

Precision medicine and Dynamic Treatment Regimes

Personalized medicine, that is the specific tailoring of disease treatment to a patient according to their individual characteristics, is somewhat an obvious notion, and dates back through the history of medicine.^{51,52} Indeed, R. Murugan, writing in the *Lancet Respiratory Medicine*, refers to Hippocrates as a 'proponent of personalized medicine', who 'assessed several factors, such as a patient's constitution, age, and build, and the time of year to help his decision-making when prescribing treatment.'⁵² The covariates of age, gender and race are clear contenders for important personalized medicine factors, well-known to be related to treatment outcomes, and are often included in subgroup and regression analyses.^{53,54} In many fields, such as oncology, a decision whether to prolong treatment or not may depend on a patient's current quality of life.⁵⁵ In short we are used to the idea of personalizing medical decisions.

Similarly the idea that chronic treatment should take into account the on-going patient response is certainly not new. On the one hand, if a disease is cured, treatment should likely cease. On the other, if a patient fails to respond to a first line treatment, often the decision is made to switch to a second or third. Examples include treatment of diseases with antibiotic resistant strains, such as tuberculosis, and treatment of cancers when a line of chemotherapy does not reduce a tumor.^{56,57}

What is a fairly recent idea however, is that in the age of big data, high performance computing, artificial intelligence and machine-learning, the opportunity to tailor treatment to the individual algorithmically now exists.^{18,19} To distinguish the notion of using precise algorithmic, formulaic and somewhat

mathematical rules of how a patient should be treated, often factoring in advanced measurements and variables such as those involving genomics and proteomics, from the basic notion that each patient should be treated as an individual, the term precision-medicine is often used.⁵⁸ And with the advance of computing and technology, the opportunity for precision-medicine is blossoming.²⁰

In the statistical literature precision-medicine rules/algorithms to treat each individual patient are often referred to as either individualized treatment rules, emphasizing the dependence on individual patient characteristics, or else either adaptive treatment strategies, or dynamic treatment regimes, emphasizing the dependence on patient response to on-going treatment.^{59,60} In this article we just use the designation of dynamic treatment regime (DTR) to denote these concepts.

The precise notion of a dynamic treatment rule that is then optimal for the population, may be formulated as follows:

First consider the problem of deciding on a one-off treatment for a patient, where N treatment options exist. We notate the treatment option a patient is given by T , and then we assume $T=1,\dots,N$. For each patient we have an outcome Y , a (one-dimensional) measure of the success of treatment - we assume a convention that higher values of Y correspond to more successful treatment, and thus are preferable. We denote the i^{th} patient's potential outcome were they to be given treatment T as $Y^*_i(T)$. Assume now that the clinicians have collected information X from each patient (X may be a vector including many different covariates), which they believe provide potentially predictive information as to the results of treatment T for the patient. Then to the clinicians' best knowledge, the i^{th} patient with potential outcome $Y^*_i(T)$, may be predicted to have an expected outcome of $E[Y^*(T)|X_i]$, where the random variable $Y^*(T)$ is the potential outcome for a given

treatment, over patients sampled from the appropriate population. That is, conditional on the treatment and patients' particular covariates X_i , we cannot distinguish patients' outcomes. The clinicians' task then becomes for each patient, choose T to maximize the expected outcome $E[Y^*(T)|X]$. We will term this T as the optimal treatment choice.

We note that this is of course not the sole definition of the optimal treatment. For example, perhaps the optimal treatment might reasonably be defined to be the one which gives the highest median, not mean, outcome over the population.⁶¹ Or perhaps we may want to consider a multidimensional Y , which contains different (possibly competing) outcome measures.^{62,63} Or perhaps we might want to balance the success of treatment with its cost, regarding a small increase in success not worthwhile if it is accompanied by a dramatic rise in treatment cost.⁶⁴ Such extensions have been considered. However defining the optimal treatment as simply that which maximizes the mean outcome is perhaps the most interpretable definition, perhaps the definition most amenable to analysis, and certainly the most prevalent definition in the precision-medicine literature.

So the task of assigning an optimal treatment, that is maximizing the expected outcome $E[Y^*(T)|X]$, becomes essentially bound up with the problem of estimating how $E[Y^*(T)|X]$ varies with X for a given T , that is with estimating the function $E[Y^*(T)|X]=f(X,T)$. One obvious way of doing this would be to posit and solve a regression model for Y^* in terms of X and T , for which standard and well-practiced techniques and methods may be used. However other methods are certainly available. The fact that we often might require the covariate space X to be high-dimensional could cause problems with the modeling. To ameliorate this problem we might turn to machine-learning methods to assist with the regression.^{65,66,67} Alternatively, other techniques may be used. For example, instead of regarding the problem as a

regression where the treatment outcome must be estimated, it might be regarded as a classification problem, where each patient is classified by their personal optimal treatment group. In this way the problem of estimating the outcome $Y^*(T|X)$ is circumvented. Outcome-weighted-learning is a technique of this type, which employs the support vector machinery to give decent performance with a higher dimensional covariate space.^{68,69} In short, there are a large number of methods to estimate the optimal treatment, and these topics are a very active area of biostatistical research.^{34,29,33,35}

The situation becomes more elaborate when there are a number of treatment decisions to be made. We may model this situation as having a (discrete) number, M , of timepoints t_1, t_2, \dots, t_M , and at timepoint t_j , we have treatment options $T_j=1, \dots, N_j$ (where $T_j=1$ might represent an entirely different treatment from $T_i=1$ if $i \neq j$). Again we consider maximizing an ultimate hypothetical outcome $Y^*(T_1, \dots, T_M|X)$, which is now dependent on each of the M treatment choices, and again conditional on patient covariates X . However the situation is different from the single treatment circumstance above, in that it is complicated by the fact that the covariate space X may include not only time varying coefficients that may be changing between timepoints, but also measured response to treatments already given. The problem is often stated as to repeatedly select treatment at each subsequent timepoint to maximize the patients ultimate outcome as a function of treatment at that timepoint $Y^*(T_j|X(j))$, where the patient covariates $X(j)$ at timepoint t_j now include the patient history of all measured covariates, from timepoints t_1 to t_j , including the previous treatments assigned at timepoints t_1, \dots, t_{j-1} .

