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Parametric Co-Variability in the Standard Model of the Saccadic Main Sequence

Claudio Busetini, PhD and J. Braswell Christy, PT, PhD

Department of Optometry and Vision Science and Vision Science Research Center (CB), and Department of Physical Therapy (BD), University of Alabama at Birmingham, Birmingham, Alabama

Abstract

Significance: Saccades present a direct relationship between the size of the movement (SACSIZE) and its peak velocity (SACPEAK), the main sequence, which is traditionally quantified using the model $SACPEAK = V_{max} \times (1 - e^{-SACSIZE/SAT})$. This study shows that V_{max} and SAT are not veridical indicators of saccadic dynamics.

Purpose: Alterations in saccadic dynamics are used as a diagnostic tool. Are the 95% confidence intervals of V_{max} and SAT correctly quantifying the variability in saccadic dynamics of a population?

Methods: Visually-driven horizontal and vertical saccades were acquired from 116 normal subjects using the Neuro Kinetics Inc. Concussion Protocol with a 100 Hz I-Portal NOTC Vestibular System and the main sequence models were computed.

Results: The 95% confidence intervals of V_{max} , the asymptotic peak-velocity, and SAT, the speed of the exponential rise towards V_{max} , were quite large. The finding of a strong correlation between V_{max} and SAT suggests that their variability might be, in part, a computational interaction. In fact, the interplay between the two parameters greatly reduced the actual peak velocity variability for saccades less than 15°. This correlation was not strong enough to support the adoption of a 1-parameter model, where V_{max} is estimated from SAT using the regression parameters. We also evaluated the effects of interpolating the position data to a simulated acquisition rate of 1 kHz. Interpolation had no effect on the population average of V_{max} and brought a decrease of the average SAT by roughly 8%.

Conclusions: The 95% confidence intervals of V_{max} and SAT, treated as independent entities, are not a veridical representation of the variability in saccadic dynamics inside a population, especially for small saccades. We introduce a novel 3-step method to determine if a data set is inside or outside a reference population that takes into account the correlation between V_{max} and SAT

Keywords

saccade; main sequence; dynamics; eye movements; concussion

Saccadic eye movements are very rapid transfers of gaze between objects of interest and involve a large number of cortical, subcortical and cerebellar brain areas. Evaluating alterations in their dynamics as a clinical tool presents a major challenge, readily evident by performing a review of the methods sections in the saccadic literature. There is poor agreement in how to quantify saccadic dynamics and how to define “normal” and “abnormal” saccades. There is even less agreement on how to compare saccadic dynamics between two subjects or between different data sets from the same subject. When studying saccadic eye movements, we need to keep in mind that in the execution of a saccade there are two main sequential processes involving different brain areas. The first process is the programming of the saccadic goal. The second is the actual execution of the saccade. Once the goal is set, which determination may itself be affected by brain injury and disease, usually as altered gain, higher number of errors, and longer latencies, the saccadic motor command is generated. A spatio-temporal process converts the desired angular rotation into a temporal sequence of neuronal spikes, controlled by a neural local feedback, which will drive the movement. A key consequence of the 2-step mechanism generating a saccade is that the dynamic characteristics of the movement are linked to the programmed size of the saccade and not to the stimulus that was presented to the subject. This has major implications in how best to compare the dynamics of different subjects or of different data sets from the same subject. The same 10° target step may have generated an 8.1° saccade in one set, and a 10.5° saccade in the comparison set. The dynamics, everything else being equal, will be different, because the eye movement is driven by a neuronal spike train linked to the 8.1° goal in one case and to the 10.5° goal in the other: saccadic dynamics is determined by a variable that we cannot directly control. Most naturally occurring saccades in humans have magnitude of 15° or less, with larger gaze shifts usually achieved in combination with head movements. In head-fixed humans, large target steps often elicit a hypometric primary saccade followed by one or more secondary saccades, making the dissociation between target step and saccadic size even more significant.

A key biological characteristic of the saccadic system can help to address this issue. There is a strong relationship between the size of the movement (SACSIZE) and the peak of the eye velocity (SACPEAK) reached during the rotation, called the saccadic main sequence. This relationship is traditionally quantified using the exponential model $SACPEAK = V_{max} \times (1 - e^{-SACSIZE/SAT})$, where V_{max} is the asymptotic peak velocity and SAT is a constant defining the speed of the exponential rise towards V_{max} . In the model equations reported in this and the accompanying paper, bold characters identify their parameters. As long as, among the data sets to be compared, the range of SACSIZE values and their distribution inside the range are similar and the data allow a reliable determination of the main sequence of each set, the fact that the actual SACSIZE and associated SACPEAK values in each data set differ can be, up to a point, ignored. Thus, the values of V_{max} and SAT could be used as quantifiers of the overall saccadic dynamics of each set, irrespective of the precise location of the data points along the main sequence curve.

PURPOSE

The specific question addressed by this study is if the 95% C.I.s (Confidence Intervals) of V_{max} and SAT of a subject population can be used to define the range of saccadic dynamics

variability of the population. The data reported in this study are from 116 participants, selected as our control population for future studies. We will first compute the main sequence models for the 116×4 saccadic directions (right, left, up, down) data sets and determine the 95% C.I.s of $V_{\max}$ and SAT of our population. The discovery of a strong correlation between $V_{\max}$ and SAT suggests the possibility of adopting a 1-parameter model where $V_{\max}$ is estimated from SAT using the regression parameters of the correlation. We will test this 1-parameter model on data sets that maximally deviate from this correlation to test if this parameter reduction is acceptable. We will then introduce a new 3-step process to determine if a data set is inside or outside our reference population that takes into account the strong correlation between $V_{\max}$ and SAT. On 35 subjects we acquired two saccadic sets and we will use these data to test the reproducibility between sessions of our findings. Finally, we will analyze how the parametric variability correlates with the actual variability in saccadic dynamics.

As is true for most clinical video eye trackers included in integrated vestibular units, the video cameras tracking the eyes in our system have a 100 Hz frame rate. In Appendix 1 we describe the effect on the main sequence parameters of using a same-weight 10-point (10x) cubic spline interpolation instead of a 1x (i.e., no interpolation) cubic spline on the position traces. A 2-point backward differentiation is then used to compute the eye velocity in both cases. A simulation study by Mack et al. suggests that interpolation can compensate for the underestimation of the peak velocity values caused by the 100 Hz video frame rate and we tested this approach on our data.

METHODS

Participants (or parent or legally authorized representative for minors) gave written informed consent and all protocols and procedures were conducted in accordance with the Declaration of Helsinki and were approved by the University of Alabama at Birmingham Institutional Review Board.

