existing clinical conditions diagnostic of AIDS and those who were younger than 18 years were excluded from enrollment. At semiannual visits, men returned to the clinics to provide specimens for laboratory analyses, undergo a physical examination, and complete self-administered data forms and an interviewer-administered questionnaire. HIV-1 seropositivity was determined by a positive ELISA confirmed by a Western blot with bands corresponding to at least two of the *gag*, *pol*, and *env* proteins of HIV-1.

T-cell subset levels at each visit were obtained from peripheral blood mononuclear cells stained with mAbs by a whole blood lysing method and analyzed by two-color flow cytometry (6, 7) and mAbs specific for CD3, CD4, and CD8. Absolute numbers of cells per ml of blood were calculated by using the complete blood count with automated 10,000 cell differential.

**Methods for Determining Individual CD3**<sup>1</sup> **Lymphocyte IPs.** To characterize whether individual  $CD3<sup>+</sup>$  lymphocyte trajectories were indicative of homeostasis failure, we developed a method to determine the time at which a change in trajectory, denoted as the T-cell IP*,* was most likely to have occurred. The method was required to be applicable to any series of  $CD3<sup>+</sup>$  cell counts, regardless of infection status or disease stage. A (possible) T-cell IP was defined as the midpoint in time between any two semiannual participant visits. At least three  $CD3<sup>+</sup>$  cell counts were required before and after the midpoint to ensure that slopes around the IP were evaluated by using several observations. Thus, only individuals with at least six  $CD3^+$  cell counts were included in the present analysis. Additionally, the  $CD3<sup>+</sup>$  lymphocyte count was required to decrease between the two visits immediately surrounding the midpoint, because  $CD3<sup>+</sup>$  cell counts were hypothesized to decline after homeostasis failure. Because this algorithm assigned an IP only between decreasing  $CD3<sup>+</sup>$  cell counts, there were individuals for whom an IP could not be estimated (e.g., those with monotonically increasing  $CD3<sup>+</sup>$  cell counts).

Denote  $Y_{ij}$  as the log<sub>10</sub> of the *j*th of  $n_i$  CD3<sup>+</sup> lymphocyte counts on the *i*th individual, collected at time  $t_{ij}$ . Let  $t_i^{(k)}$  be the time of the *k*th eligible time of inflection for the *i*th individual (i.e.,  $t_i^{(k)}$  is a midpoint point between two consecutive  $t_{ij}$  where  $CD3<sup>+</sup>$  cell counts decline and there are at least three measurements both before and after  $t_i^{(k)}$ ). Using all available  $Y_{ij}$ (not just the six required measurements around  $t_i^{(k)}$ ), a segmented regression model was fit with the form:

$$
Y_{ij} = \beta_{i0}^{(k)} + \beta_{i1}^{(k)}(t_{ij} - t_i^{(k)})^- + \beta_{i2}^{(k)}(t_{ij} - t_i^{(k)})^+ + \varepsilon_{ij}^{(k)},
$$

where  $(t_{ij} - t_i^{(k)})$ <sup>-</sup> equals  $t_{ij} - t_i^{(k)}$  if  $t_{ij} < t_i^{(k)}$  and equals zero if  $t_{ij} > t_i^{(k)}$ ,  $(t_{ij} - t_i^{(k)})^+$  equals  $t_{ij} - t_i^{(k)}$  if  $t_{ij} > t_i^{(k)}$  and equals zero if  $t_{ij} < t_i^{(k)}$ , and  $\varepsilon_{ij}^{(k)}$  represents a normal (Gaussian) error term with mean 0 and SD  $\sigma_i^{(k)}$ . The parameter  $\beta_{i0}$  can be interpreted as the estimated  $log_{10} CDS^+$  cell count at IP<sub>i</sub>, and  $10^{\beta i1}$  and  $10^{\beta i2}$  represent the relative (proportional) rate of change in  $CD3^+$  cell counts before and after IP<sub>i</sub>, respectively.