As before this may be regarded as a sequence of regression problems, positing models for $Y^*(T_j|X(j))$ in terms of $X(j)$, and then choosing T_j at each timepoint t_j to maximize the patient's expected final outcome, measuring results at timepoint

t_{j+1} , and selecting a next hoped for optimal treatment until the patient finishes treatment at timepoint t_M . However we now have the problem of low power, that is if there are many treatment options at a number of timepoints, the total number of treatment combinations may be very large. Hence, the number of patients we observe at each timepoint on each treatment path may be very low and not sufficient to estimate the regression parameters accurately.

Q-learning is one work around for this issue of low power when there are many potential treatment sequences.^{29,33,34,35} This compensates for a low number of samples of each treatment path by estimating the optimal outcome achievable for each particular patient at a timepoint, and then (theoretically) reassigning them so that the optimal treatment path has a significant number of patients on it. More specifically, Q-learning begins by looking at the last timepoint M and regressing to find the optimal treatment T_M^* , and predicted optimal outcome $Y^*(T_M|X(M))$, for each patient dependent on their covariates and history. Then it pretends each patient in fact received the best treatment possible at timepoint t_M , replacing the actual outcome of the patient $Y(T_M)$ with the estimated $E[Y^*(T_M^*|X(M))]$. In this way it estimates for each patient at timepoint t_{M-1} the optimal expected outcome *if* the best treatment had been given at the subsequent timepoints (in this case only one final stage). This is termed the Q-function. Then the optimal final expected outcomes of patients currently at timepoint t_{M-1} can be regressed as a function of T_{M-1} and $X(M-1)$, and then the best treatment for each patient at timepoint t_{M-1} may be estimated, along with corresponding outcome. The Q-function is updated to represent the optimal final expected outcome of the patients as a function of $X(M-2)$ and T_{M-2} assuming the optimal treatments are then given subsequently. Again the optimal T_{M-2} is chosen and this recursive choice of best onwards treatment and updating of the optimal final expected outcome is repeated, moving back through all the stages, until the best treatment T_1 at timepoint t_1 is estimated. At this point the optimal treatment sequence for each patient, and the optimal expected outcome

if this best treatment regime is adhered to, has been estimated, and each of the solved regressions provides a decision rule for how to assign optimal treatment to a new patient at each stage. In effect we have found the optimal dynamic treatment rule.^{29,33,34,35}

Other machine-learning methods instead of Q-learning may be applied. Outcome-weighted-learning has extensions for example that also attempt to combat the low power due to the possible large number of treatment options, such as backwards-outcome-weighted-learning and simultaneous-outcome-weighted-learning.^{68,69} Again the various possible methods for finding dynamic treatment regimes and their pros and cons are a subject of very active biostatistical research.^{29,33,34,35}

One major statistical issue with the estimation of dynamic treatment regimes is that few of the methods have satisfactory inference methods. That is, while the optimal dynamic treatment regime may be estimated, the results of following this and, importantly, how close this estimate is (in some sense) to the true optimal treatment regime are very non-trivial to estimate.^{70,71} Progress continues to be made on this subject.^{72,73}

SMART Studies and Dynamic Treatment Regimes

To calculate dynamic treatment regimes, whether by a regression based method of estimating $E[Y^*(T_j) | X(j)]$ at a given timepoint j , as essentially required in Q-learning, or whether by classifying patients into groups corresponding to their optimal treatment, as required in outcome-weighted-learning, will require high

quality data, detailing measurements of outcomes and relevant covariates at each timepoint.

Observational data may certainly be used to calculate dynamic treatment regimes, however certain assumptions are necessary.^{33,74} We must make the consistency assumption, which states the actual outcome Y for each patient (and the covariates $X(j)$) observed at each timepoint t_j is indeed the potential outcome for that treatment sequence (that is $Y_i=Y_i^*(T)$ when the i^{th} patient does receive treatment T).⁷⁵ We must make the stable unit treatment value assumption, which states that a patient's outcomes and covariates are not affected by how treatment is assigned to them (or assigned to the other patients).⁷⁶ And we must make the assumption of no unmeasured confounders, essentially an assumption that treatment assignment is independent of any unmeasured patient covariates.⁷⁵

The important assumption of no unmeasured confounders is unverifiable from observational data.⁷⁷ However if treatment is assigned at random (conditional on measured covariates $X(j)$ at timepoint t_j) it is automatically met.³⁴ Hence one proposed method for generating data amenable to calculate dynamic treatment regimes is the Sequential Multiple Assignment Randomized Trial (SMART).^{25,28}

In a SMART, patients may be re-randomized to different treatments at subsequent timepoints, with the randomization options and possibilities based on patient characteristics, including previous treatments received and response to them.^{28,29} In this way, the investigator hopes that enough relevant treatment combinations are explored over time so that the statistical analysis may pick out salient features influencing outcome, and from this predict how future patients should be treated to maximize each patient's expected individual outcome.

It may be argued that a SMART study may be more realistic than a classical clinical trial (where patients are randomized independent of response), as it permits non-responders to be switched to a different treatment, as often rightly happens in real-life clinical decisions.^{59,78} Nevertheless, there are perhaps inherent difficulties in the implementation (and more so in the associated analyses as discussed above) of a SMART beyond those for classical clinical trials. Increased efforts may need to be made to collect, and process, large enough amounts of data to hope to data-mine dynamic treatment regimes with enough precision, and the possible large number of treatment paths may give requirements for extra and unfamiliar administration and logistics, particularly if treatment re-randomization depends on real time patient responses.