Horizontal and vertical visually-driven prosaccades in a no-gap modality were acquired from 116 volunteers (61 females), mean age of 26 years (± 11 SDEV, range 8 to 49). The data reported here were acquired with the horizontal and vertical random saccadic tasks of the Neuro Kinetics Inc. Concussion Protocol using a 100 Hz I-Portal NOTC Clinical Rotary Chair. The recording session included several other tests, not part of this commercial protocol, outside the rotary chair enclosure. A subset of 35 volunteers (19 females), mean age of 19 (± 4 SD, range 9 to 24) repeated the entire sequence of tests twice, usually one sequence after the other on the same day, in three cases a few days apart. When on the same day, the two saccadic sessions were separated by approximately one hour of other oculomotor, vestibular and postural tests inside and outside the vestibular enclosure. Thus, the setting of the subject in the recording apparatus and the oculomotor calibration had to be redone between the two saccadic acquisitions. We used this strategy to maximize the variability between sessions linked to technical aspects as well as potential dynamical alterations due to tiredness, which was reported by several of the subjects. Prior to testing, all volunteers had a full eye exam performed by a licensed optometrist and completed a health questionnaire. Participants were excluded from this study if they reported a history of

concussion, a history of playing contact sports at a competitive level, a history of neurological and/or psychiatric conditions that could affect their oculomotor, vestibular and/or postural responses, and if they had ever received drugs that are known to be toxic to the vestibular system. Participants were asked to stop using meclizine (for motion sickness), alcohol or nicotine for 48 hours before testing and needed to be able to see the target without corrective glasses. Contact lenses do not interfere with video eye tracking. All participants were naïve to oculomotor, vestibular and postural testing.

Experimental Setup and Tasks

In this initial study, our sequence of saccadic tasks in terms of number of acquisitions, positions of the targets, and timings strictly followed the commercial NKI Concussion Protocol to allow direct data comparison with our target groups and with similar facilities. Participants were seated on a vertical-axis rotational chair in a light-sealed cylindrical enclosure, wore a set of seat belts and ankle belts, used for the vestibular tests (not described here) and the head was immobilized by temporal pads and a head back-support. A two-way communication system and an infrared camera allowed continuous monitoring of the participant, delivery of instructions about upcoming tasks, and feedback from the participant. Participants were asked to limit blinking and to keep their eyes fully open to obtain good eye tracking data. Periods of rest between tasks with eyes closed helped to achieve that. If the participant was wearing mascara, it was removed before the tests because of interference with eye tracking.

The participants were in total darkness, with the exclusion of the target. The binocular infrared (940 nm) video eye tracking system was embedded inside a scuba-like mask and the frame rate of each eye camera was 100 Hz. The eye tracking of this system is based on the principle of the dark pupil, with adjustable luminance threshold and selectable ROI in each eye. The eye sensors have 640×480 pixels and the location of the center of the pupil is determined as the center of mass of the selected dark area with a geometrical correction based on cross-compensated polar correlation for the measure of torsion, which was not recorded. 0.1° is given by the manufacturer as the horizontal and vertical resolution, with theoretical $\pm 30^\circ$ horizontal and $\pm 20^\circ$ vertical ranges. Our experience showed actual usable ranges of approximately $\pm 20^\circ$ horizontal and $\pm 15^\circ$ vertical. All data, including the eye traces and the analog position feedback signals from the mirror galvanometers controlling the target position, were acquired at 100 Hz and stored in raw format on disk, without any analog or digital filtering. The targets (1 mm = 0.06° in diameter @ 960 mm distance) were generated with a red (650 nm) laser beam projected onto the black wall of the cylindrical chair enclosure at a distance of 960 mm from corneal apex. The beam projection angle was controlled by a fast x-y set of mirror galvanometers. Saccades were elicited by discrete jumps of the laser beam. The <10 ms transition of the target from one location to the next was fast enough to not be detectable by the observer, simulating a standard no-gap task. At the beginning of the session, the participant was asked to fixate $\pm 10^\circ$ targets along the horizontal and vertical meridians for 4 times and these values were used to calibrate all subsequent eye data.

Visually-driven horizontal and vertical saccades were acquired separately. In the horizontal test, the target moved along the horizontal meridian, while in the vertical test the target moved along the vertical meridian. The target steps (TSTEP) were 2°, 4°, ..., 26°, 28°, 30°, randomly presented in terms of direction (right or left in the first sequence, up or down in the second sequence), step size, and timing [range 1.1 to 2.0 s between target steps]. The target sequence was identical for all participants. With the recording session including several other tests and the time allocated to each test necessarily limited, each step value was presented only once. Thus, for each saccadic direction we had up to 15 data points (min 12 valid points for the set to be accepted for analysis) to determine the main sequence model. The starting position of the target for the next trial was the position at the end of the previous trial, with no re-centering. Due to the usable oculomotor range limitations of video-oculographic systems, to record large saccades, in our case up to 30°, the eyes need to start from an offset position to fit well into the trackable range. This has the drawback that, when the target is at the eccentric edge of the range, the participant may have predicted that the next step will be centripetal. This predictability, with potential impact on latency, which is not considered in this study, may have also slightly affected saccadic dynamics following the study by Bieg et al. Potential latency and dynamical differences between centripetal and centrifugal saccades, considering that several large saccades crossed the center, were also not taken into consideration in this study. As we will illustrate in the discussion, there is the need to have the widest possible range in saccadic sizes, which is very difficult to achieve with a standard video-oculographic method by starting at the center at each trial.

Data Analysis

The raw data were converted into ASCII text files and sent to a Linux RedHat computer where the main analysis was conducted. In most of the data sets the reported measures are from the version traces, i.e., for the horizontal tests the average of the left-eye and right-eye horizontal traces and for the vertical tests the average of the left-eye and right-eye vertical traces. All tasks were conjugate saccadic tasks with no change in depth and the two eyes were expected to execute almost identical movements with the exclusion of the well-known intrasaccadic vergence transient. For each data set, a direct graphical comparison of the right-eye and left-eye saccadic size and of the right-eye and left-eye saccadic peak velocity values was performed to identify trials with possible tracking artifacts, seen as major breaks in conjugacy. If this occurred, these trials were deleted from further analysis after visual verification from the raw traces of the actual presence of tracking artifacts. If, during the initial inspection of the data, the traces from one eye were significantly worse than from the other eye, with evident tracking artifacts throughout the session, the data from the eye with the best traces were used instead of the version data. Saccades contaminated by concurrent blinks were also manually deleted. They were easily identifiable by the transient binocular loss of eye tracking signal due to the covering of the pupils by the upper eyelids, which generated “nan” in the eye traces, and the stereotypical transients in the vertical eye traces associated with blinks. The eye tracker has no algorithm compensating for partial pupil occlusions by canthi and/or eyelids, and, unless sufficiently asymmetric to be detectable during the conjugacy control, these data passed the preliminary inspection and were included in the data set.

Eye velocity traces were computed using a 2-point backward differentiation after a cubic spline of the position traces. The weight of the cubic spline was identified using the optimization method suggested by Eubank applied to the raw unfiltered position traces. This weight optimization search is traditionally applied on repeated measures associated with the stimuli giving the highest response dynamics, which are the limiting elements in the choice for the optimal spline weight. The algorithm searches for the optimal compromise between the reduction in local noise (strong filtering, i.e., weak maximum curvature of the fit) at the level of the single position traces and the preservation of the temporal profile of the average eye position trace (weak filtering, i.e., strong maximum curvature of the fit). A visual post-comparison between the average velocity traces obtained applying the 2-point backward differentiation to the raw position traces and to the splined position traces is then performed to confirm that this preservation of the average profiles in the position domain applies also to the average velocity profiles. In our case, the test sets, one for each direction, were generated by pooling the saccade with the highest peak velocity from each of the 116 subjects. With the time expressed in ms and the time resolution 10 ms (100 Hz sampling rate), the optimal weight was $10^{-1.4} = 0.04$. Albeit, in our case, each trace was coming from a different subject, the overall profile preservation between the average unfiltered and filtered velocity traces was very high. The same-weight spline filter, with a 10x interpolation, was temporarily used in the search for the saccadic onset and offset. The determination of SACSIZ and SACPEAK were then made using the non-interpolated position and velocity profiles. The results obtained using the 10x interpolated profiles also in the determination of SACSIZ and SACPEAK will be described in Appendix 1.