We obtained one triplet of parameter estimates  $(\hat{\beta}_{i0}^{(k)}, \hat{\beta}_{i1}^{(k)})$  $\hat{\beta}_{i2}^{(k)}$ ) for each eligible  $t_i^{(k)}$  of the *i*th individual. The  $t_i^{(k)}$  that resulted in the smallest residual variability between the data and the fitted line (i.e.,  $\min_k \sum_{j=1}^{n_i} [\hat{\epsilon}_{ij}^{(k)}]^2$ ) was chosen as the estimated IP  $(IP_i)$  for the *i*th individual. Fig. 1 illustrates the selection method for a hypothetical set of serial  $CD3<sup>+</sup>$  cell counts on an individual. The eligible times for the IP, denoted with an asterisk along the *x*-axis, do not include all midpoints because of the requirements of decreasing  $CD3<sup>+</sup>$  cell counts and the occurrence of at least three  $CD3<sup>+</sup>$  cell counts before and after the midpoint.



FIG. 1. Graphical illustration of IP model. Post-SC  $log_{10}$  CD3<sup>+</sup> cell counts are represented by points  $(•)$ , and eligible times for inflection are denoted by  $\ast$ . The IP for individual *i* (IP<sub>i</sub>) is the time for which the segmented regression model (solid lines) gives the smallest residual variability.

After applying the above methods, estimates of the IP  $(\text{IP}_i)$ and each of the regression coefficients ( $\beta_{i0}$ ,  $\beta_{i1}$ ,  $\beta_{i2}$ ) were obtained for each individual. The  $CD3$ <sup>+</sup> lymphocyte trajectories before  $(\beta_{i1})$  and after  $(\beta_{i2})$  the IP are key parameters for evaluating the methods relative to the T-cell homeostasis hypothesis. For individuals who are maintaining T-cell homeostasis, we would expect  $\beta_{i1} \approx \beta_{i2} \approx 0$ . For those who have lost T-cell homeostasis, we would expect  $\beta_{i1} \approx 0$  and  $\beta_{i1} \gg \beta_{i2}$ , so that either the difference  $(\beta_{i2} - \beta_{i1})$  or the post-IP slope  $(\beta_{i2})$  would be a measure discriminating those with homeostasis loss from those preserving homeostasis. Below, we describe the methods to address the important question of which of these variables provides better discrimination.

**Application of the Methods and Evaluation of IPs.** We primarily were interested in comparing the regression parameters among two groups:  $(i)$  HIV+ men who had developed AIDS as of  $6/97$ , and were expected to have lost T-cell homeostasis (referred to as the  $HIV+ / AIDS$  group), and (*ii*)  $HIV+$  men who were AIDS-free as of  $6/97$  and therefore were expected to have maintained T-cell homeostasis (referred to as the  $HIV+ /AIDS$ free group). T-cell counts from  $HIV$  men, who obviously were expected to have maintained T-cell homeostasis, were used as controls in the analysis. AIDS surveillance and reporting are conducted continuously in the MACS. Our definition of AIDS included only clinical illnesses diagnostic of AIDS (8) that were confirmed by review of medical records. Individuals with CD4<sup>+</sup> cell counts below 200 cells/mm<sup>3</sup> without clinical disease were not classified as having AIDS.  $CD3<sup>+</sup>$  lymphocyte counts from the baseline visit of the seroprevalent (SP) men and measurements before and within 1 year after seroconversion of the seroincident men were not used, to avoid changes occurring around seroconversion.

We restricted AIDS cases to those occurring before 10/94 to obtain an unbiased evaluation of the interval between the IP and AIDS. If AIDS cases after 10/94 had been included in the analysis, IPs would have been forced to occur before onset of AIDS because of insufficient follow-up after AIDS. To ensure that all incipient cases of AIDS were excluded, only  $CD3<sup>+</sup>$  lymphocyte counts obtained up to 10/94 were included among those AIDS-free through  $6/97$ . Men with AIDS before  $10/94$  were required to have six  $CD3<sup>+</sup>$  cell counts before AIDS, although counts after AIDS were used in estimating the IP and trajectories.