One major issue with the design and implementation of a SMART is that the lack of inference methods regarding the estimation of optimal treatment regimes means powering a SMART for the sole purpose of estimating these is difficult.⁷³ While theoretical progress on the problem continues to be made, one way around this is to explore the performance through simulation studies. Another simple solution is to power the SMART to perform a classical analysis for a question of interest, such as treatment of embedded fixed non-dynamic treatment regime (or even a pre-chosen dynamic treatment regime).^{28,48,17} In the LIBERTI trial we show how this may be done, where the ultimate question of interest is establishing whether there are treatment effects.

Thus SMART studies and their designs, protocols, and analyses may tend to be more complicated than classic randomized clinical trials, and this means extra care may need to be taken in detailing, presenting and explaining these to the appropriate

stakeholders. These issues notwithstanding, SMART studies have already been very usefully employed in many areas, with researchers in psychiatry, oncology and behavioral medicine in particular exploring their advantages and benefits.^{79, 80, 81, 82, 83, 84, 34}

Short-Term Effect Statistical Modeling/Power Calculations

We study the short-term effect using the change in Vancouver Scar Score at four months and testing three hypotheses regarding the short-term effect. Denoting the change in patient Vancouver Scar Score at four months after treatment with CO₂ laser, pulsed-dye laser and just medical therapy as V_{CO_2} , V_{PDL} , V_{MED} respectively, we may rewrite the short-term null hypotheses as:

Short-Term Null Hypothesis 1: $E[V_{PDL}] = E[V_{MED}]$.

Short-Term Null Hypothesis 2: $E[V_{CO_2}] = E[V_{MED}]$.

Short-Term Null Hypothesis 3: $E[V_{CO_2}] = E[V_{PDL}]$.

We will test the short-term hypotheses, using 2-sided t-tests and (a Hochberg modification of) the Bonferroni multiple comparison procedure, with an overall Type I error rate of 5%.^{45, 85} We will reject any of the short-term hypotheses with 80% power, at overall size 5%, adjusting for multiple comparisons, if there is an effect size of more than 0.63 standardized units (using standard t-test theory). Pilot studies suggest that we then have an 80% power of observing a minimal clinically significant difference of 0.9 Vancouver Scar Score units in treatment

effect.

Long-Term Effect Statistical Modeling/Power Calculations

Our proposed comparison of the long-term (two-year) change in Vancouver Scar Score between sequences of three treatment blocks is less standard than the simple short-term (four-month) change examination. We study the long-term effect using the change in Vancouver Scar Score at twenty-four months and testing two hypotheses regarding the long-term effect. Due to the large number of possible treatment combinations possible over the twenty-four month period, and the need to isolate the effects of differing laser treatments from each other, we must set-up a non-trivial regression model and structure tests carefully.

Specifically, we propose a regression model applied to the treatment effects in each of the blocks. We denote a treatment sequence by a triplet (i, j, k) with each of i, j, k corresponding to (randomized) treatment in the first, second and third block, respectively, and being set to 0, 1, or 2, to represent solely non-surgical medical therapy, CO₂ laser, and pulsed-dye laser, respectively. We let the change in Vancouver Scar Score over the study for any given participant on treatment sequence (i, j, k) be denoted by $z_{i, j, k}$. We model the change in scar score by a normal variable, with a global constant variance, as:

$$z_{i, j, k} \sim N(\mu_{i, j, k}, \sigma^2), \quad E[z_{i, j, k}] = \mu_{i, j, k} = \mu + \alpha_{1, i} + \alpha_{2, j} + \alpha_{3, k} + \beta_{i, j} + \gamma_{i, k},$$

subject to the constraints:

$$\sum_i \alpha_{x,i}=0, \sum_x \alpha_{x,i}=0, \sum_j \beta_{p,j}=0, \sum_i \beta_{i,q}=0, \sum_a \beta_{a,a}=0, \sum_k \gamma_{q,k}=0, \sum_j \gamma_{j,r}=0, \sum_a \gamma_{a,a}=0.$$

This model we propose seems clinically reasonable; for example it contains the 'usual' regression model of non-temporal effects and two-way interactions between first and second treatments and also between second and third treatments. The imposed constraints should force the model to identify 'better' and 'worse' treatment options at a given timepoint, as well as 'better' and 'worse' treatment interactions between treatments in the first and second blocks and also between treatments in the second and third blocks. This identification will simply correspond to the signs of the $\alpha_{x,p}$, $\beta_{i,j}$, $\gamma_{j,k}$ respectively. Focusing on the identification of 'better' and 'worse' treatments rather than exact estimation of average treatment group outcomes and effects will potentially give us increased power to determine whether or not there is a laser effect, and subsequently whether or not there is a difference in effect between lasers.

Our mean model has in total 28 parameters, allowing for all values i, j , and k (including those corresponding to unobserved treatment groups). However, the constraints ensure we have only eleven free parameters. As we have twelve overall treatment groups, only one more treatment group than free parameters, we cannot significantly relax the model further, and the requirement to have our given constraints is somewhat unavoidable (in particular a three-way interaction term must be omitted).

We may interpret these parameters as follows: μ is the grand mean, $\alpha_{x,p}$ represents the main order effect of having treatment p at timepoint x , $\beta_{p,q}$ represents the interactive effect of treatment p at the first timepoint and treatment q at the

second, and $\gamma_{p,q}$ represents the interactive effect of treatment p at the second timepoint and treatment q at the third.

We note $\mu + \alpha_{x,w}$ corresponds to the expected outcome for participants assigned treatment w at timepoint x and randomized at other timepoints equally between treatments. Other more elaborate interpretations may similarly be given. Thus if, for example, $\alpha_{x,u} - \alpha_{x,0} \geq q$, we have an interpretation that there is a treatment, u , with an average outcome different from the current standard by more than q .