The calibration set was used for a linear recalibration of the eye position traces. The onset and offset were determined with the 2-segment fitting procedure described in Busettini and Mays applied to the horizontal (for horizontal tasks) and vertical (for vertical tasks) calibrated 10x interpolated velocity traces. This procedure does not rely on a velocity or an acceleration threshold. Briefly, once a saccade is localized (a velocity above 50°/s), its peak is determined. A 60 ms interval starting at the point where the velocity goes above 50% of the peak value and going backward in time is defined as the interval where the search for the saccadic onset will be performed. A 120 ms interval starting at the point where the velocity goes back below 50% of the peak value and going forward in time is defined as the interval where the search for the saccadic offset will be performed. A 2-segment function, with one segment with free offset and zero slope and the second segment with the same offset (to guarantee continuity) but free slope, is fit inside each of the two search intervals. The joint point of the two segments in each interval is defined as saccadic onset and offset, respectively. These determinations are visually inspected and the starting points of both intervals and lengths can be manually adjusted, for example for saccades with decelerating phases longer than 120 ms or with complex profiles showing multiple peaks. In the latter case, the onset search interval is moved before the first peak and the offset search interval is moved after the last peak. As pointed out by the authors, this fitting method is preferable to a threshold method because it is independent of saccadic dynamics, working well also for very small saccades where threshold and peak velocity become comparable, and it is largely insensitive to local noise and pre- and post-saccadic drifts. It works well also when the saccades occur during ongoing smooth pursuit responses or asymmetric vergence responses

without having to rely on acceleration traces, which can be very noisy. The joint points of the 2-segment functions can be seen as the transition points between fast and slow dynamics. Using the 10x onset and offset estimates, the nearest points in time on the 1x traces were selected as onset and offset. Saccadic size was determined as the change in eye position between onset and offset. Peak velocity was determined as the maximum eye velocity inside the saccadic interval. The first saccade after the target step was identified as the primary saccade and the analysis was limited to the primary saccade. Traditionally, rightward and upward target steps and eye movements are indicated as positive values and leftward and downward target steps and eye movements are indicated as negative values. To ease the comparisons between saccadic directions, in this paper all measures are shown as positive values.

To avoid inflating the quality of the parametric estimates of the main sequence model, determined using the Gauss-Newton method with least-square optimization, the point (0 ; 0), i.e., peak velocity = 0°/s for saccadic size = 0°, was not included in the estimations. The reported R^2 is the mean-corrected R^2 , which is the most conservative of the R^2 values. The amplitude of the 95% C.I.s is the difference between the upper $P = .975$ and the lower $P = .025$ limits, i.e., the full amplitude of the interval, not the $\pm$ value.

All statistical distributions were tested for normality. The χ^2 statistical test for normality implemented in Systat is based on subdividing the data range in 10 equal-size bins without ceiling adjustments. Thus, the default degrees of freedom for a normal distribution test is 7. This test performs poorly with bins empty or with only a few observations. If the number of observations in some bins is too low, which often occurs at the edges of the data range, adjacent bins are fused together, reducing the actual number of bins and therefore also the degrees of freedom. The χ^2 statistical test for normality becomes unreliable for small data sets. For the repeated saccadic tests ($n=35$) we used the Shapiro-Wilk test. For both tests we adopted an α level of 0.01.

All the histograms illustrated in this and the accompanying paper have 12 equal-size bins on a ceiling-adjusted and distribution-adjusted range, which is identified in each histogram with vertical dotted lines. To make the comparisons between saccadic directions easier, the x-axis range was then adjusted to be identical for the 4 saccadic directions but we maintained the original bin size. This approach was preferred to the use of the widest range among the 4 saccadic directions in determining the bin size due to the associated loss of histogram resolution for the horizontal sets, which have ranges of variability significantly narrower than the vertical sets.

RESULTS

Estimate of the Standard Model of the Saccadic Peak Velocity vs. Size Main Sequence

The left panel in Fig. 1 illustrates typical eye position and eye velocity temporal profiles for increasing amounts of eye rotation, i.e., saccadic size, indicated at the end of the position traces. The larger the saccadic size, the higher the peak velocity of the eye rotation. Non-interpolated traces are in black and 10x interpolated traces are in red. With the same color code, the peak velocity vs. size main sequence for all the saccades ($n=15$) of this leftward

data set is shown in the right panel of Fig. 1, superimposed with the traditional main sequence model $SACPEAK = V_{max} \times (1 - e^{-SACSIZE/SAT})$. We will focus here on the 1x (non-interpolated) data. See Appendix 1 for a discussion of the 10x interpolated data in this and subsequent figures and tables. The parametric results, shown above the x-axis of the right panel, are somewhat surprising, considering the quality of the fit ($R^2 = 0.968$), with wide confidence intervals. For all 116 participants x 4 saccadic directions sets we determined the parameters V_{max} and SAT. The model performed best for leftward saccades, with a R^2 range from 0.747 to 0.996 and mean value 0.959, and worst for downward saccades, with a R^2 range from 0.465 to 0.995 and mean value 0.912. Figure 2 shows histograms of the distributions of the V_{max} values and Fig. 3 of the SAT values for all saccadic directions. The parameters of the normal distribution models are reported in Tab. 1. Rightward and leftward directions were almost identical in terms of scatter and in the parameters of the normal distributions. Upward and downward directions had larger scatter and wider parameter variability than the horizontal directions. Some of the larger scatter for vertical saccades may be due to tracking interferences by the upper and lower eyelids or by the eyelashes for large upward and downward eye eccentricities, causing alterations in the velocity profiles. The 95% C.I.s of the two parameters V_{max} and SAT were quite large in all directions. By using the maximum likelihood method implemented in Systat and the χ^2 test of normality, we verified that these distributions could be modeled as normal distributions, with $P < .01$ selected as the criteria for rejection of the normal distribution hypothesis (χ^2 , df and P values in Tab. 1). As population ranges for V_{max} and SAT, reported in Tab. 1, we determined the $P = .025$ and $P = .975$ values of V_{max} and SAT using the normal distribution models. The V_{max} and SAT mean values were similar among directions ($P > .01$), with one exception: both paired and unpaired 2-tail t-tests indicated that upward V_{max} and SAT means were statistically different ($P < .01$) with respect to the other directions, albeit with wide overlaps in the 95% C.I.s among all directions.

