



Harmony Search Optimization for HDR Prostate Brachytherapy

Aditya Panchal

Rosalind Franklin University of Medicine and Science

Department of Medical Radiation Physics

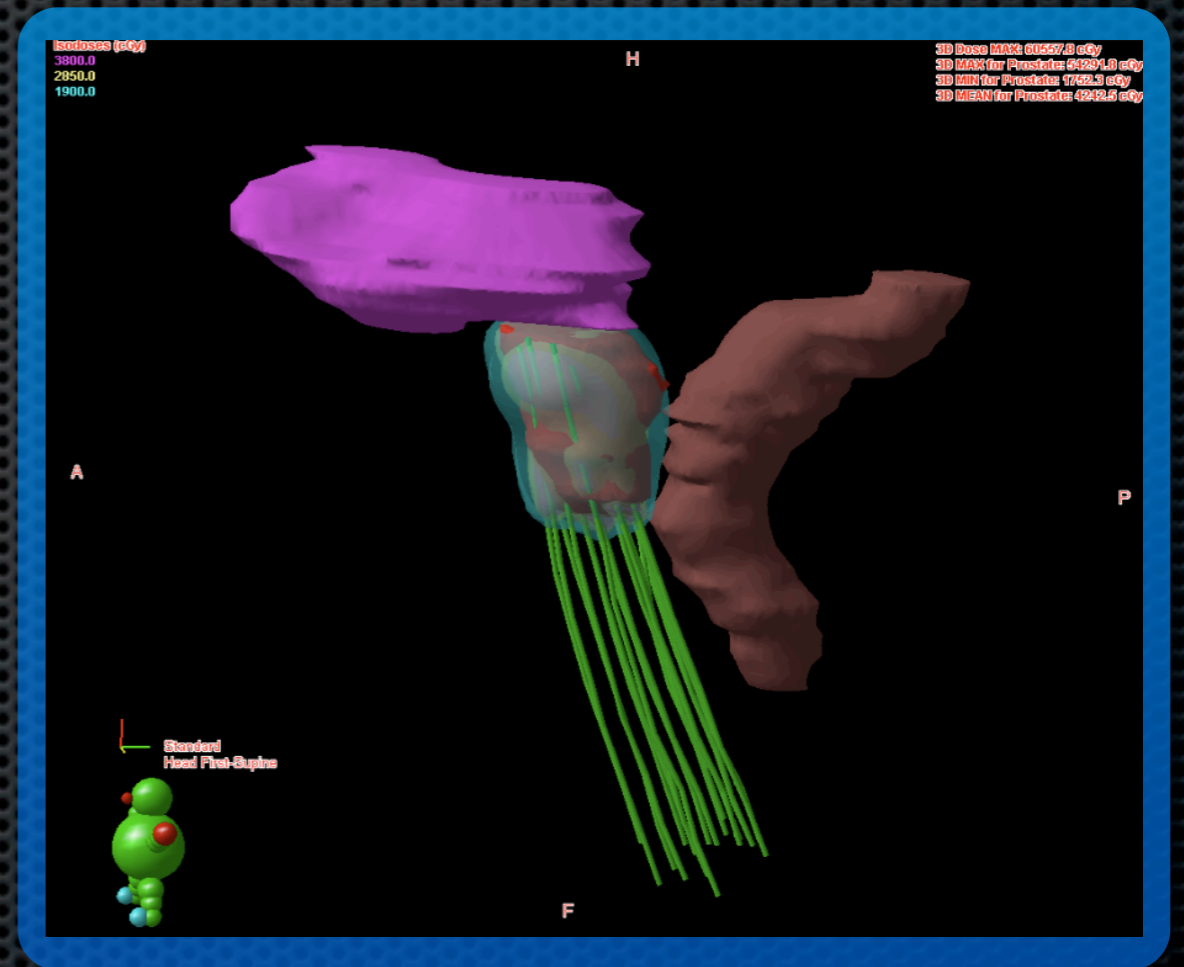
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Outline

- ✦ Harmony Search Optimization for HDR Prostate Brachytherapy
 - ✦ Goals
 - ✦ Background
 - ✦ Materials and Methods
 - ✦ Results and Discussion
 - ✦ Conclusions

HDR Prostate Brachytherapy

- ✦ Multiple catheters inserted into the prostate
- ✦ OARs include: urethra, bladder, rectum
- ✦ DVH-based prescription
- ✦ Delineation of catheters
- ✦ Optimization of dwell times in order to meet prescription goals



Anatomy and catheter reconstruction in 3D in Varian BrachyVision

Main Goals

- ✦ Main objective is to apply a new algorithm, Harmony Search, for DVH-based HDR Prostate brachytherapy optimization
- ✦ Harmony Search parameters will be investigated in order to determine the best settings for optimization
- ✦ Harmony Search will be compared against the genetic algorithm (4x improvement)