Regarding this SMART trial as a subset of experimental runs of a full 3^3 factorial trial,^{17,31,32} the $\alpha_{x,w}$ have a nice interpretation as the main treatment effects and indeed $\mu + \alpha_{x,w}$ are then marginal effects in the sense that they average the treatment effects of specifying treatment in one block, or factor, over the levels of the remaining two factors.

Under the null hypothesis of no laser effect, the model is certainly true, and all parameters except μ are 0, in particular all the $\alpha_{x,i}$ must be 0. Further if there is no difference between the effect of CO₂ and pulsed-dye laser, the standard regression estimators of the coefficients must yield $\alpha_{x,1} = \alpha_{x,2}$ for each timepoint x . Testing $\alpha_{x,i}$ to determine if they obey these relationships is then a valid test of the long-term null hypotheses. Focusing on determining whether there is a laser effect using just the $\alpha_{x,w}$, not all the coefficients in the model, should hopefully increase the power by reducing the degrees of freedom in the tests. We may write (relaxations of) our long-term hypotheses then as:

Long-Term Null Hypothesis 1: (No laser effect) $\alpha_{1,0} = \alpha_{2,0} = \alpha_{3,0} = 0$.

Long-Term Null Hypothesis 2: (No difference in lasers) $\alpha_{1,1}-\alpha_{1,2}=\alpha_{2,1}-\alpha_{2,2}=\alpha_{3,1}-\alpha_{3,2}=0$.

For testing both these long-term null hypotheses, we may then use this regression model and $F(2,157)$ -tests with Type I errors of 5%. We regard the more important determination in the investigation of long-term effects to simply be whether there is any laser effect (that is testing Long-Term Null Hypothesis 1), as opposed to whether there is a difference between effects corresponding to different types of laser (that is testing Long-Term Null Hypothesis 2). Therefore to maximize power when we examine the more important aspect, we use step-down testing, first testing Long-Term Null Hypothesis 1, and only if this is rejected testing Long-Term Null Hypothesis 2. Step-down testing will preserve an overall total Type I error rate of 5%.^{46,47,86}

The sample size will give good power to reject the long-term null hypotheses (according to standard linear model theory). The precise conditions on the coefficients which match with a particular test power are slightly difficult to interpret. However we may make the following observations:

1: the power of rejecting Long-Term Null Hypotheses 1 is over 80%, if choosing solely non-surgical medical therapy at a particular timepoint, and assigning random treatment at the other timepoints, results in an outcome difference of more than 0.35 standardized units in comparison to simply randomly assigning treatment at all timepoints.

2: the power of rejecting Long-Term Null Hypotheses 2 (if Long-Term Null Hypotheses 1 is rejected) is over 80%, if choosing CO₂ laser therapy at a particular

timepoint, and assigning random treatment at the other timepoints, results in an outcome difference of more than 0.37 standardized units in comparison to assigning pulsed-dye laser therapy at the given timepoint then assigning random treatment at the remaining two timepoints.

More involved power estimates and their corresponding clinical interpretations convince us that we have more than sufficient power. We therefore believe this is a powerful and effective model to compare the overall population effects of the twelve sequences, with the focus being more to identify better and worse options than to precisely extrapolate other unobserved treatment sequences or effects. The model also seems statistically reasonable and it appears to have very good power for rejecting our hypotheses, despite having comparatively large degrees of freedom (as is needed to realistically model the effects of twelve treatment sequences).

Precision Medicine Dynamic Treatment Statistical Modeling/Power Calculations

We intend to analyze optimal patient individualized dynamic treatment regimes using machine-learning techniques involving Q-learning^{23,87,34} and Outcome-Weighted-Learning.^{68,69} We will then contrast this with the estimated effects of a population-level treatment regime, hence obtaining insights into possible benefits of personalizing treatment, or otherwise, in this field.

Accurate estimation of individualized dynamic treatment regimes is the Holy Grail of the research (providing answers automatically to the other hypotheses) but is also expected to be the most challenging, due to the complicated estimations that

will need to be performed.

We will not specify the precise analysis we will use, for we expect significant advances in the precision-medicine methodology whilst the study is underway, and we intend to take advantage of these. We do intend our first exploration to be with the Q-learning framework,³⁴ and we will also explore the use of the simultaneous-outcome-weighted-learning framework.^{68,69}

Explicit sample size calculations are not possible in any straightforward manner for applying Q-learning or outcome-weighted-learning to the data from LIBERTI. However the sample size of 180 (including 10% inflation to allow for dropout) is predicted to be sufficient to provide good insights into an individualized dynamic treatment regime. More specifically, we expect to find a superior personalized treatment (with results within approximately 90% of the true optimal treatment) with probability at least 80%, based on published simulation results for similar studies.⁵⁰

Simulation Studies

The modeling and power calculations we detailed for testing the short-term hypotheses are standard and straightforward. However those for testing the long-term hypotheses are less so, therefore for further reassurance we should explore somewhat the performance of our procedure through simulation studies. As explained, modeling and power calculations for a precision-medicine dynamic treatment regime is extremely difficult, and simulations should definitely be used to evaluate the

feasibility of estimating these from data generated by the LIBERTI trial.

Simulations suggest that our models and analysis will on the one hand have very good power to detect a laser effect, and on the other be likely to construct a beneficial dynamic treatment regime for patients. We present two of our simulations below for illustration.

To demonstrate possible performance of the regression model to detect laser effect on a two-year outcome, we take a somewhat Bayesian stance. We simply model the two-year mean expected change in Vancouver Scar Score for each of the twelve treatment sequences as random independent samples from a normal distribution with mean 0 and variance hyperparameter σ_μ^2 . That is we model $\mu_{i,j,k} \sim N(0, \sigma_\mu^2)$ for each of the twelve sequences (i, j, k) to be observed. We then model 168 patients, equally distributed between these twelve treatment sequences, who have a two-year change in Vancouver Score Scar given by independent samples from $z_{i,j,k} \sim N(\mu_{i,j,k}, \sigma^2)$, where $z_{i,j,k}$ is the outcome for a given participant on treatment path (i, j, k) . As no relation is assumed between similar treatment paths (eg. knowing the results of even an apparently close treatment path imparts nothing at all about the results of another) this is a worst case scenario for our regression model, which benefits when there are predictable main effects and treatment interactions.