Correlation between V_{max} and SAT

When fitting data with a model with two or more parameters, one of the guiding principles in the selection of the model equation is to have the parameters as orthogonal in the parameters' space as possible. This maximizes the stability of the convergence of the model and minimizes the ASE and 95% Wald C.I.s, with each parameter independently controlling one single aspect of the data set. In theory, V_{max} , the asymptotic peak velocity value of the standard main sequence model, and SAT, the speed with which this value is reached, could be independent, but is this the case for the human saccadic main sequence? Panel A of Fig. 4 illustrates the effects of keeping the value of SAT equal to the average of the SAT 1x values in Tab. 1 ($SAT = 9.9^\circ$) while varying the value of V_{max} between the lowest 1x $P = .025$ value ($294^\circ/s$) and the highest 1x $P = .975$ value ($785^\circ/s$). Panel B of Fig. 4 illustrates the effects of keeping the value of V_{max} equal to the average of the V_{max} 1x values in Tab. 1 ($V_{max} = 517^\circ/s$) while varying the value of SAT between the lowest 1x $P = .025$ value (4.5°) and the highest 1x $P = .975$ value (16.3°). It is evident that, inside our ranges of SACSIZE, V_{max} and SAT, V_{max} acts also on the slope of the rising phase of the main sequence and SAT acts also on the overall amplitude. This suggests a strong crosstalk between the 2 parameters, which is indirectly seen in the large asymptotic standard errors (ASE) and wide 95% Wald C.I.s even for the highest R^2 . The striking results reported in Fig. 5 are clear evidence that, in the

human saccadic main sequence standard model, the two parameters $V_{\max}$ and SAT are strongly correlated. To quantify this correlation, we used a simple linear model, $V_{\max} = \mathbf{A} + \mathbf{B} \times \text{SAT}$, in order to determine how well $V_{\max}$ can be predicted from the SAT value. The values for intercept A, slope B and R^2 are remarkably similar for the 4 saccadic directions. The average value of the 4 intercepts is $179^\circ/\text{s}$ [range $175 - 182^\circ/\text{s}$] and the average of the 4 slopes is 34.3 s^{-1} [range $32.7 - 35.3 \text{ s}^{-1}$]. For all sets, quadratic and cubic parameters of a polynomial fit had their 95% Wald C.I.s including zero, indicating a strong linear relationship, and are not included in the fit estimates.

Estimating $V_{\max}$ from SAT

The correlation between SAT and $V_{\max}$, illustrated in Fig. 5, makes it biologically plausible that the non-linearity of the main sequence, quantified by SAT, is the determinant element of the main sequence profile, with $V_{\max}$ an indirect consequence of SAT. An important clinical question is if brain damage and disease can alter this relationship. To evaluate the range of variability of this correlation in our population, for each data set we determined the statistical distribution of $V_{\max} - V_{\max\text{est}}$, i.e., of the deviation of the actual $V_{\max}$ of the set with respect to the $V_{\max\text{est}}$ estimated from the SAT value using the regression coefficients reported in Fig. 5 for its saccadic direction. The results are illustrated in Fig. 6 and in Tab. 2, with similar layouts of Figs. 2 and 3 and Tab. 1. Starting from Fig. 6 and Tab. 2, all reported results are from non-interpolated data and the labeling as such was discontinued for brevity. The χ^2 test statistic for a normal distribution gave a probability $P = .01$ for all sets, suggesting that a normal distribution of $V_{\max} - V_{\max\text{est}}$ is an acceptable assumption for all saccadic directions, with $P < .01$ the criteria for rejection of the normal distribution hypothesis. For horizontal saccades, the prediction of $V_{\max}$ from SAT was remarkably robust, with the largest $P = .025$ or $P = .975$ value of $V_{\max} - V_{\max\text{est}}$ of $65.7^\circ/\text{s}$. For vertical saccades, the prediction was not as strong, with the largest $P = .025$ or $P = .975$ value of $V_{\max} - V_{\max\text{est}}$ of $111.5^\circ/\text{s}$. A key clinical consequence of these results is that, for each SAT value, our reference population shows a range of actually observed $V_{\max}$ values which is only a fraction of the full 95% C.I. in Tab. 1. Values of $V_{\max} - V_{\max\text{est}}$ outside these ranges might indicate a breakdown in the natural relationship between SAT and $V_{\max}$, even if both values are well inside their respective 95% C.I.s.

Quantification of the Main Sequence Using SAT Alone

A direct consequence of the linear correlation between $V_{\max}$ and SAT is that for the data sets along the regression line, $V_{\max}$ can be computed from SAT using the equation $V_{\max} = \mathbf{A} + \mathbf{B} \times \text{SAT}$, with the values of A and B given in Fig. 5 for each saccadic direction. Quantifying the main sequence with a single parameter would allow direct comparisons between data sets using the parameter's 95% Wald C.I.s. The question is how the 1-parameter model in SAT, $\text{SACPEAK} = (\mathbf{A}_{\text{FIG5}} + \mathbf{B}_{\text{FIG5}} \times \text{SAT}_{1\text{-par}}) \times (1 - e^{-\text{SACSIZE}/\text{SAT}_{1\text{-par}}})$ behaves when a data set is far from the linear regression. Is the 1-parameter $\text{SAT}_{1\text{-par}}$ model an acceptable approximation? As test sets we used the two data sets indicated with a green dot in the leftward direction panel (points A and B) and the two data sets indicated with a green dot in the upward direction panel (points C and D) in Fig. 5. These sets are among the furthest away from the regression lines in the horizontal and vertical directions respectively. We fitted their main sequence with both the 1-parameter ($\text{SAT}_{1\text{-par}}$) and the 2-parameter model

($V_{\max}$; SAT) in order to determine the degradation of the fit using the 1-parameter model, and the results are illustrated in Fig. 7. In each panel, the black curve is the 2-parameter model and the red curve is the 1-parameter model. The green curve labeled " $V_{\max\text{est}}$ " is the main sequence model with the original SAT value of the data set and $V_{\max} = V_{\max\text{est}}$ from the linear regression to illustrate the amount of deviation of the actual main sequence profile from the model with the same SAT but on the regression line. When $V_{\max}$ is below $V_{\max\text{est}}$ (points A and C) there is a decrease of $\text{SAT}_{1\text{-par}}$ from the original SAT value in an attempt to curtail the gain effect of SAT at the larger SACSIZ values, illustrated in the right panel of Fig. 4. The change in the SAT value results in a more rapid rise of the 1-parameter model for small SACSIZ values and a flattening of the curve at higher SACSIZ values when compared with the 2-parameter model. This effect is evident for point C, where the 1-parameter model clearly fails. In a mirror-image behavior, when $V_{\max}$ is above $V_{\max\text{est}}$ (points B and D) there is an increase of $\text{SAT}_{1\text{-par}}$ in an attempt to maximize the gain effect of SAT at the larger SACSIZ values. The change in the SAT value results in a slower rise of the 1-parameter model for small SACSIZ values but this rise continues for the larger SACSIZ values. The effect is quite dramatic for point D, where the 1-parameter model is not applicable to this data set. The actions on the main sequence profiles by the two parameters $V_{\max}$ and SAT are too dissimilar, albeit strongly interacting, for $\text{SAT}_{1\text{-par}}$ to be able to compensate for the difference between $V_{\max}$ and $V_{\max\text{est}}$ without introducing unacceptable distortions. Although points C and D are outliers, the results in Fig. 7 show that the correlation between SAT and $V_{\max}$ is not strong enough to be able to support a 1-parameter model of the main sequence with $V_{\max}$ estimated from SAT, particularly for the vertical directions. We also tested the 1-parameter square-root model of the peak velocity main sequence, proposed by Lebedev et al. in 1996. It performed similarly to the 1-parameter model in SAT but with a higher number of data sets where it failed to fit the data. The main reason for these failures is that the square root function has a gradual curvature for increasing SACSIZ values and it fails to reproduce the main sequence saturation at the larger SACSIZ values when the saturation is strong, i.e., for data sets with small SAT values, like the one reported in Fig. 10 (SAT=7.1).