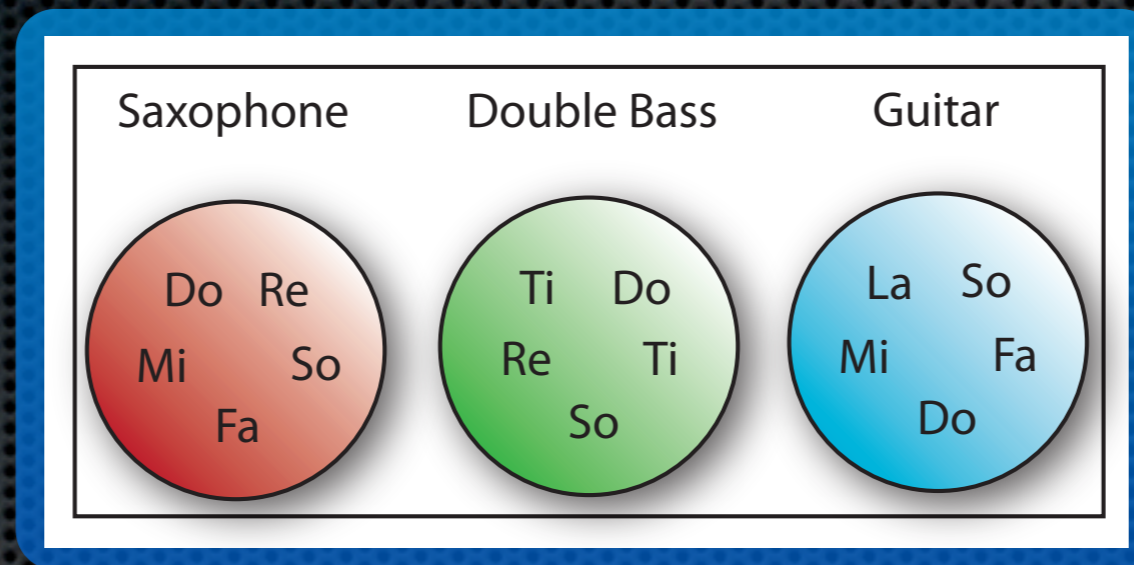
Harmony Search

- ✦ Analogy of music improvisation process
- ✦ Consider an ensemble continually searching for better harmony
- ✦ The combination of pitches are evaluated and remembered in a Harmony Memory of a fixed size
- ✦ New harmonies are created from pitches of existing harmonies
- ✦ Better combinations replace inferior harmonies

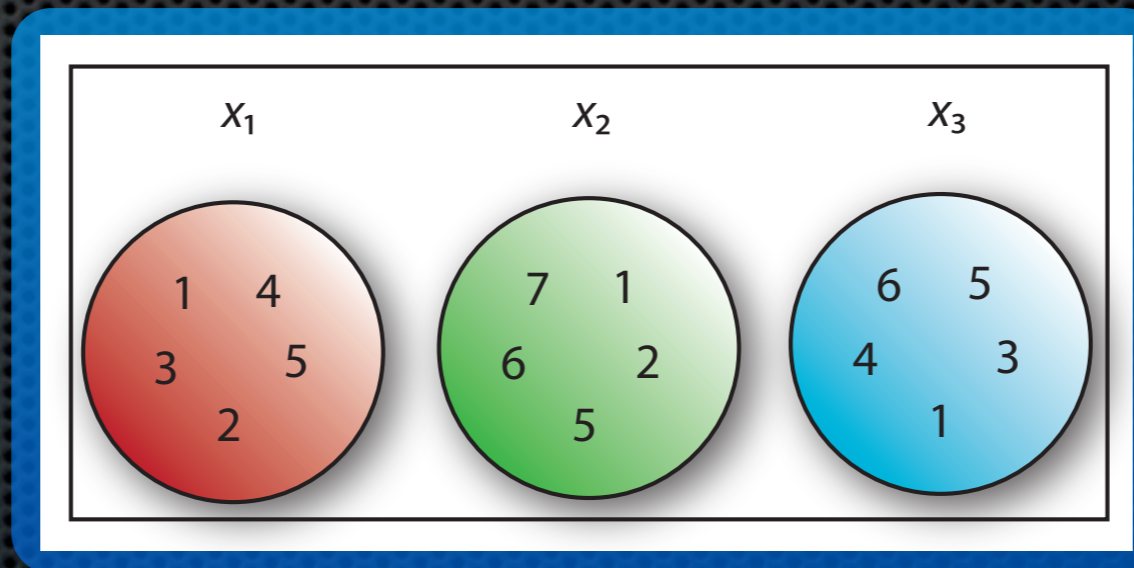
Harmony Search

- ✦ Harmony Search process:
 - ✦ Initialize a Harmony Memory (HM)
 - ✦ Compose a new harmony from HM
 - ✦ If new harmony is better than the minimum harmony in HM, replace it
 - ✦ If the stopping criteria has not been satisfied, compose a new harmony again

Harmony Search



Representation of Harmony Memory for a jazz trio



Representation of Harmony Memory for HDR dwell times

Harmony Search

- ✦ Important parameters for Harmony Search include:
 - ✦ Harmony Memory Size (HMS)
 - ✦ Harmony Memory Considering Rate (HMCR)
 - ✦ Pitch Adjusting Rate (PAR)
 - ✦ Stopping criteria

Current State of HDR Prostate Brachytherapy Optimization

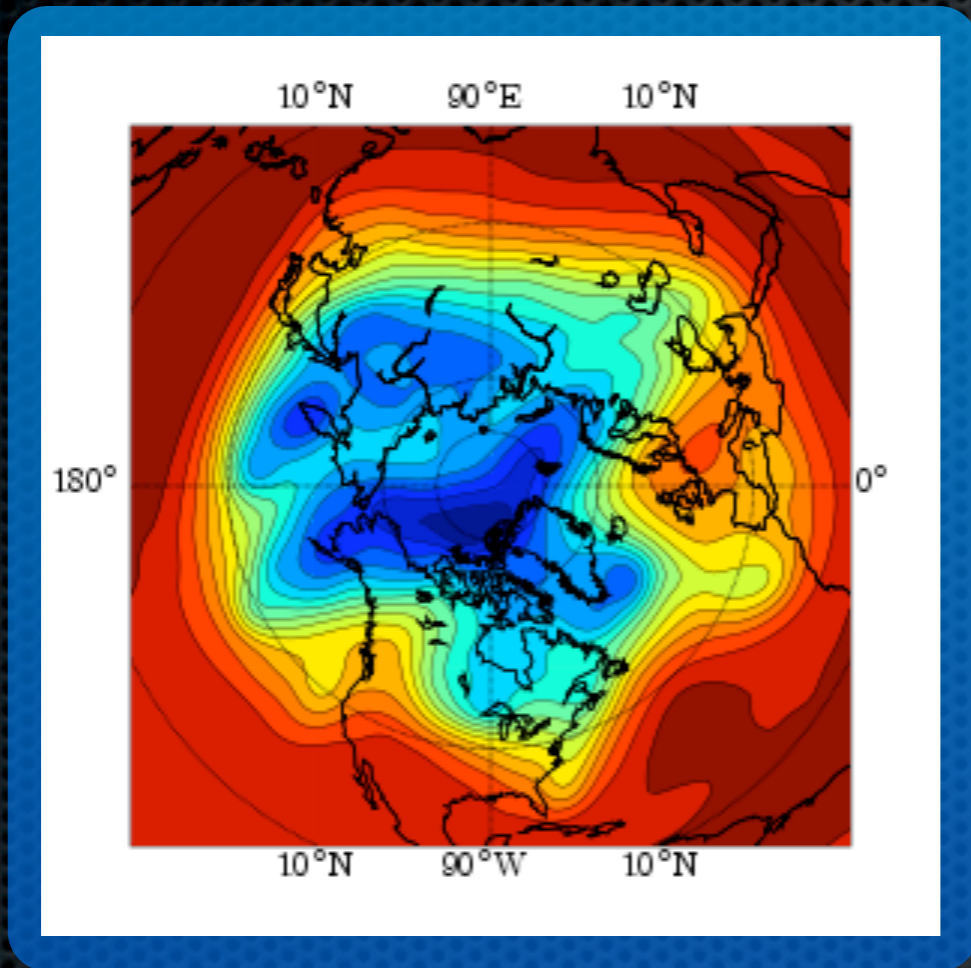
- ✦ Simulated annealing, linear programming, geometrical optimization, genetic algorithm
- ✦ Most recent work in 2006 - Attraction-repulsion model
- ✦ Two main research groups:
 - ✦ Lahanas et. al.
 - ✦ Lessard, Pouliot, et. al.