We apply the regression model to our simulated data and determine the power as a function of σ_μ/σ . The corresponding power curves for rejecting Long-Term Null Hypothesis 1, (no treatment effect), and for rejecting both firstly Long-Term Null Hypothesis 1, and then subsequently Long-Term Null Hypothesis 2 (no difference between types of lasers) are shown in Figure 2. It appears we have good power in these circumstances, with the power becoming acceptable when the variance between

the expected mean outcomes of the treatment paths means, σ_{μ}^2 , approaches that of the variance of actual patients on each path, σ^2 . This can be regarded as an appropriate minimal clinically significant difference we would want to detect in this scenario.

Next we also simulate two tailoring variables for each patient (which in this set-up have no effect whatsoever on patient outcome, but just add challenging noise to the estimation of dynamic treatment regimes). We use basic Q-learning (approximating the Q-functions by linear regressions in tailoring variables, current treatment and interactions of current treatment and tailoring variable) to determine a dynamic treatment regime. The precise process is detailed further below in the details for the second main simulation. A further 1680 patients are simulated and treated according to this dynamic treatment regime. Figure 3 shows the results of the experiment. We might expect Q-learning to do very little in this scenario, as there is no structure to exploit between the treatment outcomes. We observe that while the dynamic treatment regime does not always produce a particularly good outcome (for example not infrequently the expected patient benefit under the dynamic treatment regime is above 0), it is reassuringly almost always superior to randomly assigned treatment (even though the Q-functions are extremely misspecified).

To explore the effects of Q-learning in a more realistic set-up, we explore various models for the laser effect. For example we may model percentage change in scar score from one stage to the next as a log-normal variable with mean dependent on current scar score, and a binary time-independent variable representing race, with the added mechanism that the scar score may not increase by more than some percentage randomly assigned to each patient. We may choose coefficients to represent pilot data somewhat, and we may build in certain rules such as: a time

varying effect with treatment in block 2 leading to greatest change, a race effect, such as one laser has no effect on one race, a scar score interaction effect such that one laser is likely beneficial for higher scar scores, but detrimental for lower scar scores, and complex interaction effects such as the effect of laser two being multiplied by the number of treatments of laser one received.

Precisely, we present a simulation where Vancouver Scar Score (VSS) changes throughout treatment according to the following rules:

Patients have tailoring variables of: (Race), which we simulate as binary, and VSS before each treatment is received. We denoted VSS after the i^{th} treatment block is received as $(VSS)_i$ for $0 \leq i \leq 3$. That is $(VSS)_0$ is patient initial VSS before treatment, $(VSS)_1$, that after the first treatment block, $(VSS)_2$ that after the second, and $(VSS)_3$ that after the third and final treatment. We assume no further improvement from the results of the final treatment to the longer-term Vancouver Scar Score at the two-year mark.

Our population is initially simulated by generating 168 patients, with (Race) distributed binomially with $p=0.5$, and $(VSS)_0 \sim \min(N(10.2, 1), 13)$ a normal with mean 10.2, variance 1, and truncated above at 13.

For each patient, we simulate:

$$(VSS)_1 \sim \min((VSS)_0 \times \exp(N(a, 0.3^2)), 0.800 \times (VSS)_0 + U[0, 0.4], 13),$$

where N is a normal variable with the value of a determined by:

$$a = -0.500(\text{PDL1})(\text{Race}) - 0.500((VSS)_0 - 6)(\text{CDL1})(1 - 5(\text{Race})/6)$$

with $PDL1=1$ if pulsed-dye laser is assigned in treatment block 1, 0 otherwise, and $CDL1=1$ if CO_2 laser is assigned in treatment block 1, 0 otherwise, and U is a uniform random variable.

Next, we simulate:

$$(VSS)_2 \sim \min((VSS)_1 \times \exp(N(b, 0.15^2)), 0.800x(VSS)_0 + U[0, 0.3], 13),$$

where b is determined by:

$$b = -0.625(PDL2)(Race) - 0.625((VSS)_1 - 6)(CDL2)(1 + PDL1)(1 - 5(Race)/6)$$

and now $PDL2=1$ if pulsed-dye laser is assigned in treatment block 2, 0 otherwise, and $CDL2=1$ if CO_2 laser is assigned in treatment block 2, 0 otherwise.

Finally, we simulate:

$$(VSS)_3 \sim \min((VSS)_2 \times \exp(N(c, 0.15^2)), 0.900x(VSS)_0 + U[0, 0.2], 13),$$

where c is determined by:

$$c = -0.375(PDL3)(Race) - 0.400((VSS)_2 - 6)(CDL3)(1 + PDL1 + PDL2)(1 - 5(Race)/6)$$

and now $PDL3=1$ if pulsed-dye laser is assigned in treatment block 3, 0 otherwise, and $CDL3=1$ if CO_2 laser is assigned in treatment block 3, 0 otherwise.

We repeatedly model the scar score trajectories of 168 patients under such rules, then apply Q-learning to predict an optimal dynamic treatment regime. We use a very

simple model for the Q-functions, that is we approximate them through linear regressions (which then necessarily must be misspecified). More precisely, we choose the outcome for the Q-function at each stage to be $(VSS)_3 - (VSS)_0$, model each Q-function as a normal variable of unspecified variance, and model population means as follows:

$$E[Q_j] = (a_j + b_j(\text{Race}) + c_j(VSS)_{j-1}) + (d_j + e_j(\text{Race}) + f_j(VSS)_{j-1})(PDL(j)) \\ + (g_j + h_j(\text{Race}) + i_j(VSS)_{j-1})(CDL(j))$$

for each $j=1,2,3$. $PDL(j)$ is 1 if the j^{th} treatment is pulsed-dye laser, 0 otherwise, and $CDL(j)$ is 1 if the j^{th} treatment is CO_2 laser, 0 otherwise.