Although not strong enough to allow the reduction of the standard main sequence model to a 1-parameter model, the correlation between $V_{\max}$ and SAT (Fig. 5), combined with their crossed non-linear interaction (Fig. 4), has devastating effects on the stability and reproducibility between sessions of their values. These effects are evident when comparing the values of $V_{\max}$ of the two sessions in our 35 subjects from which we have repeated data (Fig. 8) and they are even more dramatic when comparing the values of SAT (Fig. 9). While there is some reasonable reproducibility between sessions of $V_{\max}$ for the horizontal sets, it is very poor for the vertical sets. There is no reproducibility for SAT in any direction.

Based on the R^2 values, the 2-parameter model $\text{SACPEAK} = V_{\max} \times (1 - e^{-\text{SACSIZ}/\text{SAT}})$, which is the most used method to quantify the main sequence, is a robust numerical quantification of human main sequence profiles. At the same time, ignoring the correlation between $V_{\max}$ and SAT and simply adopting the overall 95% C.I.s of $V_{\max}$ and SAT (Tab. 1) as the range of saccadic dynamics of a reference population is clearly invalid. Only a fraction of the possible $V_{\max}$ and SAT pairs is actually observed. The reproducibility of the

$V_{\max}$ and SAT values between sessions is also very poor. In the discussion, we will present a 3-step process that overcomes these issues by including the correlation in the determination of whether a data set is inside or outside a reference population and how the interplay between $V_{\max}$ and SAT directly affects the main sequence profiles.

DISCUSSION

Quantification of the Saccadic Dynamics Range of a Reference Population

A typical process, often used in commercial clinical systems, is to gather a large number of SACPEAK vs SACSIZ data points from a reference population and build a threshold main sequence curve. A participant from a target population with a high number of data points below this threshold curve, following a statistical criterion of some kind, will be flagged as showing abnormally slow saccadic dynamics. Although it offers a rapid visual determination of the results from a clinical standpoint, it is difficult to translate this process into a compact numerical form. It is also not applicable when comparing two data sets. From the average R^2 of the fits, the $V_{\max}$ and SAT values of the standard main sequence model $SACPEAK = V_{\max} \times (1 - e^{-SACSIZ/SAT})$ offer a robust numerical quantification of the main sequence profiles. These values are much less representative when we consider their wide ASE and 95% Wald C.I.s. A 2-parameter model requires a much higher number of data points than a 1-parameter model for comparable statistical significance, particularly when the two parameters are strongly correlated. Even small changes in the main sequence profiles can cause large changes in the model parameters, affecting stability and reproducibility of the parametric results.

Figure 7 shows that the 2-parameter standard main sequence model cannot be reduced to a 1-parameter model in SAT (SAT_{1-par}) using the correlation between $V_{\max}$ and SAT to estimate the value of $V_{\max}$ from SAT. This negative result is most likely to exacerbate when dealing with patients with altered main sequences. Their $V_{\max}$ and SAT values may fall further away from the regression lines than our examples in Fig. 7. Nonetheless, simply using the 95% C.I.s of $V_{\max}$ and SAT reported Tab. 1 vastly overestimates the actual parametric variability of a population. Due to the correlation between the two parameters, only a fraction of all the potential $V_{\max}$ and SAT pairs defined by these two C.I.s are actually observed. The 3-step process described below offers a better approach to determine whether a data set is inside or outside the reference population by taking into account this correlation. For each saccadic direction, the reference population in this process is defined by 8 parameters: the traditional upper and lower limits of the 95% C.I.s of $V_{\max}$ and SAT, the intercept and slope of the linear regression between $V_{\max}$ and SAT, and the upper and lower limits of the 95% C.I. of $V_{\max} - V_{\maxest}$. The first step is the traditional estimate: are the $V_{\max}$ and/or SAT values of the data set under evaluation inside the $V_{\max}$ and SAT 95% C.I.s of the reference population in Tab. 1? If the answer is no, the set is flagged as “outside” the reference population and both the traditional and the 3-step processes conclude. If both the $V_{\max}$ and SAT values are inside the reference ranges, the traditional process flags the set as “inside” and the process concludes. We propose two additional steps, in order to take into account the correlation between $V_{\max}$ and SAT. The second step is to determine the $V_{\maxest}$ value from the SAT of the data set, using the regression reported in Fig. 5. The third step is

to determine the $V_{\max} - V_{\max\text{est}}$ value and whether this value is inside or outside the 95% C.I. of the reference population, given in Tab. 2. An example of this process is illustrated in Fig. 10 for a rightward data set obtained from one of our patients. Is the patient's rightward main sequence inside or outside the reference population? The main sequence of this patient, illustrated in the left panel of Fig. 10, has a remarkable $R^2 = 0.985$, with $V_{\max} = 382^\circ/\text{s}$ and $\text{SAT} = 7.1^\circ$ (red dot in Fig. 10 right panel). Both $V_{\max}$ and SAT values are inside the 95% C.I.s in Tab. 1 for rightward saccades, i.e., they are inside the grey area in the right panel of Fig. 10. The dashed lines are parallel to the regression line and shifted by the upward and downward values of the 95% C.I. of the $V_{\max} - V_{\max\text{est}}$ distribution. This panel clearly illustrates how the actual 95% range of variability of $V_{\max}$ and SAT, i.e., the area simultaneously contained inside the grey area and the dashed lines, is only a fraction of the total grey area. The $V_{\max\text{est}}$ value is $427^\circ/\text{s}$ (green dot in Fig. 10 right panel), estimated using the rightward regression parameters in Fig. 5, and therefore $V_{\max} - V_{\max\text{est}} = -45^\circ/\text{s}$. For rightward saccades, the $P = .025$ value for $V_{\max} - V_{\max\text{est}}$ in Tab. 2 is $-64.8^\circ/\text{s}$. Following our criteria, the main sequence for the rightward saccades of this patient is inside the 95% adjusted C.I. of the reference population. Note that this method does not necessarily require the correlation between the model parameters to be linear, the distributions to be normal or the C.I.s to be the 95% C.I.s, once proper adjustments are adopted to deal with non-linear estimates of $V_{\max\text{est}}$, non-Gaussian distributions or different P limits of the C.I.s.

The process described above can be used to determine, for each saccadic direction, the variability between sessions of the correlation between $V_{\max}$ and SAT and to see how many of the ($V_{\max}$; SAT) pairs from the first and the second session are outside the reference area determined by the first session. The results are illustrated in Fig. 11 for the 4 saccadic directions ($n=35$). The dynamics variability associated with the first session, defined as in Fig. 10, is identified by the dashed polygon in each panel. The black dots are the ($V_{\max}$; SAT) pairs from the first session and the red dots are the pairs from the second session. All directions present two common features. A comparable number of pairs (3) from the two sessions fall outside the $V_{\max}$ and SAT C.I.s. from the first session, which is consistent with the use of 95% C.I.s and not absolute ranges. The slope of the regression associated with the second session (in red) is lower than the slope of the regression associated with the first session (in black). For three directions, its value is outside the 95% C.I. of the slope of the first session. This slope rotation causes some additional pairs from the second session (4) to fall below the reference area defined by the first session. Several of the subjects told us that they were tired after the first sessions and struggling to remain focused on the task and to keep their eyes fully open, which is possibly reflected in the data as degraded dynamics. Note that no pair from the second session is above the reference area defined by the first session. These results are quite remarkable when compared with the poor between-session reproducibility of $V_{\max}$ and SAT, illustrated in Figs. 8 and 9. In fact, most reliability studies have avoided the use of $V_{\max}$ and SAT. Roy-Byrne et al. used a 3-parameter main sequence model to determine, by interpolation, the saccadic peak velocity of 20° saccades as representative of the overall dynamics of the subject and used these estimated values for their reliability analysis. Meyhofer et al. used a fixed size of the target steps (rightward or leftward 10°), ignoring the actual variability of saccadic gain and therefore associated variability in peak velocity for a given target step and potential rightward/leftward

asymmetries. In a detailed oculomotor reliability study, Balgary et al. used the 1-parameter square-root model of the main sequence. Although a proper reproducibility study is needed, our preliminary data suggest a step in the right direction in offering a robust definition of the range of dynamic variability of a population.