Methods and Materials

- ✦ Construction of simulation environment
- ✦ Anatomy and catheter reconstruction
- ✦ Dose calculation and generation of DVH
- ✦ DVH-based objective function
- ✦ Optimization algorithm parameters

Methods and Materials

Construction of simulation environment



Example of an isocurve plot
from Matplotlib

- Open source toolkits and libraries used:
 - Python, wxPython
 - NumPy, Matplotlib



Methods and Materials

Anatomy and catheter reconstruction

- ✦ DICOM RT (structure set and treatment plan)
- ✦ DCMTK used to convert DICOM RT to XML format
- ✦ XML parsed into native Python object

Methods and Materials

Dose calculation and generation of DVH

- ✦ Dose calculation matrix was created based on a minimum bounding box for each structure
- ✦ Delaunay triangulation, Heron's formula and serial slice linear interpolation were used to calculate the volume of each structure
- ✦ Dose calculation points were uniformly distributed and stored in a 3D NumPy array

Methods and Materials

Dose calculation and generation of DVH

- AAPM TG-43 point source model was used to calculate dose to each point
- Φ_{an} was set to 0.98 as recommended for ^{192}Ir
- A cumulative DVH was constructed based on the calculation points

Methods and Materials

DVH-based objective function

$$f = \sum_i c_i \left\{ \sum_k u_{ik} (d_i(V_{i,k}) - D_{i,V_k})^2 \right\} \quad (3)$$

$$f = 5 \times (90 - D100_{prostate})^2 + (1 - V125_{urethra})^2 \\ + (1 - V75_{bladder})^2 + (1 - V75_{rectum})^2 \quad (4)$$

- RTOG Protocol 0321-based constraints:

Volume	Constraint	Expected	Weight
Prostate	D100	90%	5
Urethra	V125	1 cc	1
Bladder	V75	1 cc	1
Rectum	V75	1 cc	1

Methods and Materials

Algorithm parameters - Harmony Search

- ✦ Harmony Memory Size set to 5
- ✦ Harmony Memory Considering Rate set to 0.95
- ✦ Pitch Adjusting Rate set to 0.9

Methods and Materials

Algorithm parameters - Genetic Algorithm

- ✦ Population size set to 5
- ✦ Generations set to 100

Methods and Materials

Optimization parameters

- ✦ Minimum dwell time set to 0
- ✦ Maximum dwell time set to 20
- ✦ Number of iterations set to a high number
- ✦ Both integer and floating point modes tested

Results and Discussion

- ✦ Validation of volume calculation
- ✦ Dose calculation validation
 - ✦ Isodose curve validation
- ✦ Comparison of Harmony Search and Genetic Algorithm
- ✦ Harmony Search Parameters