The Q-functions are hence seen to be very misspecified, for example due to modeling $(VSS)_3 - (VSS)_0$ using a normal distribution instead of $\log((VSS)_3 / (VSS)_0)$, due to not allowing for a truncation effect, and due to not explicitly allowing for interactive treatment effects. Nevertheless we solve the corresponding regressions using the data from our 168 patients (assuming that of the original 180 patients 10% dropout), and theoretically reassigning patients to their most beneficial treatment at each stage, then estimate the dynamic treatment regime generated by these Q-functions.

Next we then model the results of applying this dynamic treatment regime to 1680 new patients. Figure 4 shows a plot of simulated final scar score against initial scar score for one simulation run of trial patients, and then new patients following the estimated dynamic treatment regime. It is observable that the dynamic treatment regime appears to weed out less effective or detrimental treatments, and favors better personalized treatments.

Over 100 simulations the average decrease in scar score for the trial patients is 5.6 units, but for the new patients is 7.4 units, roughly a 40% improvement. This, and other simulations, both for the LIBERTI study, and results exploring Q-learning in general, suggest the Q-learning framework may be most beneficial.

We note that the not insignificant performance in these simulations was obtained using even a very crude form of Q-learning, (modeling the Q-functions through linear regressions, with misspecified models for the Q-functions).

We finally also remark how our regression model for examining the long-term null hypotheses would have performed in this second simulation. A laser effect and then subsequently a difference in effect between lasers would be detected, that is both Long-Term Null Hypothesis 1 and Long-Term Null Hypothesis 2 would be rejected in over 80% of these simulations.

Patient Variables/Evaluation

From each patient, data will be gathered in several broad areas including:
Demographic Data, Injury Factors, Treatment Factors, and Study Assessment Factors.

Demographic Data will include routine information such as:

Age, Gender, Ethnicity, Fitzpatrick Type (a measure of skin pigmentation and response to ultra-violet light),⁸⁸ Height, Weight, Body Mass Index (BMI), Medical

Comorbidities, Participant Zip Code, and Alcohol, Tobacco, and/or Recreational Drug Use.

Injury and Treatment Factors related to burn injury will include:

Mechanism of Injury, Total Burn Surface Area (TBSA),⁸⁹ Utilization of Medications Prescribed for Burn Scars (including narcotics, narcotic analogs, non-steroidal anti-inflammatory drugs (NSAIDs), antihistamines, GABA analogs, antidepressants), Time From Injury to Presentation, and Length of Hospital Stay. □

Study Assessment Factors will include: Skin Measurements, Validated Scar Assessment Scales, Quality of Life Metrics, and Photography/Videography Records. □

The study assessment factor category denotes the variables that may be used to determine impact of lasers on hypertrophic burn scars. These variables, measured at baseline and each treatment, may also be important tailoring variables. It is therefore most important that these variables are precisely quantified and measured.

For skin measurements, a representative 1cm² area that best reflects the overall scar pattern will be chosen by the investigator and participant for skin measurement at the participant's first treatment visit. This anchor spot will be photographed and identified on a representative diagram with appropriate measurements to allow for continued tracking throughout the study. A similar area of healthy skin will also be identified at the participant's first treatment visit and measured for purposes of color and elasticity comparison. Two nearby spots that are also representative of the overall scar pattern will also be selected. These

will be 1cm² areas within 5cm of the anchor spot and at least 1cm apart from each other. At each visit a series of measurements will be recorded for the anchor spot and the two nearby spots. Skin measurements will consist of the following:

Elasticity (assessed using a Cutometer® dual MPA 580 (CK Electronics, Cologne, Germany) with an 8 mm spot size),

Color/Hyperemia (assessed using a CR-400 Chromo Meter (Konica Minolta Sensing Americas, Ramsey, NJ) with an 8 mm spot size),

Scar Density/Thickness: (assessed utilizing 2D imaging with a Sonosite M-Turbo (FUJIFILM Sonosite, Inc., Bothell, WA)). □

We will use two validated scar scoring systems to assess the scar, the Vancouver Scar Scale and the Patient and Observer Scar Assessment Scale.^{90,42} We will also record the UNC 5p Scar Scale.³ The VSS is a 14-point scale based on standardized descriptions of pigmentation (0-3), vascularity (0-3), pliability (0-5), and height (0-3). The POSAS is a combined patient and observer scoring system with each part containing six items scored on 10-point scales with standardized descriptions. The clinical observer rates the scar on its vascularity, pigmentation, thickness, relief, and pliability. The patient rates the pain, itching, color, stiffness, thickness, and irregularity of the scar. The UNC 5p consists of a 15-point scale for pruritus (0-3), pain (0-3), paresthesia (0-3), pliability (0-3), and perception (0-3).

To assess overall quality of life, a validated, standardized questionnaire will be used. For adults, this will be the SF-12 Health Survey, which is a modified version of the original SF-36.⁹¹ For children under the age of 18, this will be the

Pediatric Quality of Life Inventory.⁹²

Standardized digital photography will be performed to document the locations of the selected study area and anchor spot. Changes to scar appearance over time will also be documented with photographs. Video will be obtained to document changes in scar characteristics with mobility that cannot be captured with still photography. Photo and video images are for documentation purposes, and for controlling the quality of measurements. They will not be used in the scar assessment scales.