Distributions of the three model parameters  $(CD3<sup>+</sup>$  cell count at  $IP_i$ , slope before  $IP_i$ , and slope after  $IP_i$ ) were compared graphically. We also investigated whether larger post-IP declines  $(\beta_{i2})$  were associated with shorter times between IP and AIDS. The sensitivity and specificity for the development of AIDS was calculated by using varying levels of  $CD3<sup>+</sup>$  lymphocyte slopes after the IP as cutoffs for identifying those with ''true inflection,'' with graphical representation facilitated through use of a receiver operating characteristic (ROC) curve (9). ROC curves plot sensitivity versus  $(1$ specificity) over all possible cutoffs and allow for comparison of classification properties independent of any particular cutoff. ROC curves defined by parameters that better distinguish those with or without the onset of AIDS (our gold standard for the sensitivity and specificity calculations) manifest a larger area under the curve.

The preceding classification scheme does not take into account the variability of an individual's  $CD3<sup>+</sup>$  lymphocyte data. Thus, although two individuals might show a decline of 10% per year, this decline may fall within the range of variability for one individual but not the other. As an alternative to classifying individuals based on the ROC curves, we also used a statistical criterion based on the statistical significance of F-statistics. For each individual, suppose

$$
F = \frac{(SS_{\rm H} - SS_{\rm A})/2}{SS_{\rm A}/(n-4)}
$$

is computed for testing whether the segmented regression model is appropriate, where  $SS_H$  represents the residual sums of squares under the linear regression model ( $\beta_{i1} = \beta_{i2}$ ), and SSA represents the residual sums of squares under the twophase regression model. This statistic has an  $F_{(n-4)}^2$  distribution when the time of inflection is fixed (or known independently of the data) (10). That is, if the time of inflection were known for each individual, we could compare the F-statistic to an F-distribution cutoff to determine whether the  $CD3<sup>+</sup>$  cell trajectory after the IP was statistically different from the trajectory before the IP (10). However, our method estimates the IP from each individual's T-cell data, and the standard F-distribution has been shown to be inappropriate for the segmented regression model when the time of inflection is not fixed but estimated from each individual's data (11–13). To address this problem, simulation methods were used to approximate the required critical values for the F-statistic as described in the *Appendix*. Using these values for determining statistical significance, we classified individuals as ''true inflectors'' and investigated the sensitivity and specificity of true inflection for the onset of AIDS within 3 years.

## **RESULTS**

Fig. 2 depicts the numbers of individuals included after we applied the different restriction criteria. Of the 5,579 men enrolled in the MACS, 2,195 were HIV SP, and 491 of 3,384 seronegative (SN) individuals were observed to seroconvert as of  $6/97$ . The impact of requiring at least six  $CD3<sup>+</sup>$  cell counts



FIG. 2. MACS study population and final sample. Seroconversion and AIDS events are as reported by June 1997.  $\ast$ , 136 SP men and 53 SC men with AIDS after 10/94 were excluded in this analysis to allow for at least three follow-up visits after AIDS.

is shown in the second to last line. The final line displays the number of individuals for whom the method estimated an IP.

Fig. 3 displays the distribution of two different estimated parameters from the IP model for individuals in each of five groups resulting from subdividing the AIDS-free and AIDS groups by whether they were SP or seroconverter (SC). There were virtually no differences in these variables between the SP and SC men in either those developing or those not developing AIDS, suggesting that the duration of HIV infection did not affect our conclusions.