Results and Discussion

Validation of volume calculation

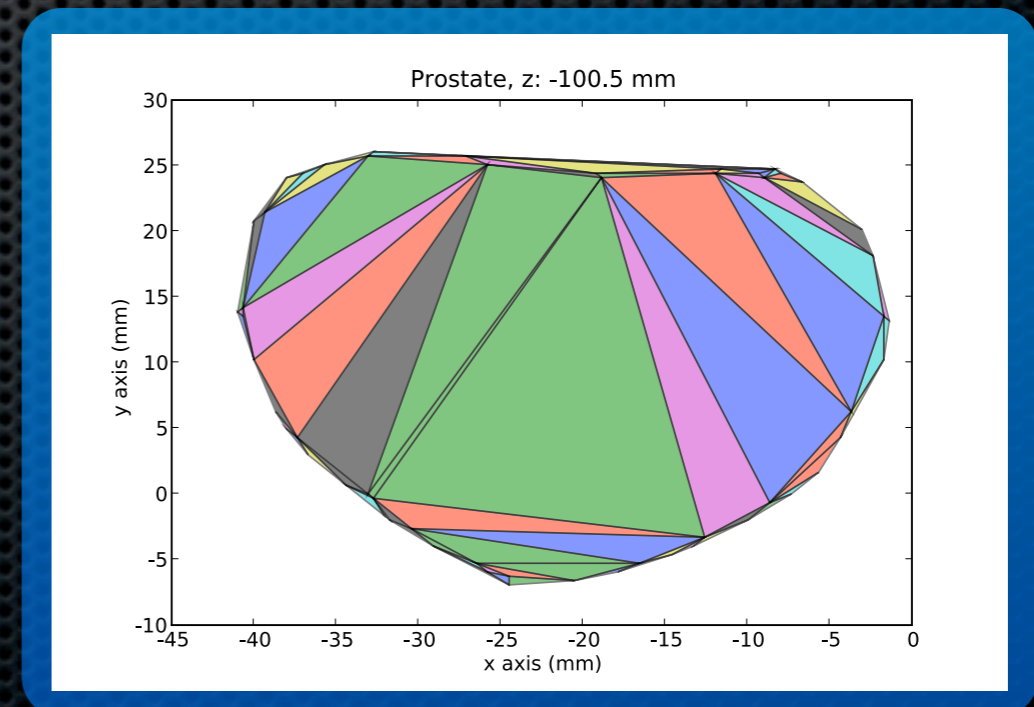
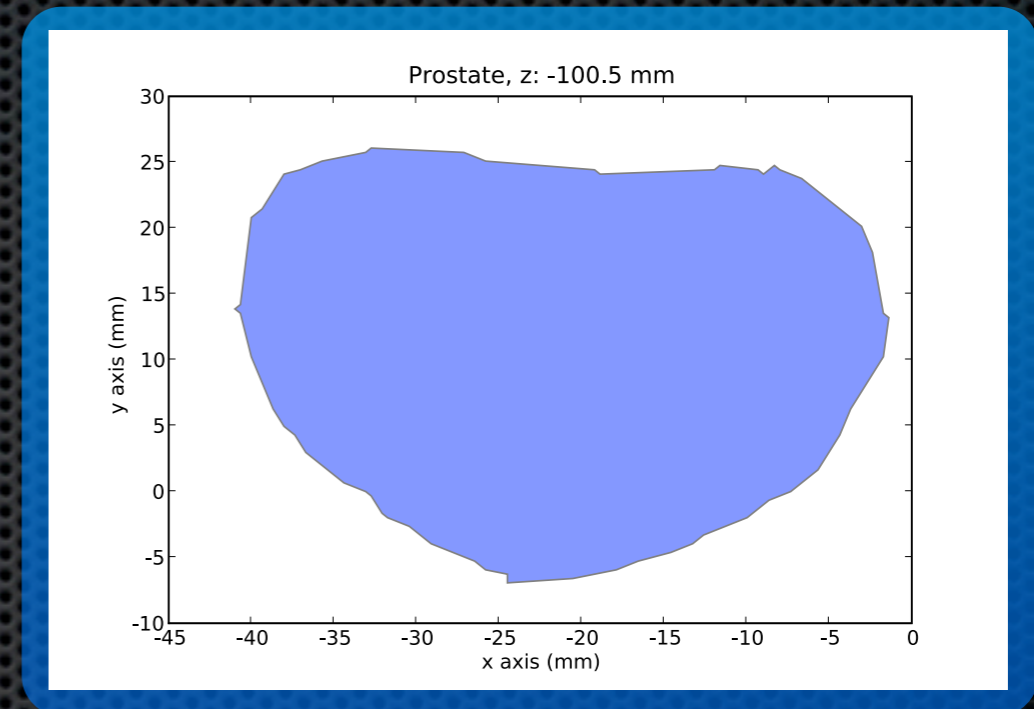
- Volumes of 9 patients were calculated and compared to Varian BrachyVision values
- Delaunay triangulation, Heron's formula and serial slice interpolation were used to calculate volume

Volume	Prostate	Urethra	Bladder	Rectum
Average Percent Difference	0.55%	6.32%	3.02%	1.26%