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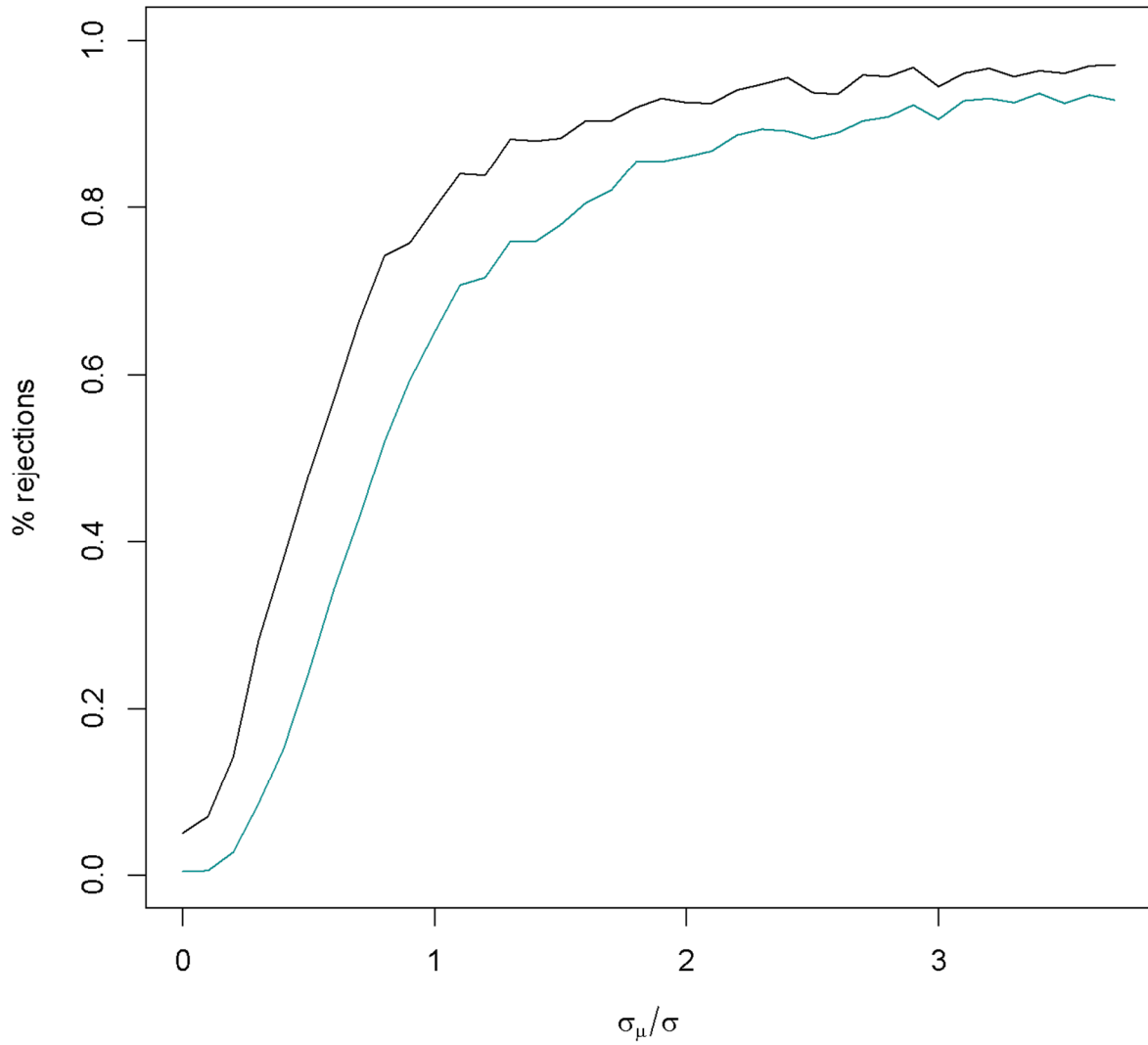


Figure 2: Power curves showing, in black, percentage of times H_{01} was rejected in simulations, and, in blue, percentage of times both firstly H_{01} and then H_{02} was rejected in simulations, as functions of σ_μ/σ .