Fig. 3  $\alpha$  and  $\beta$  describes the slopes in CD3<sup>+</sup> cell counts around the IP. Fig.  $3a$  shows the slope of  $CD3^+$  cell counts before IP in terms of the percentage change in  $CD3<sup>+</sup>$  cell counts per year [i.e.,  $(1 - 10^{\beta_{i1}}) \times 100$ ]. Although variable, the distributions were essentially symmetric around 0.0 with median (inter-quartile range, IQR) annual change of 0.5%  $(-7.7\%$  to 7.8%) for the groups developing AIDS, 2.0%  $(-5.2\%$  to 9.7%) for the groups not developing AIDS, and  $1.5\%$  (-6.3% to 8.5%) for the SN group. This finding is consistent with the homeostasis hypothesis, which predicts a stability in  $CD3<sup>+</sup>$  cell counts before the IP.

Fig. 3b displays the post-IP CD3<sup>+</sup> lymphocyte slopes, also expressed in terms of the percentage change of  $CD3<sup>+</sup>$  cell counts per year [i.e.,  $(1 - 10^{\hat{\beta}^2}) \times 100$ ]. The distribution of this parameter was also very close to symmetric around  $0.0$  for the  $HIV -$  group (median  $-0.3\%$ , IQR  $-5.0\%$  to  $+5.0\%$ ), and the HIV+ group remaining AIDS-free (median change  $-1.9\%$ , IQR  $-8.7\%$  to  $+5.5\%$ ). However, the distribution for the groups developing AIDS was clearly distinct from these, with a median (IQR) annual decline of 32.0% ( $-50\%$  to  $-11.8\%$ ). An examination of the exponentiated difference (ratio) of pre-IP and post-IP slopes  $(10^{(\hat{\beta}z-\hat{\beta}i)} = 10^{\hat{\beta}z}/10^{\hat{\beta}i}$  also shows similarity between the HIV – group and the  $HIV+$  group without onset of AIDS and much larger declines in the group developing AIDS, although the distributions are not as distinct as in Fig. 3*b*. Both the discordance in the distributions of post-IP among those with onset of AIDS and the similarity of pre-IP and post-IP slopes for the  $HIV-$  and  $HIV+$  men with no onset of AIDS strongly suggest that the methods are identifying a meaningful time point among those with onset of AIDS and a nonmeaningful time point among the other two groups.

The groups developing AIDS had slightly lower  $CD3<sup>+</sup>$ lymphocyte levels just before the estimated IP (median 1,354, IQR 1,010 to 1,761) than the SP and SC groups not developing AIDS (median 1,572, IQR 1,232 to 1,952) and the SNs (median 1,601, IQR 1,275 to 1,970). The median  $CD4<sup>+</sup>$  lymphocyte count for the groups developing AIDS (346) was much lower than the median for the groups remaining AIDS-free (619), which was lower than the median for the SNs (1,109). However, the groups developing AIDS had slightly higher  $CD8<sup>+</sup>$  cell counts (median 1,054) relative to the groups remaining AIDSfree (median 1,015) and higher than the  $CD8<sup>+</sup>$  cell count at IP for the SNs (median 653).

The distribution of time differences (in years) between the estimated IP and the diagnosis of AIDS were nearly identical for the SP and SC groups. The median (IQR) times from the estimated IPs to AIDS were 1.73 (0.68 to 2.69) and 1.71 (0.81 to 2.99) years for SC and SP groups, respectively. Overall, the vast majority (87%) of IPs were estimated to occur before the onset of AIDS, despite using  $CD3<sup>+</sup>$  cell counts occurring before and after AIDS. There was a dose–response relationship between post-IP slope and time to AIDS, in which larger post-IP  $CD3$ <sup>+</sup> lymphocyte declines were associated with shorter times between IP and an onset of AIDS ( $P < 0.0001$ , data not shown).

