**AUGMENTING THE GREEDY METHOD WITH**

**CURRENT-DISPLACEMENT**

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## Definitions

**DNR** = *dose-non-uniformity ratio*, defined as $V_{150,t}/V_{100,t}$

**CN** = *conformation number*, defined as $(V_{100,t}/V_t)(V_{100,t}/V_{100})$

$\mathbf{D}_{X,x}$ = *minimum dose covering X% of tissue x*

$\mathbf{V}_{X,x}$ = *volume of tissue x receiving at least X% of prescibed dose*

## 1 Introduction

The basic idea presented here is one possible approach to use currents, both forward and adjoint, as a means to improve the results given by the Greedy method. Furthermore, another methodology is given using current-displacement as a sole driving force in a Greedy optimization scheme.

## 2 Greedy Heuristic with Dose Update

For the initial investigation, a two-dimensional version of the Greedy method with dose update was implemented. The discrete ordinates code DANTSYS was used to generate the adjoint function for sample target, rectum, urethra, and normal tissue regions. These functions in turn were used to calculate the so-called *adjoint ratio*, defined

$$ratio(i) = \frac{w_r R(i) + w_u U(i) + w_n N(i)}{w_t T(i)} \tag{1}$$

where $R(i)$, $U(i)$, $N(i)$, $T(i)$ are the rectum, urethra, normal, and target adjoint functions at the $i$th location, and the $w$'s are their respective weights.

The adjoint ratio gives to us a means to quantify the dose-to-target relative to tissue-sparing for a radioactive seed placed at a given location. Possible seed positions (confined to the target region and possibly also to a treatment grid) are ranked via their adjoint ratio value in increasing order; in other words, the lower the adjoint value at position $i$, the better a seed placed at $i$ is able simultaneously to impart dose to the target region and to spare healthy tissues. Using this ranking as the *greedy criterion*, seeds can be placed sequentially until a given target dose is reached.

However, to avoid seed clustering, a dose-update is performed to re-rank seed positions. The adjoint ratio is scaled by the current dose profile after each seed placement. In this way, the adjoint ratio in the region about a seed is scaled *up* proportional to that seed's dose; subsequently, open seed positions in that region are (far) less likely to be selected next.

The implementation of this method seemingly works as it should. As has been noted, confining treatment solely to a plane excludes many better configurations possible in a three-dimensional solution space. Therefore, we do not expect various evaluation parameters for this case to match those found for proper three-

dimensional problems in the literature; rather, we shall generate such parameter values for this test case using the aforementioned Greedy method and use those as a benchmark for our cases employing current-displacement.

# 3 Current-displacement as an 'Adjustment'

The initial conception of using current in seed placement was in the context of adjusting a given placement from the Greedy method. In a sense, the Greedy gives to us an initial value from which we can converge toward a better solution using the more detailed information intrinsic to adjoint currents. That is to say, given the adjoint (and forward) current contains angular information and not just a scalar quanitity, it necessarily provides better insight to the physical nature of the problem. Subsequently, it was thought such information could–if used properly–yield better results.

## 3.1 Defining Current-displacement

Using the same DANTSYS models for the tissue regions, the angular flux can be generated from which we may calculate the respective cell-centered adjoint current for each tissue. In this case, the current has only a vertical and horizontal component. A special utility was created to perform such calculations. In addition to tissue adjoint currents, we can also find the *forward* current produced by a simple seed model.

We may sum the sensitive tissue horizontal currents to produce a total horizontal current via

$$J_x^{tot}(i) = J_x^r(i) + J_x^u(i) + J_x^n(i) \tag{2}$$

and doing likewise for the vertical component, we have

$$J_y^{tot}(i) = J_y^r(i) + J_y^u(i) + J_y^n(i) \tag{3}$$

where $J_x^{tot}(i)$ ($J_y^{tot}(i)$) denotes the horizontal (vertical) current at the $i$th location. We can write the current more succintly using the notation

$$\mathbf{J}^{tot}(i) = \hat{x}J_x^{tot}(i) + \hat{y}J_y^{tot}(i). \tag{4}$$

From the Greedy method, we are given an initial seed placement. We may then superimpose onto our total current at each seed location the forward current calculated via the simple seed model.