Results and Discussion

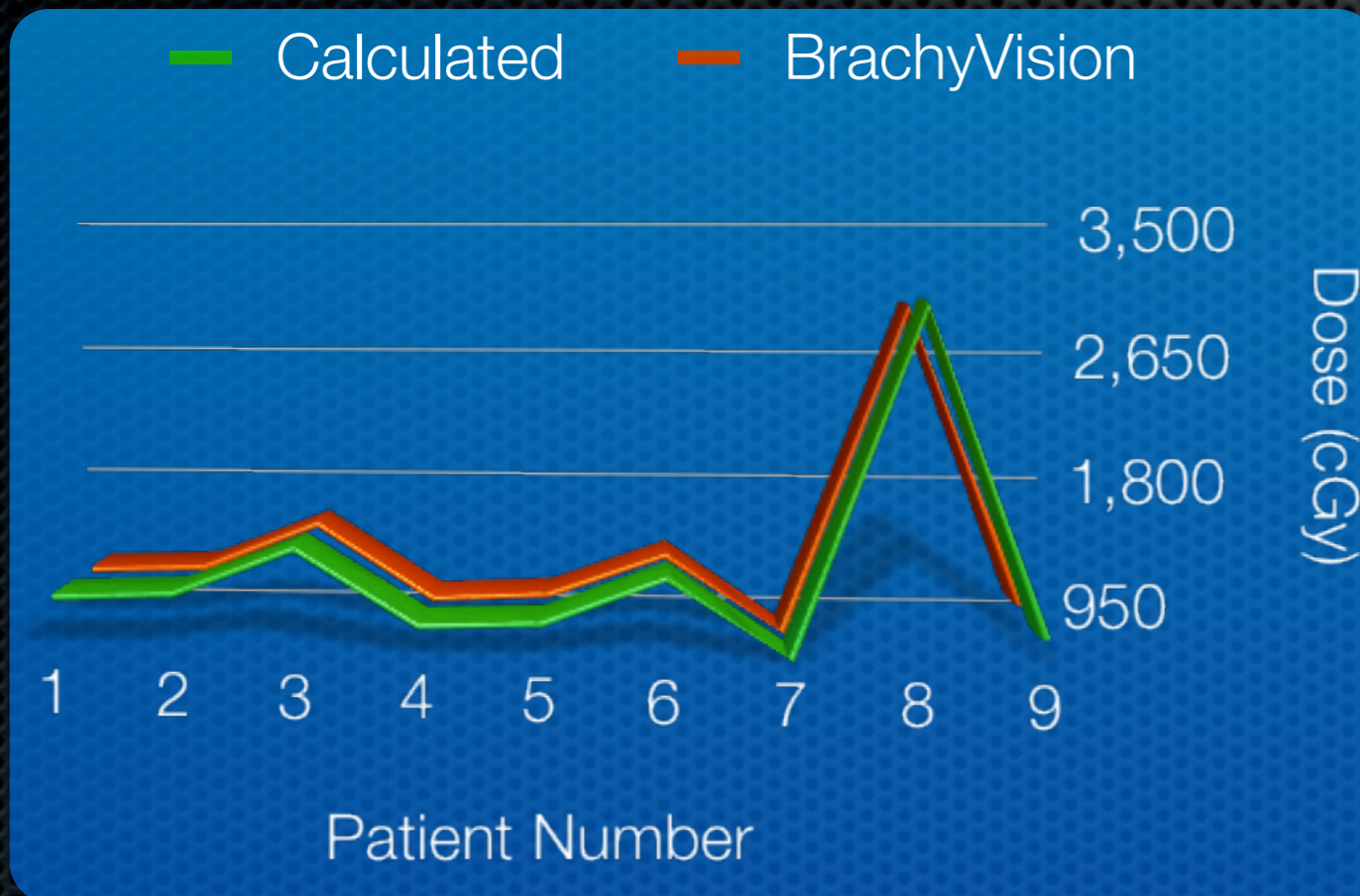
Validation of volume calculation

- ✦ Calculations slightly overestimate volume
 - ✦ Delaunay triangulation
 - ✦ Linear interpolation
 - ✦ Urethral volume



Results and Discussion

Dose calculation validation



- ✦ Dose to a reference point of 9 patients were calculated and compared to Varian BrachyVision values