Fig. 4 displays longitudinal  $CD3<sup>+</sup>$  counts and model estimates for three individuals who had representative slopes for the three subject groups:  $HIV - (Fig. 4a)$ ,  $HIV + but without$ AIDS onset (Fig.  $4b$ ), and HIV+ developing AIDS (Fig.  $4c$ ). The individuals selected for this figure were among those with preinflection and postinflection slopes closest to the median



FIG. 3. Boxplots (light middle bar denotes median, ends of dark boxes denote 25th and 75th percentiles, brackets indicate 150% of IQR outside the quartiles, outliers are indicated with points) displaying the distribution of estimated parameters by group. (*a*) CD3<sup>+</sup> slope (expressed as change in CD3<sup>+</sup> count per year) before IP  $[(1 - 10^{\beta i}) \times 100]$ . (*b*) CD3<sup>+</sup> slope (change per year) after IP  $[(1 - 10^{\beta i2}) \times 100]$ .

preinflection and postinflection slopes for each of the three groups. Before the estimated IP, the slopes for all individuals were slightly positive  $(+1.6\%, +2.8\%, \text{ and } +2.0\%$  per year, respectively). After the IP, however, the HIV- and HIV+/ AIDS-free individuals showed very modest declines  $(-0.5\%$ and  $-2.9\%$  per year, respectively) but the individual who developed AIDS showed a clear change in T-cell trajectory (to  $-31\%$  per year) occurring 2.3 years before AIDS. Fig. 4 illustrates the need to distinguish true inflection from trajectory changes estimated in the presence of the natural variability of serial T-cell counts.

We evaluated the operating characteristics (sensitivity, specificity) that result from classifying individuals with and without onset of AIDS as ''inflectors'' or ''noninflectors'' by using only the magnitude of the parameter estimates  $\hat{\beta}_{i1}, \hat{\beta}_{i2}, \hat{\beta}_{i} - \hat{\beta}_{i1}$  from the model. For example, by using a post-IP slope  $(\hat{\beta}_{i2})$  cutoff of  $-20\%$  per year to define inflection, each individual could

be classified as an inflector or noninflector. When these data then were combined with our gold standard of disease defined by an AIDS diagnosis, we could compute the sensitivity and specificity associated with this classification rule. In the analysis, shown in Fig. 5, we did not include the 92 individuals with an estimated IP occurring after AIDS, although the analysis was nearly identical with them included. The slope before IP  $(\hat{\beta}_{i1})$  was a poor parameter to distinguish those developing and not developing AIDS, because it fell very close to the diagonal line. In contrast, the slope after IP better distinguished groups. The change in slopes  $(\hat{\beta}_{i2} - \hat{\beta}_{i1})$  did not give as good characteristics as  $\hat{\beta}_{i2}$  alone, as indicated by a smaller area under the curve, but performed much better than  $\hat{\beta}_{i1}$ .

The cutoff of  $\hat{\beta}_{i2}$ , which maximized both sensitivity and specificity (i.e., closest to the upper left corner in Fig. 5) was very close to  $log_{10}(.90)$  (Fig. 5, arrow). Thus, by using the criteria that post-IP  $CD3<sup>+</sup>$  cell counts, which fall by more than 10% per year represent



FIG. 4. Representative T-cell lymphocyte counts (solid lines and points) for three men who were: (*a*) HIV-, (b) HIV+ without AIDS onset, and (c) HIV+ with AIDS onset. The best-fit segmented regression model is denoted by the dashed line with the  $*$  denoting the estimated IP. "A' indicates the date of onset of clinical AIDS. The fitted regression lines are curved because of the linear structure used to model the log10 transformed values, and we have exponentiated the values to plot the data and the regression estimates in the original scale (cells per mm3).