Unfortunately, this method is not applicable when comparing two data sets, for example pre- and post-concussion sets from the same athlete. The strong non-linearity of the main sequence and the fact that the SACSIZ_E values in the pre-concussion (SACSIZ_E_{pre}) and post-concussion (SACSIZ_E_{post}) sets do not normally match preclude the use of traditional ANOVA statistical methods. For example, the athlete might present deeply altered saccadic gain after a concussion but the movements have normal dynamics for a given saccadic size, consistent with the fact that saccadic gain and dynamics are determined in different brain areas. In this case, we may apply an approach similar to the one that we used in our sedation study. The 2-parameter main sequence model of the pre-concussion set (SACPEAK_{pre} vs. SACSIZ_E_{pre}) is used to compute the pre-concussion peak velocity estimate (SACPEAK_{preest}) for each of the post-concussion SACSIZ_E_{post} values. This re-mapping process co-registers the pre- and post-concussion peak velocities to matching SACSIZ_E values. The SACPEAK_{post} - SACPEAK_{preest} set of values, now with matching SACSIZ_E values, is tested if significantly different from 0. A requirement of this approach is that the set used as reference, in our case the pre-concussion set, must allow a reliable determination of the main sequence model for the entire range of SACSIZ_E_{post} values. This is not required for the post-concussion set, the main sequence model of which is not computed.

Physiological Consequences of the Correlation between V_{max} and SAT

In order to understand the consequences of the correlation between V_{max} and SAT from a biological point of view, we analyzed the changes in the main sequence profiles while moving inside the adjusted 95% C.I.s of the two parameters, illustrated in Figs. 10 and 11. As main sequence profile simulations to compare, for each direction we selected three (V_{max}; SAT) pairs, based on the 95% C.I.s in Tab. 1: the $P = .025$ pair, the mean pair, and the $P = .975$ pair. For the rightward set, these are the three light-blue dots in the right panel of Fig. 10. Note that the $P = .025$ and $P = .975$ pairs, which define the lower left and upper right corners of the grey area, as well as the mean pair, are very close to the regression line. This observation applies to all directions. Thus, these pairs also well represent the changes in the main sequence profile while moving along the regression line. The results are illustrated in Fig. 12 and the values of SACPEAK @ SACSIZ_E 5°, 10°, 15°, 20°, 25° and 30° (dotted lines) are reported in Tab. 3 together with the relative % change (%) with respect to the correspondent SACPEAK value of the mean pair (in bold). When comparing Fig. 12 with Fig. 4, where SAT was kept constant but V_{max} was changed over similar ranges (left panel) and where V_{max} was kept constant but SAT was changed over similar ranges (right panel), the effects of the correlation between V_{max} and SAT are quite striking. In the following discussion, we will use the rightward data for brevity, but identical conclusions can be extracted from the other three directions, described in Tab. 3. For the $P = .025$ (V_{max}; SAT) pair, V_{max} is 30% smaller than the average V_{max} value of the population and SAT is 42% smaller than the average SAT value of the population. Due to the interaction between the two parameters, there is no change in the profiles up to SACSIZ_E ~7°. Actually, at

SACSIZE = 5° the peak velocity for the $P = .025$ pair is slightly higher than the value for the mean pair and the peak velocity for the $P = .975$ pair is slightly lower. Even at SACSIZE = 15°, which is the oculomotor range covered by most studies, including our sedation report, the peak velocity for the $P = .025$ pair is only 17% slower, a value that is much less than the 30% decrease for $V_{\max}$ and the 42% decrease for SAT. Only at SACSIZE = 30°, the peak velocity decrease (27%) is actually comparable to the decrease in $V_{\max}$ (30%), but still less than the decrease in SAT (42%). For the $P = .975$ pair, this squashing effect is even more pronounced: the green curves are closer to the black curves than the red curves. At SACSIZE = 15°, the peak velocity for the $P = .975$ pair is only 10% faster, a value that is 1/3 of the 30% change for $V_{\max}$ and less than 1/4 of the 41% change for SAT with respect to the mean values. Even at SACSIZE = 30°, the peak velocity increase is only 21%. It is important to note that a target step of 30° seldom generates a 30° saccade. Larger target steps increase the probability of the gaze transfer being achieved with a hypometric primary saccade followed by one or more correctives.

These surprising results show the absolute need to select the largest possible SACSIZE range allowed by the stimulus delivery and eye recording systems in order to get as deep as possible into large SACSIZE values, where the dynamical stabilizing effect of the correlation of $V_{\max}$ and SAT is less effective. At the same time, acquiring only large saccades would make the determination of $V_{\max}$ and SAT unreliable. A uniform coverage of saccadic sizes inside the selected range, and therefore including small saccades, is needed to have a veridical main sequence profile. A large SACSIZE range is a significant challenge, both technically and physiologically. Video-oculographic recording systems struggle to get reliable data beyond 15° eccentricities, particularly in the upward and downward directions. Our protocol, with the target position at the start of the next trial being the position at the end of the previous trial, can be designed to cover saccades as large as the total oculomotor range of the eye tracker, but this methodology has shortcomings. When the target is at an eccentric position, it is likely that the next step will be centripetal, adding predictability to the protocol and potential alterations in the latency measures. It may have also slightly affected saccadic dynamics. An additional fully randomized protocol with the target starting at the center at every trial is required for proper latency estimates. It is also difficult to obtain large primary saccades, in some subjects more than in others, irrespective of the technology used.

SUMMARY

Although the 2-parameter model $SACPEAK = V_{\max} \times (1 - e^{-SACSIZE/SAT})$ is widely accepted as the standard method to quantify the saccadic main sequence, our study shows that the two parameters $V_{\max}$ and SAT are linearly correlated. This correlation is not strong enough to be able to estimate the value of $V_{\max}$ from SAT and therefore to reduce the 2-parameter model to a 1-parameter model, but it has major repercussions in determining whether a data set is inside or outside a reference population. We propose a 3-step process that takes into account this correlation and making this determination much more robust. Furthermore, the interaction between the two parameters generates a strong squashing effect on the variability in the main sequence profiles when compared with the variability of $V_{\max}$.

and SAT. Particularly for small saccades, variations in $V_{\max}$ and SAT greatly overestimate the actual variations in the main sequence profiles.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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APPENDIX

Appendix 1, available at [LWW insert ink]: video eye tracking systems with 100 frame/s cameras are very common, particularly in clinical integrated vestibular/oculomotor recording systems, but are considered too slow for saccades. Sampling frequencies less than 200–300 Hz cause an underestimation of saccadic peak velocity. Mack et al. have demonstrated that numerical oversampling can reduce this effect. In the Appendix, we analyzed the effect of 10-point oversampling of the eye position traces on the $V_{\max}$ and SAT estimates.