- ✦ AAPM TG-43 point source formalism was used

Volume	Prostate Point
Average Percent Difference	0.38%

Results and Discussion

Dose calculation validation

- ✦ Discrepancy can be attributed to:
 - ✦ BrachyVision uses AAPM TG-43 line source model
 - ✦ More accurate model of source dose distribution

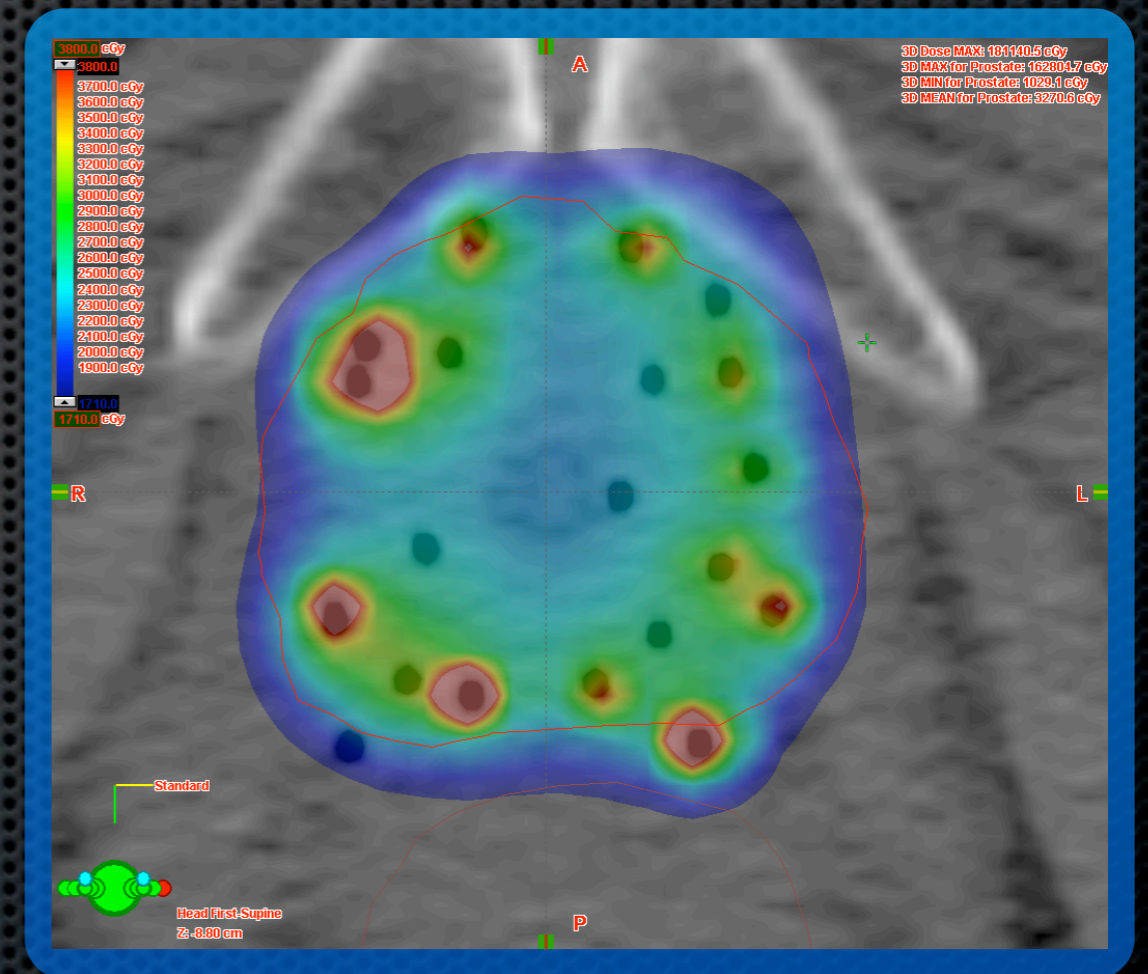
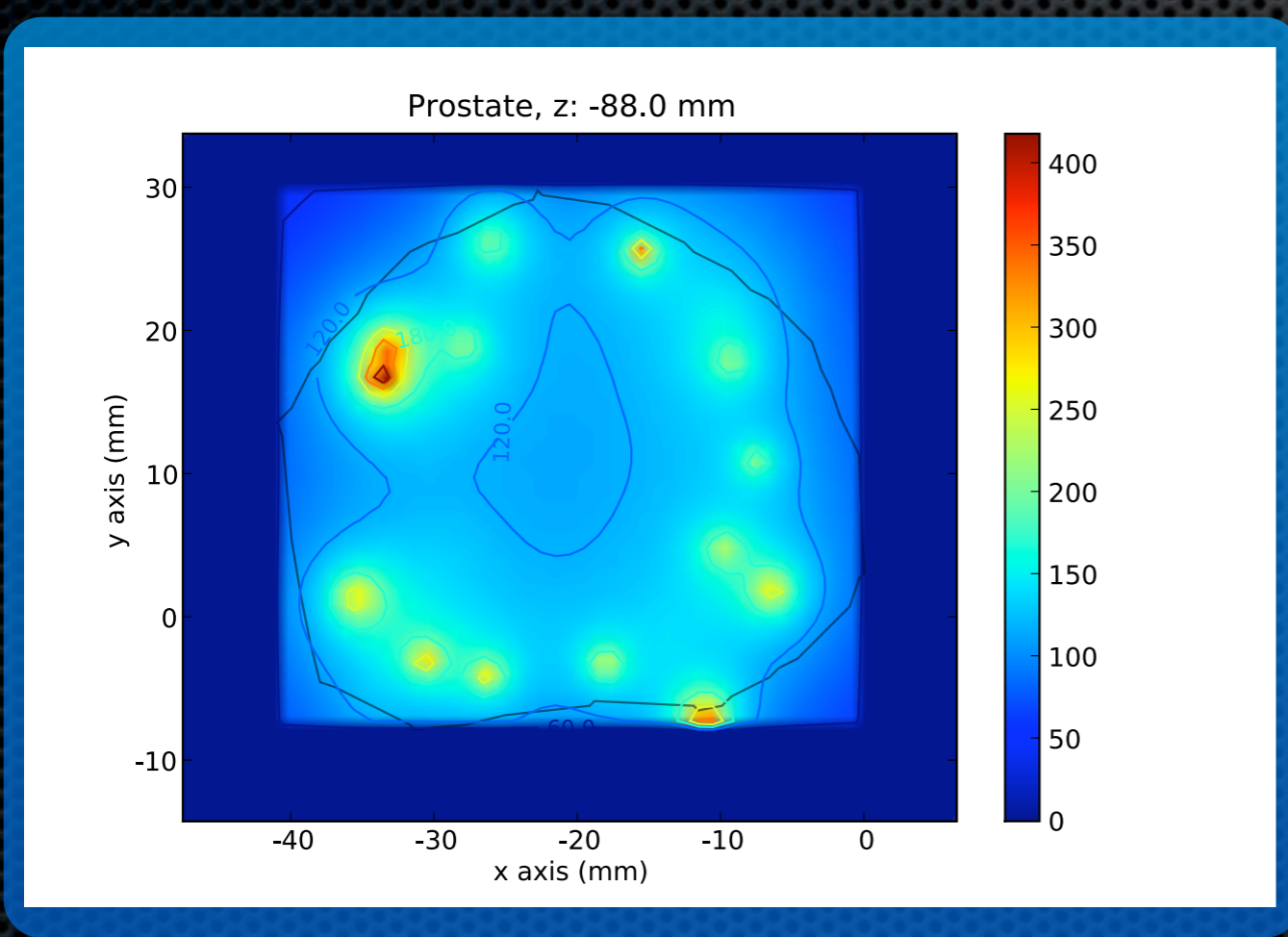
Results and Discussion