FIG. 5. ROC curves (sensitivity vs.  $1 -$  specificity) when distinguishing AIDS and AIDS-free men (SC and SP groups combined) using three different criteria: CD3<sup>+</sup> slope before IP ( $\hat{\beta}_{i1}$ ), CD3<sup>+</sup> slope after IP ( $\hat{\beta}_{i2}$ ), and the change in log<sub>10</sub>(CD<sub>3</sub><sup>+</sup>) slopes from before IP to after IP ( $\hat{\beta}_{12}$ <sup>2</sup>)  $\hat{\beta}_{i1}$ ). The arrow indicates the point of maximal sensitivity and specificity.  $*$  and  $+$  denote the characteristics when distinguishing individuals by using the statistical criteria (i.e., classification based on F-statistics) for all individuals and those with 15 or more visits, respectively.

true inflection, 77.5% of the men developing AIDS had true inflection as opposed to only 23.1% of the men remaining AIDS-free. These values were nearly identical when including the 92 men with IP after onset of AIDS (69, or 75%, of whom declined by more than 10% after IP). Among the SNs, 12%  $(264/2,152)$  showed a post-IP decline of this magnitude or more. Using the cutoff that maximized the sensitivity and specificity for the difference in slopes, there was slightly less discrimination: 71.8% of the men developing AIDS and 27.9% of the men remaining AIDS-free showed this pattern of decline.

The discrimination using the statistical criterion based on individual F-statistics provided a lower sensitivity (proportion of men developing AIDS who showed inflection) of 38.4% and a correspondingly higher specificity (proportion of men remaining AIDS-free classified without inflection) of 88.8%. These characteristics are plotted as an asterisk in Fig. 5, where we can see the criterion based on the ROC curves performing better in terms of the sensitivity and specificity. Furthermore, approximately  $8\%$  of the SNs showed significant CD3<sup>+</sup> lymphocyte inflections, which was only slightly higher than the 5% expected as a consequence of how the empirical distribution was simulated to generate the 95th percentile cutoffs.

Because the statistical criterion depended on the number of  $CD3<sup>+</sup>$  lymphocyte counts available, an immediate concern was the statistical power for detecting a decline in  $CD3<sup>+</sup>$  cell counts when few data were available. In a separate set of simulations, we estimated the power to detect a  $10\%$  drop in CD3<sup>+</sup> cell counts per year to be  $30\%$  when six semiannual  $CD3^+$  cell counts were available but greater than 99% when 15 or more semiannual visits were available. Examining only those individuals with 15 or more visits, we found an increase in the percentage of men developing AIDS with inflection by the statistical criterion (54%) and a slight decrease in the men remaining AIDS-free with significant inflection (13%) (Fig. 5,  $+$ ). Both the sensitivity and specificity when using the post-IP slope cutoff  $(\beta_2)$  among those with 15 or more  $CD3^+$  cell counts also increased slightly, to 81%.

#### **DISCUSSION**

The data obtained in this study and described by our methods lend strong support to the hypothesis that the loss of T-cell homeostasis is important in the pathogenesis of the severe immunodeficiency that characterizes the late stages of HIV infection. Based on our hypothesis regarding the patterns of  $CD3<sup>+</sup>$  changes over time, we constructed a segmented regression model with different  $CD3<sup>+</sup>$  trajectories before and after an IP. Criteria were developed for determining whether an individual could be considered as having a true inflection. We

found that the optimal criteria for discriminating men who did and did not develop AIDS was whether their post-IP  $CD3$ <sup>+</sup> lymphocyte counts declined by more than 10% per year.

Supported by the methods for identifying individuals with true inflection, we applied our model to a variety of groups in the MACS to evaluate the blind T-cell homeostasis hypothesis  $(2, 3, 14-16)$ . Consonant with this hypothesis, in which CD8<sup>+</sup> cells compensate for  $CD4<sup>+</sup>$  loss to maintain a constant number of circulating  $CD3<sup>+</sup>$  cells, the trajectories before the IP were closely distributed around zero. Furthermore, there were no differences in the pre-IP trajectories of the  $HIV-$  and  $HIV+$ men remaining free of AIDS, who were expected to have maintained homeostasis, and the  $HIV+$  men with onset of AIDS, who were expected to have lost homeostasis, but only after the IP. Independent from whether homeostasis is perfectly maintained (versus a slight decline over time), the individual trajectories after the IP observed in the men who developed AIDS indicated a rapid decline in  $CD3<sup>+</sup>$  cell counts preceding the onset of AIDS in the vast majority of these men.