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Figure 1.

Sample eye traces and peak velocity main sequence. Black: non-interpolated data. Red: 10x interpolated data. Left panel: eye position and eye velocity traces over time, showing evident increase in peak velocity for increasing size of the saccade, indicated at the end of the position traces. Right panel: Peak velocity vs. size main sequence for all the saccades in this data set (#22065 leftward saccades; n=15). The fit of the main sequence function has a remarkable R^2 of 0.968 (1x data) and R^2 of 0.961 (10x data). The values of the parameters $V_{\max}$ and SAT together with their asymptotic standard error (ASE) and Wald 95% C.I. limits are reported in the right panel near the x-axis.

Figure 2.

Histograms of the distributions of the $V_{\max}$ values of the standard main sequence model for the 116×4 saccadic directions. The histograms and the normal distribution models reported as solid curves are applied to the non-interpolated data. The dashed curves are normal distribution models applied to the interpolated data. The two dotted vertical bars identify the ceiling-adjusted and distribution-adjusted range selected for each histogram. This range was then parsed into 12 equal-size bars. To ease the comparison between directions, each x-axis was then resized to be identical for all saccadic directions while maintaining the original bin size.

Figure 3.
Histograms of the distributions of the SAT values of the standard main sequence model for the 116×4 saccadic directions. Identical layout of Figure 2.

Effects of Changing the Values of the Parameters $V_{\max}$ and SAT
in the Main Sequence Model $SACPEAK = V_{\max} \times (1 - e^{-SACSIZE/SAT})$

Figure 4.

Crossed effects of $V_{\max}$ and SAT on the main sequence profiles. Panel A: Main sequence simulated profiles obtained by keeping SAT constant at the average 1x SAT from Table 1 (9.9°) and varying $V_{\max}$ between the extremes of the 1× 95% Wald C.I.s. Panel B: Main sequence simulated profiles obtained by keeping $V_{\max}$ constant at the average 1x $V_{\max}$ from Table 1 (517°/s) and varying SAT between the extremes of the 1× 95% Wald C.I.s.

Correlation between $V_{\max}$ and SAT in the Main Sequence Model **Figure 5.**

Correlation between $V_{\max}$ and SAT for the 4 saccadic directions. The dots and the black linear regression lines are for the non-interpolated data. The red linear regression lines are for the 10x interpolated data. The R^2 values are indicated near the regressions lines. The values for intercept A and slope B, together with their asymptotic standard error (ASE) and Wald 95% C.I. limits are reported near the x-axis. The four green dots in the LEFT and UP graphs indicate the 1x data sets that will be utilized in Figure 7 to evaluate if a 1-parameter model in SAT is an acceptable approximation.

Figure 6.

Histograms of the distributions of the $V_{\max} - V_{\max\text{est}}$ values for the 116×4 saccadic directions. $V_{\max}$ is the actual value of the set. $V_{\max\text{est}}$ is estimated from the SAT value of the set using the regression parameters reported in Figure 5 for its saccadic direction. The solid curves are normal distribution models. Identical layout of Figure 2.

Failure of a 1-parameter Peak Velocity Main Sequence Model Using SAT as Free Parameter (SAT_{1-par}) **Figure 7.**

Behavior of the 2-parameter (V_{max} ; SAT) and 1-parameter (SAT_{1-par}) main sequence models applied to the data sets labeled A, B, C and D in Figure 5. In each panel, the black curve is the 2-parameter model and the red curve is the 1-parameter model. With the same color code, the R^2 of the fits are indicated near the respective curve and the model parameters are reported near the x-axis. The green curve labeled " V_{maxest} " is the main sequence model with the original SAT value of the data set and $V_{max} = V_{maxest}$.

Figure 8.

Comparison of the $V_{\max}$ estimates between the first session ($V_{\max 1}$) and the second session ($V_{\max 2}$) for the 35 subjects we have repeated saccadic acquisitions. The black lines are linear regression lines, which R^2 values are indicated near the regressions lines. The values for intercept A and slope B, together with their asymptotic standard error (ASE) and Wald 95% C.I. limits are reported near the x-axis.

Figure 9.
Comparison of the SAT estimates between the first session (SAT1) and the second session (SAT2) for the 35 subjects we have repeated saccadic acquisitions. Same layout of Figure 8.

Figure 10.

Graphical illustration of the 3-step process used to determine if a data set of a patient (#21073 rightward set) is inside the parametric range of the reference population. Left panel: main sequence and standard 2-parameter main sequence model (red curve) of the data set, the parameters of which are reported also in the right panel as the red dot. The R^2 of the model is indicated near the fit, and the model parameters are reported near the x-axis. The green curve labeled “ $V_{\max\text{est}}$ ” is the main sequence model with the SAT value of the data set and $V_{\max} = V_{\max\text{est}}$, represented also in the right panel as the green dot. The right panel replicates the rightward data from Figure 5. The grey area is delimited by the 95% C.I.s of $V_{\max}$ and SAT from Table 1. The dashed lines are parallel to the regression line and shifted by the upward and downward limits of the 95% C.I. of the rightward $V_{\max} - V_{\max\text{est}}$ distribution from Table 2. Only data sets with $V_{\max}$ and SAT simultaneously inside the grey area and the dashed lines are considered inside the reference population. The three light-blue dots identify the $P = .025$, mean, and $P = .975$ ($V_{\max}$; SAT) pairs from Table 1 (rightward) used in Figure 12.

Session Variability of the Correlation between $V_{\max}$ and SAT **Figure 11.**

Comparison of the results from the first and the second session ($n=35$) utilizing the 3-step process introduced in Figure 10. The reference areas associated with the first session (dashed polygons) are determined as in Figure 10. Superimposed to this reference area are, in black, the ($V_{\max}$; SAT) pairs from the first session with the associated linear regression. The data from the second session are in red. With the same color code, the R^2 values are indicated near the regressions lines and the values for intercept A and slope B, together with their asymptotic standard error (ASE) and Wald 95% C.I. limits are reported near the x-axis.

Effects of the Correlation between $V_{\max}$ and SAT on the Main Sequence Profiles **Figure 12.**

Main sequence simulations using the $P = .025$, mean and $P = .975$ ($V_{\max}$; SAT) pairs in Table 1 for the 4 saccadic directions. The peak velocity values of these models @ SACSIZ 5°, 10°, 15°, 20°, 25° and 30° (dashed lines) are reported in Table 3.

Table 1.

Parameters, for each of the 4 directions, of the normal distribution models of the 116 $V_{\max}$ and SAT values in Figs. 2 and 3. The “1x” rows list the results for the non-interpolated data and the “10x” rows for the 10x interpolated data (“Spline” column). Each row reports mean, standard deviation σ , value of the χ^2 test statistic of normality with in parenthesis the degrees of freedom of the estimation (df), probability of the χ^2 test statistic, value of the parameter @ $P = .025$ and @ $P = .975$, and size of the 95% C.I., defined as the difference between the values @ $P = .975$ and @ $P = .025$. A $P < .01$ in the probability of the χ^2 test statistic was selected as rejection threshold of the normal distribution model, and all distributions had a $P > .01$. The single asterisks in the $V_{\max}$ section indicate a weak significance in the difference between the 1x and 10x mean values ($P < .01$). The double asterisks in the SAT section indicate the extremely significant shift in the mean SAT values for the 10x models with respect to the 1x models.