Isodose curve validation

- ✦ Isodose curves for patient #1 were generated for several slices and compared to Varian BrachyVision
- ✦ Generated curves were normalized to 100% of prescription dose

Results and Discussion

Isodose curve validation



Isodose and colorwash display for from patient #1 - slice: z: -88.0 mm

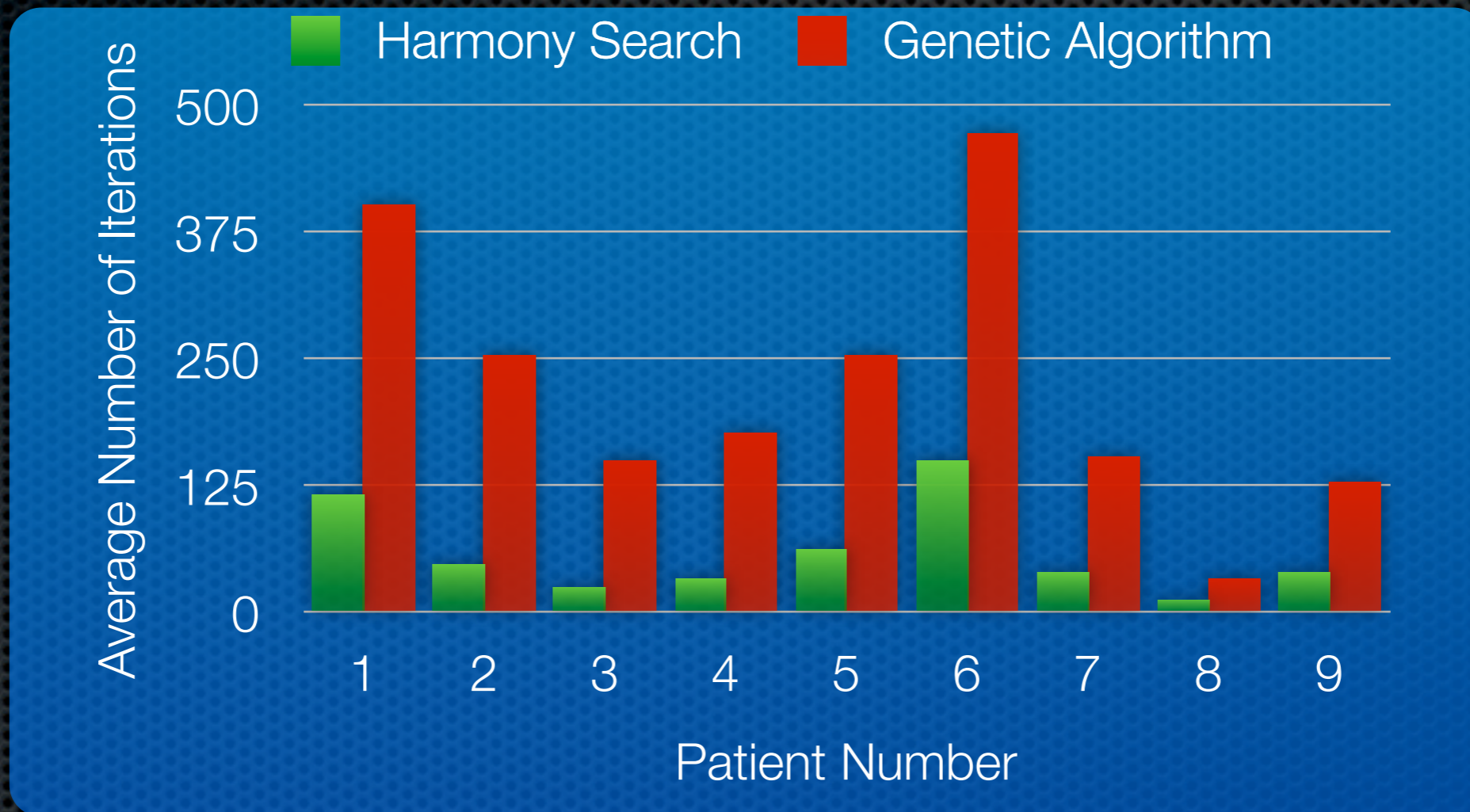
Results and Discussion

Comparison of Harmony Search and Genetic Algorithm

- ✦ Harmony Search and the genetic algorithm were used to optimize the 9 patients using the constraints from RTOG Protocol 0321
- ✦ Simulation was allowed to run to completion, allowing same end result
- ✦ Runs were repeated 5 times for each algorithm / patient combination

Results and Discussion

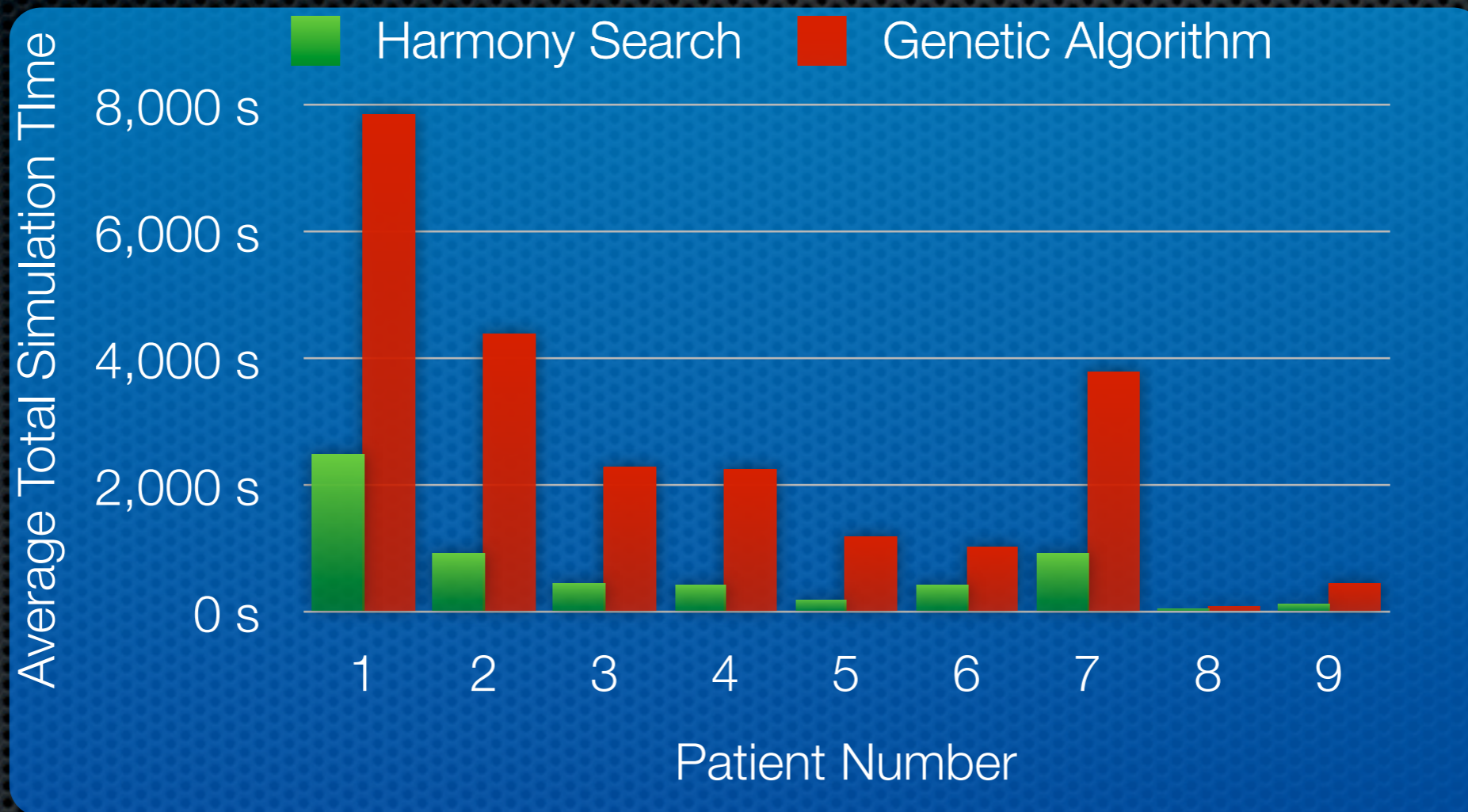
Comparison of Harmony Search and Genetic Algorithm