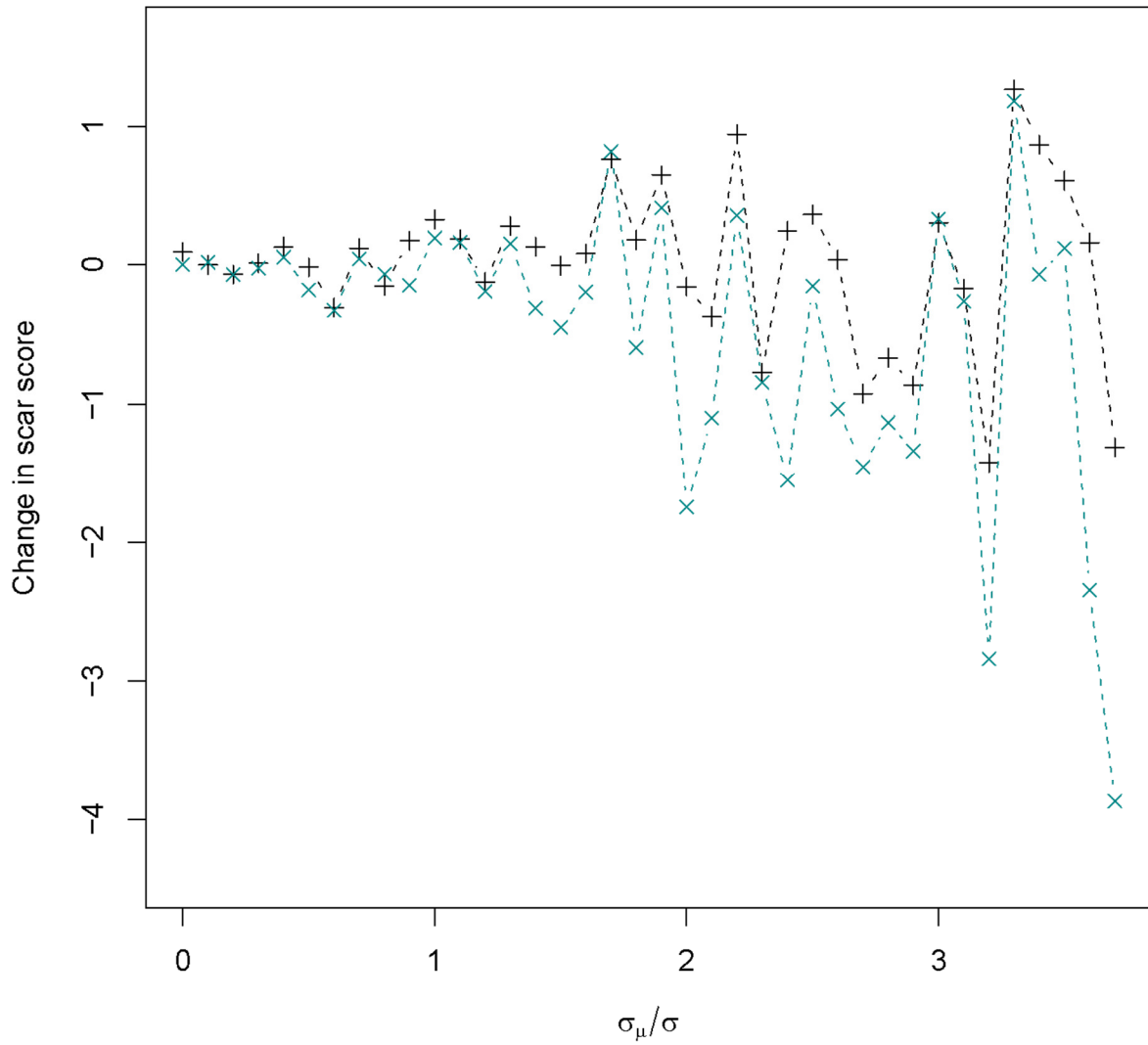


Figure 3: Simulated change of patient scar scores for patients in trial, shown as black '+', and for patients subsequently following the discovered DTR, shown as blue 'x', plotted against σ_μ/σ .

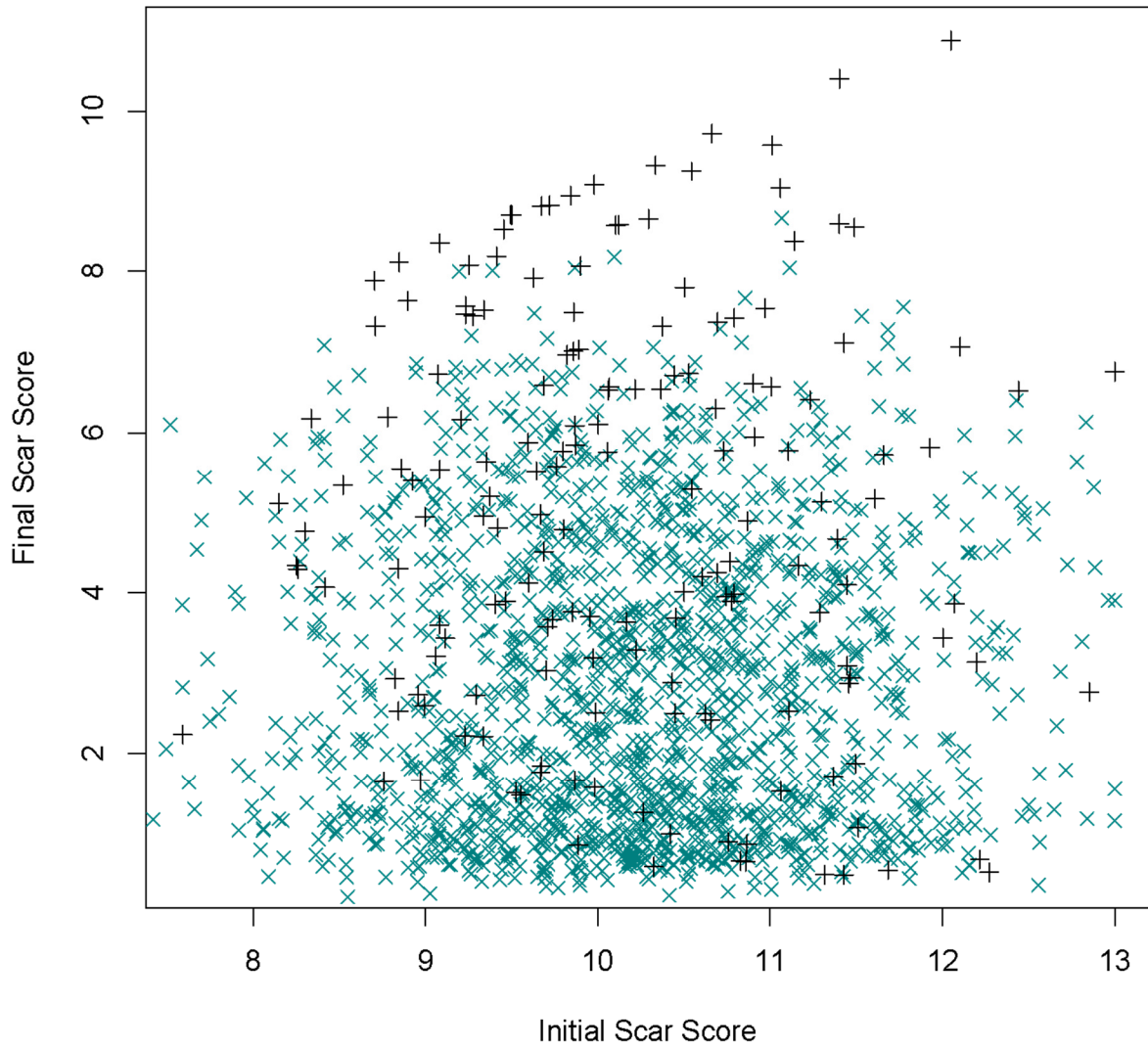


Figure 4: Plot of simulated patient final scar scores against corresponding initial scar scores, for patients in trial, shown as black '+', and for patients subsequently following the discovered DTR, shown as blue 'x'.