Asymptotic Peak Velocity $V_{\max}$ [°/s] SACPEAK = $V_{\max} \times (1 - e^{-\text{SACSIZE}/\text{SAT}})$ n=116								
Direction	Spline	Mean	σ	χ^2 (df)	P	$V_{\max}$ @ $P = .025$	$V_{\max}$ @ $P = .975$	95% C.I.
Right	1x	514	78	1.7 (3)	0.64	361	666	305
	10x	514	74	1.2 (3)	0.76	369	659	290
Left	1x	516	72	4.8 (4)	0.31	375	656	281
	10x	516	71	4.8 (4)	0.31	376	656	280
Up	1x	547	121	3.7 (5)	0.60	310	785	475
	10x	552*	114	3.7 (6)	0.71	329	776	447
Down	1x	489	99	5.6 (4)	0.23	294	683	389
	10x	493*	95	2.3 (4)	0.68	306	680	374
Saturation Coefficient SAT [°] SACPEAK = $V_{\max} \times (1 - e^{-\text{SACSIZE}/\text{SAT}})$ n=116								
Direction	Spline	Mean	σ	χ^2 (df)	P	SAT @ $P = .025$	SAT @ $P = .975$	95% C.I.
Right	1x	9.6	2.0	6.9 (4)	0.14	5.6	13.5	7.9
	10x	8.7**	1.9	7.6 (5)	0.18	5.1	12.4	7.3
Left	1x	9.6	1.7	8.6 (4)	0.07	6.3	13.0	6.7
	10x	8.8**	1.7	11.9 (4)	0.02	5.5	12.1	6.6
Up	1x	10.6	2.9	11.0 (5)	0.05	4.9	16.3	11.4
	10x	9.7**	2.6	6.4 (4)	0.17	4.6	14.8	10.2
Down	1x	9.6	2.6	9.8 (5)	0.08	4.5	14.7	10.2
	10x	8.9**	2.4	8.4 (5)	0.14	4.2	13.6	9.4

$V_{\max}$ and SAT of SACPEAK = $V_{\max} \times (1 - e^{-\text{SACSIZE}/\text{SAT}})$ normal distribution parameters.

Direction = saccadic direction; Spline = cubic spline used on the position trace. 1x: no interpolation; 10x: 10 points interpolation; Mean = mean value (normal distribution) and σ : standard deviation (normal distribution); χ^2 (df) = χ^2 value and degrees of freedom of the χ^2 test of normality; P : probability of the χ^2 test of normality; @ $P = .025$ and @ $P = .975$ = estimate of the parameter at $P = .025$ and $P = .975$ of the normal distribution model; 95% C.I. = 95% confidence interval of the normal distribution model, defined as the parameter estimate @ $P = .975$ minus the parameter estimate @ $P = .025$

Table 2.

Parameters of the normal distribution models of the $V_{\max}$ - $V_{\max\text{est}}$ values for the 116×4 data sets in Figure 6. Identical layout of Table 1.

$V_{\max} - V_{\max\text{est}}$ [°/s] n=116							
Direction	Mean	σ	χ^2 (df)	P	@ $P = .025$	@ $P = .975$	95% C.I.
Right	-0.4	32.9	4.6 (6)	0.60	-64.8	64.1	128.9
Left	2.0	32.5	14.0 (6)	0.03	-61.6	65.7	127.3
Up	0.6	56.6	9.8 (6)	0.13	-110.3	111.5	221.8
Down	-0.6	49.8	3.7 (5)	0.60	-98.2	97.0	195.2

$V_{\max\text{est}}$ and SAT of SACPEAK = $V_{\max\text{est}} \times (1 - e^{-\text{SACSIZE}/\text{SAT}})$ normal distribution parameters.

Direction = saccadic direction; Mean = mean value (normal distribution) and σ : standard deviation (normal distribution); χ^2 (df) = χ^2 value and degrees of freedom of the χ^2 test of normality; P : probability of the χ^2 test of normality; @ $P = .025$ and @ $P = .975$ = estimate of the parameter at $P = .025$ and $P = .975$ of the normal distribution model; 95% C.I. = 95% confidence interval of the normal distribution model, defined as the parameter estimate @ $P = .975$ minus the parameter estimate @ $P = .025$.

Table 3.

SACPEAK sample values of the models in Figure 12. For each direction, the table reports the peak velocity values at SACSIZES 5°, 10°, 15°, 20°, 25°, and 30° for the main sequence models associated with the $P = .025$ ($V_{\max}$; SAT) pair, the mean pair, and the $P = .975$ pair from Table 1. The relative % changes (%) with respect to the correspondent $V_{\max}$, SAT and SACPEAK value of the mean pair are reported in bold.

Actual Variation of SACPEAK Values Inside the 95% Confidence Intervals of $V_{\max}$ and SAT from Table 1									
Direction	$V_{\max}$ (%) [°/s]	SAT (%) [°]	SACPEAK @5° (%) [°/s]	SACPEAK @10° (%) [°/s]	SACPEAK @15° (%) [°/s]	SACPEAK @20° (%) [°/s]	SACPEAK @25° (%) [°/s]	SACPEAK @30° (%) [°/s]	
Right	361 (-30)	5.6 (-42)	213 (+1.9)	300 (-10)	336 (-17)	351 (-22)	357 (-25)	359 (-27)	
	514	9.6	209	333	406	450	476	491	
	666 (+30)	13.5 (+41)	206 (-1.4)	348 (+4.5)	447 (+10)	515 (+14)	561 (+18)	594 (+21)	
Left	375 (-27)	6.3 (-34)	205 (-1.9)	298 (-11)	340 (-17)	359 (-21)	368 (-23)	372 (-25)	
	516	9.6	209	334	408	452	478	493	
	656 (+27)	13.0 (+35)	209 (0.0)	352 (+5.4)	449 (+10)	515 (+14)	560 (+17)	591 (+20)	
Up	310 (-43)	4.9 (-54)	198 (-3.9)	270 (-19)	295 (-29)	305 (-34)	308 (-38)	309 (-40)	
	547	10.6	206	334	414	464	495	515	
	785 (+44)	16.3 (+54)	207 (+0.0)	360 (+7.8)	472 (+14)	555 (+20)	616 (+24)	660 (+28)	
Down	294 (-40)	4.5 (-53)	197 (-0.0)	262 (-17)	284 (-27)	291 (-32)	293 (-35)	294 (-37)	
	489	9.6	199	316	387	428	453	467	
	683 (+40)	14.7 (+53)	197 (0.0)	337 (+6.6)	437 (+13)	508 (+19)	558 (+23)	594 (+27)	

Direction = saccadic direction

$V_{\max}$ and SAT of the main sequence (used in Figure 12)

SACPEAK values estimated from $SACPEAK = V_{\max} \times (1 - e^{-SACSIZES/SAT})$ for SACSIZES = 5, 10, 15, 20, 25 and 30°.

The value in bold is the relative change with respect to the value from the main sequence associated with the mean pair, which has no entry, being the variation, by definition, zero.