With our methods for the estimation of inflection at the individual level, we could investigate issues that cannot be addressed at the population level, particularly the prevalence of inflection among those destined to develop AIDS or not within 3 years. It is not necessary that every person exhibit an IP for the phenomenon to exist in the aggregate of HIV-infected individuals. In the population averages, a few men could have accounted for the observed declines before AIDS. This was not found, however, as we estimated that 77% percent of the men developing AIDS, but only 23% of the men remaining AIDS-free, had T-cell inflection. The use of the statistical criteria qualitatively validated the difference in prevalence among men developing AIDS and men remaining AIDS-free, despite using a more conservative cutoff. Taken together, these data strongly support the idea that failure of T-cell homeostasis is an important milestone in the progression of HIV-1 infection to AIDS.

Nevertheless, even these estimates of the prevalence of  $CD3<sup>+</sup> homeostasis loss before AIDS may be conservative for$ several reasons. First, the limitations in the data available on each individual may have had an impact. Because the methods required a minimum of six  $CD3<sup>+</sup>$  cell counts, some individuals with true inflection may have been missed. Furthermore, our analysis did not exclude individuals who supplied the minimum data but who had large gaps between their visits, or those individuals who met the entry criteria with data collected much earlier than AIDS.

Second, our decision criteria used only the magnitude and statistical significance of the trajectories of  $CD3<sup>+</sup>$  lymphocyte counts. No concomitant immunologic (e.g., CD4<sup>+</sup> level,  $\beta_2$ microglobulin, neopterin), virologic (e.g., viral load), or epidemiologic (e.g., antiretroviral therapy) variables were used to assess whether there was evidence of true inflection. Using additional T-cell data might improve the sensitivity and specificity. For example, we could have required both the  $CD3<sup>+</sup>$  trajectory to be larger than  $10\%$  and the CD4<sup>+</sup> cell count to be below  $500$  cells/mm<sup>3</sup> to assess men as having evidence of true inflection. Although previous analyses have not demonstrated any influence of therapy on the loss of homeostasis (2), more research in this area is needed, particularly in the new era of highly active antiretroviral therapy.

The occurrence of inflection after AIDS suggests a more complicated relationship between loss of homeostasis and AIDS. However, further investigation of the data from these men suggested that some of the IPts after AIDS might have been consequences of the data structure. The distribution of IPs among these individuals was highly skewed so that 40% of the IPs among these individuals were within 1 year of AIDS. It is likely that many of these AIDS occurrences were within the expected random variation of the IP time from pre-AIDS time points. In addition, we found that these men had a higher median number of  $CD3^+$  cell counts (17 versus 12 in those with

IP estimated before AIDS) and that AIDS occurred earlier in these men by 1.1 years versus those with an IP estimated before AIDS. Thus, a relatively long follow-up after AIDS might have resulted in an IP estimated after AIDS. Because the method used allowed for only one IP per individual, these individuals also might have had a less dramatic inflection earlier in their disease. In support of this, when the algorithm was rerun on only pre-AIDS data, the prevalence of a pre-AIDS IP characterized by more than a  $10\%$  post-IP decline in CD3+ trajectories was nearly identical for these individuals (75%) as for those with an IP estimated before AIDS (77%).

The identification of  $CD3<sup>+</sup>$  lymphocyte inflection on an individual level provides an approach for investigating immunologic and virologic mechanisms that elucidate the pathogenesis of HIV infection. Using the methods described in this paper, studies now can be designed to examine the occurrence of landmark events (e.g.,  $CD4^{\dagger}$  lymphocyte counts less than 50  $cells/mm<sup>3</sup>$ ) relative to the timing of T-cell inflection. This type of design will be critical to resolve factors that are consequences of T-cell inflection from those antecedent factors that may help precipitate  $CD3<sup>+</sup>$  inflection.