	Iterations
Average Difference	412%±119%

Results and Discussion

Comparison of Harmony Search and Genetic Algorithm



	Speed
Average Difference	392%±133%

Results and Discussion

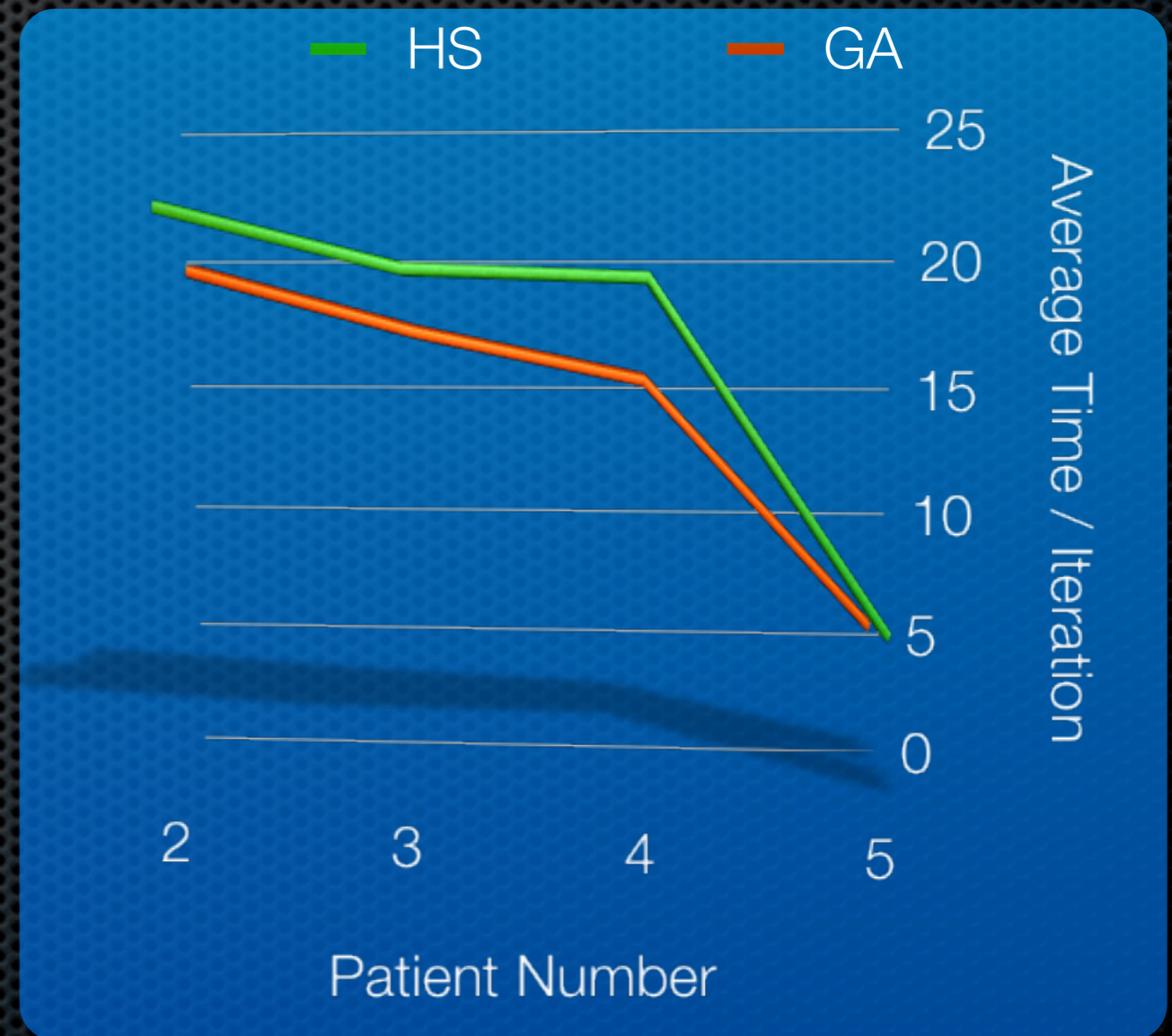
Comparison of Harmony Search and Genetic Algorithm

- ✦ Best case: HS is at least 5 times faster than GA
- ✦ Almost 400% improvement can be realized via HS
- ✦ HS selects decision variables from all vectors in HM to create a new vector
- ✦ GA only chooses 2 existing vectors to create a new vector

Results and Discussion

Comparison of Harmony Search and Genetic Algorithm

- ✦ Average time per iteration
- ✦ HS slightly slower than GA due to more involved construction of each vector



Results and Discussion

Comparison of Harmony Search and Genetic Algorithm

Optimization	Mode	Average Iterations	Time / Iteration (s)
Harmony Search	Integer	56.70	2.84
	Floating Point	69.33	3.19
Genetic Algorithm	Integer	198.20	3.21
	Floating Point	182.43	3.18

- ✦ Integer versus Floating Point
- ✦ HS still faster than GA by 300%
- ✦ Floating Point mode has infinitely more choices compared to Integer mode

Conclusions

- ✦ Harmony Search was used to solve the problem DVH-based HDR prostate brachytherapy optimization
- ✦ A comparison between Harmony Search and the genetic algorithm was presented
- ✦ The optimal parameters used in Harmony Search (HMS, HMCR, PAR) were determined
- ✦ The benefits of multiple threads in optimization was demonstrated

Conclusions

- ✦ A complete HDR brachytherapy simulation environment was developed using Python, wxPython, NumPy, Matplotlib, OFFIS DCMTK and Parallel Python
- ✦ DICOM RT data from Varian BrachyVision was used to obtain patient anatomy and HDR catheter information
- ✦ Once the structures were indexed, the volume of each structure was determined and compared to the original volume calculated in BrachyVision

Conclusions

- ✦ The results showed the volume calculation was within 2% for the prostate, 3% for the rectum and bladder, and 6% for the urethra
- ✦ The discrepancy for the urethra was mostly due to its relatively small volume

Conclusions

- ✦ Dose was calculated using AAPM TG-43 point source model of GammaMed ^{192}Ir HDR source and compared to BrachyVision
- ✦ Calculation of point dose was found to be 0.38% different
- ✦ Generated isodose curves were found to be similar to BrachyVision

Conclusions

- ✦ DVH-based objective function was created and used for optimization based on RTOG Protocol 0321
- ✦ Harmony Search and the genetic algorithm were compared for 9 different patients
- ✦ HS was found to be around 4 times faster than GA when compared over multiple data sets
- ✦ Average time/iteration was faster for GA than HS due to the work involved in creating a new vector in HS

Conclusions

- ✦ HS was still faster than GA when using Floating Point values compared to Integer values for dwell times
- ✦ When optimizing for GammaMed, Integer mode should be used since the system only accepts integer dwell times

Conclusions

Future Research

- ✦ Comparison versus other optimization algorithms
- ✦ Use HS for new techniques such as SAVI
- ✦ Parallel Python over multiple PCs
- ✦ Combination of Monte Carlo dose calculation with HS
- ✦ HS applications to IMRT, beam angle optimization