This gives to us everything we need to calculate the *current displacement* vector. The essential idea is that the currents in the x- and y-directions from the sensitive tissue may act as a *pushing* mechanism used to shift the seeds from their initial placement. However, to avoid seed clustering, we include the forward current from a seed to act on all other seeds. In this way, we define quantitatively the current-displacement for a seed at $i$

$$\mathbf{D}'(i) = a\left(-\mathbf{J}^{tot}(i) + b\sum_{\substack{j=1\\ j\neq i}}^{n}\mathbf{J}^s(i,j)\right) \tag{5}$$

where $\mathbf{J}^s(i,j)$ denotes the two-component current at $i$ from a seed at $j$, $b$ is a constant defining the relative importance of the seed currents to the tissue currents, and $a$ is a constant that converts the summed current magnitudes into a suitable seed displacement value. (The negative before $\mathbf{J}^{tot}(i)$ is included to show explicitly that the tissue currents must be negated to provide a *push*. This is because the adjoint current represents the flow of particles *to* the adjoint source, namely the tissue of interest; here, we want a flow *away* from that source.)

Given that the model investigated has a solution space of resolution 1 mm (or with a grid, 5 mm), the displacement must be an integer. It is assumed simply rounding the displacement will suffice. Hence, the applied displacement for a seed at $i$ is defined

$$\mathbf{D}(i) = \text{round}(\mathbf{D}'(i)) \tag{6}$$

Because the value $a$ is rather arbitrary, it is quite possible to set it such that only some number of seeds is actually displaced.

Preliminary results show that implementing current-displacement in this fashion can lead to better sparing of the sensitive tissues while maintaining proper target dose coverage (typically V100 $\geq$ 98% ). However, still needed are calculations of different dose homogeneity parameters.

### 3.2 Another Approach to Current-displacement

The previous discussion defined the total current-displacement vector $\mathbf{D}$, which when applied has the potential to displace all seeds simultaneously. However, if such a displacement is performed, the directions in which seeds travel might actually lead to a greater need for displacement than initially. While this has not been observed yet, it was also thought performing the all-at-once displacement might not be as *fine-tuned* as an approach focusing on a single seed at a time.

With that in mind, we can find the $L_2$ norm of each seed displacment, which for a seed at $i$ is

$$|D(i)|_2 = \sqrt{D_x(i)^2 + D_y^2(i)} \tag{7}$$

We then rank the seeds by decreasing $|D(i)|_2$ and apply the following algorithm

```
it = 0
```

```
while (V100 <= 0.98 .and. it < max)
   seed(1,1) <-- seed(1,1) + D(1,1)
   seed(1,2) <-- seed(1,2) + D(1,2)
   D <-- calcdisp(D,seed)
   [seed D] <-- rerank(seed,D)
   it <-- it + 1
end
```

where `seed(i,r)` refers to the $i$th seed's $r$th position coordinate. Here, $r = 1$ and $r = 2$ refer to the $x$ and $y$ coordinates, respectively. Similarly, the current-displacement `D(i,d)` refers to the $i$th seed's $d$th current-displacement components, again in the $x$ and $y$ directions for $d = 1$ and $d = 2$. The function `calcdisp(D,seed)` returns the new current-displacement given the updated seed coordinates contained in `seed`. The seeds are subsequently re-ranked, and the algorithm repeats until either the dose requirements are met or the number of iterations reaches a limit.

As of now, this method has not been implemented but will be shortly.

## 4 Current-displacement as the 'Greedy Criterion'

The previous discussion focused on using current-displacement as an adjustment to an initial seed placement generated via the Greedy method. Here, we discuss how current-displacement could be used as the greedy criterion.

Recall from above that the greedy criterion used was the adjoint ratio. In that method, the open seed position having the lowest ratio was selected for the next seed placement. We can establish a similar system using our adjoint currents.

Briefly, such an algorithm would resemble

```
D <-- Dtiss ! where Dtiss is displacement from sensitive tissues
[seed(1,1) seed(1,2)] <-- findmin(D)
D <-- calcdisp(D,seed)
V100 <-- calcdose(seed)
num = 1
while (V100 <= 0.98 .and. num < max)
   num <-- num + 1
   [seed(num,1) seed(num,2)] <-- findmin(D)
   D <-- calcdisp(D,seed)
   V100 <-- calcdose(seed)
end
```

where `seed(i,r)` and `calcdisp(D,seed)` are as above. The function `findmin(D)` returns the coordinates of the open position with the smallest current-displacement value, and the function `calcdose(seed)` calculates the target coverage parameter.

Of course, this is but a crude outline of what the procedure would be. Moreover, it neglects completely the use of the *target* current (only sensitive tissues!). It is not clear yet how the target tissue current would be incorporated. Perhaps as in the adjoint ratio, the target current could be used to 'weight' the sensitive tissue currents, again to establish a quantitative measure of target-coverage relative to tissue-sparing. The simplest approach for this would be to divide elementwise the total sensitive current matrix $J^{tot}$ by the absolute value of the target current, or $|J^{tar}|$. (The absolute value would ensure a simple scaling; if it weren't used, quite likely the sign of $J^{tot}/J^{tar}$ would be constant (probably negative), for when parti-

cles stream *to* the sensitive structures they likely stream *away* from the target.)