More generally, our approach demonstrates the ability of statistical models to elucidate pathogenesis mechanisms. The methods proposed could be applied to any longitudinal series of outcomes in any time scale. The segmented regression model with random IPs is particularly well-suited for investigating the timing of trajectory changes. Along these lines, they previously have been proven useful in other medical fields (e.g., respiratory medicine, ref. 17) and other scientific disciplines (e.g., allometry, ref. 18). The use of the segmented regression model in HIV research also has additional promise. For example, the application of the IP model to serial viral RNA measurements in plasma would give a formal method to test the hypothesis that a ''set-point'' exits (19). That is, one could use the methods described in this paper to examine whether longitudinal HIV RNA measurements are constant, consistently rising, or initially constant but rising as a prelude to AIDS. In the latter case, a comparison of T-cell inflection with that of HIV RNA inflection could shed important light on the relative timing of viral events (e.g., the emergence of viral quasi-species  $(20, 21)$  and macrophage-tropic variants (22)) and of immunologic events (e.g., immununologic exhaustion (23, 24) and changes in receptor expression (25).

#### **APPENDIX**

The following methods were used to approximate the critical values used for testing whether the segmented regression model or a linear model was most appropriate for an individual's  $CD3<sup>+</sup>$ cell counts. They are approximate because the exact distribution depends on the exact spacing of the observations (12) and simulated critical values used only equally spaced observations. For a fixed value of  $N_i$  (the total number of  $CD3^+$  cell counts), the algorithm can be described in three steps. Note that our algorithm is similar to that described by Kiuchi *et al.* (11) except that they generate independent observations in step 1.

*Step 1: Generate a series of*  $N_i$   $CD3^+$  *counts under the null hypothesis assumption that*  $\beta_{i1} = \beta_{i2} = 0$ . We assumed the log<sub>10</sub>  $CD3<sup>+</sup>$  responses followed a multivariate normal distribution with mean  $\beta_{i0}$  and a variance-covariance structure described by a damped-exponential model (26). The damped-exponential regression model is a very flexible and parsimonious method for modeling correlated data and has been specifically used to describe markers of HIV infection (27). The model includes a covariance of responses *s* years apart described by  $\sigma^2 \gamma^s$ . Estimates for  $\beta_{i0}$  and the covariance parameters were obtained by applying a regression model of this form to a subset of  $CD3^+$  cell counts for 500 HIV - individuals ( $\hat{\beta}_{i0} = 3.24$ ,  $\hat{\sigma}^2 = 0.0203$ ,  $\hat{\gamma} =$  $0.643, \theta = 0.126.$ 

*Step 2: Apply a linear model and a segmented regression model to this series of CD3<sup>+</sup> counts.* Standard linear regression (i.e., a model with no IP) and the segmented regression model algorithm described in *Methods* were applied to the simulated data generated in step 1.

*Step 3: Compute the F-statistic for testing the appropriateness of a linear model versus a segmented regression model.*The F-statistic

$$
F_i = \frac{(SS_{\rm H} - SS_{\rm A})/2}{SS_{\rm A}/(N_{\rm i} - 4)}
$$

was computed, where  $SS_H$  represents the residual sums of squares under the linear regression model ( $\beta_{i1} = \beta_{i2}$ ), SS<sub>A</sub> represents the residual sums of squares under the segmented regression model with the breakpoint estimated by using methods described in *Methods*.

*Step 4: Repeat steps 1–3 to generate an empirical distribution for the F-statistics.* We repeated steps 1–3 a total of 3,000 times ( $i =$ 1,. . . ,3000) to obtain 3,000 F-statistics. We then ordered the F-statistics and computed the 95th percentile. This value is the critical value we need whereby, given the null hypothesis ( $\beta_{i1}$  =  $\beta_{12}$ ), only 5% of the F-statistics will exceed this critical value.

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