

Model Analytics辅助的智能放疗计划建模

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【摘要】目的:利用瓦里安公司开发的Model Analytics(MA)工具减少人工处理RapidPlan模型离群值的繁琐和主观因素导致模型构成的不确定性,评估MA工具在效率、改善统计学参数及模型优化效果等方面的表现。**方法:**①选取81例优质计划导入RapidPlan系统并建立初始模型;②将初始模型上传MA进行自动分析统计,根据报告提示对离群值进行批量统计学确认,比较模型验证前后统计学指标的变化;③利用20例测试病例评估统计学确认前后RapidPlan模型的剂量学表现,并与原临床计划比较。**结果:**MA只需几分钟便可得到构成模型计划的几何学、剂量学等特征统计,5轮分析共找出8个股骨头剂量学离群值,分别高于各自预测范围上限的11.11%、5.88%、5.56%、5.56%、5.00%、5.26%、5.56%和5.88%, R^2 由0.32提高至0.45;仅用一轮分析便找出所有3个膀胱几何和剂量学离群值,其中几何离群值分别高于均值62.22%或低于均值55.35%,剂量学离群值高于预测范围上限3.33%,处理完离群值后, R^2 由0.35升至0.37。测试计划表明,RapidPlan计划质量显著优于人工计划($P<0.05$),使用验证前后的模型可分别降低股骨头剂量23.15%和27.55%,降低膀胱剂量8.14%和6.79%。**结论:**使用MA工具可快速获取模型构成计划的整体描述,并准确查找出模型中的离群值,从而提高智能放疗计划建模的效率,但统计学确认对模型的剂量学表现影响不大。

【关键词】智能计划;RapidPlan;Model Analytics;机器学习;建模

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Modeling for knowledge-based plan assisted with Model Analytics

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Abstract: Objective To reduce the component uncertainty induced by the complexity and subjectivity of outlier processing during the RapidPlan model verification with the use of Varian Model Analytics (MA), and to evaluate the efficiency, statistical and dosimetric performances of MA. **Methods** An initial RapidPlan model was configured with 81 best-effort plans. The established initial model was uploaded to the MA for automated statistical analysis, and MA suggested that outliers were processed batch by batch. Statistical indexes were compared before and after verification. The dosimetric outcomes of 20 validation cases were re-planned by the RapidPlan models before and after verification, and compared with the clinical manual plans. **Results** MA took a few minutes to analyze the geometric and dosimetric statistics of the plans. Eight dosimetric outliers were reported in 5 rounds of verifications, which were higher than the estimated upper limits by 11.11%, 5.88%, 5.56%, 5.56%, 5.00%, 5.26%, 5.56% and 5.88%, respectively. R^2 value was improved from 0.32 to 0.45 after statistical verification. Only performing 1 round of verification, we found out all 3 outliers for urinary bladder, where the values of geometric outliers were 62.22% higher or 55.35% lower than the majority average values. The value of dosimetric outlier was 3.33% higher than the estimated upper limit. The R^2 value was improved to 0.37 from 0.35 after statistical verification. Validation cases suggested that RapidPlan plan prevails over conventional manual plan significantly ($P<0.05$), in which the dose to femoral head was reduced by 23.15% and 27.55% using model before and after verification, respectively, and the dose to urinary bladder was reduced by 8.14% and 6.79%, respectively. **Conclusion** Statistical features of RapidPlan plans can be acquired quickly using MA which detects outliers hence

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enhances the efficiency of model configuration for knowledge-based planning. The effect of statistical verification on the dosimetric outcome is marginal.

Keywords: knowledge-based plan; RapidPlan; Model Analytics; machine learning; modeling

前言

从2012年 Appenzoller 等^[1]和 Yuan 等^[2]团队各自将机器学习技术应用于放疗计划设计,到瓦里安近期上市的商用系统 RapidPlan,基于人工智能的放疗计划已经在效率^[3]、质量(包括头颈^[4]、肺^[5]、食管^[6]、乳腺^[7]、肝^[8]、前列腺^[9]、宫颈^[10]、直肠^[11-12]等病种)、一致性^[13-14]等众多方面展示出优于人工设计的特点。甚至有学者预言十年内自动计划将取代传统人工设计^[15]。基于历史数据建立和调试剂量体积直方图(DVH)预测模型是实现智能计划的关键过程,虽然 RapidPlan 可以生成各种复杂的统计学参数和图表,但依靠设计者本人的统计学知识判断处置离群值和强影响点(以下统称离群值)以改进模型不仅费时费力,而且文献报道的方法和效果也莫衷一是^[10, 16-17]。

为减少人工处理离群值的繁琐和主观因素导致模型构成的不确定性,瓦里安公司最近开发了基于 web 的 Model Analytics (MA) 工具,并免费供给 RapidPlan 用户试用。作为常规临床前测试和质控,本工作系统评估了 MA 工具在运行效率、改善统计学参数及模型优化效果等方面的表现。

1 材料与方法

1.1 RapidPlan 模型的建立

北京大学肿瘤医院直肠癌术前同步推量 SIB VMAT 模型的建立方法、统计确认及验证结果详见早前报道^[11-12, 17-19],现简要总结如下:81例历史计划经高年资物理师逐一精修后被导入 RapidPlan 系统,其中处方剂量、解剖结构、布野方式、剂量分布等关键数据被自动提取并拟合成 DVH 预测模型。所有计划均采用单个整弧、10 MV 光子、5°准直器角度,在配置 Millenium 120 MLC 的加速器上实现 95% 计划肿瘤靶区 (PGTV) 及计划靶区 (PTV) 分别大于等于 50.6 和 41.8 Gy 的处方剂量,分 22 次完成。人工统计学确认过程包括逐个检查所对应计划的几何离群值 (Z-scores) 大于 3.5、剂量学离群值 (Studentized Residual, SR) 大于 3、强影响点数据 (Cook's Distance, CD) 大于 4。其中, Z-scores、SR 和 CD 值分别反映离群值与样本均值的差异、残差与预测标准差之商,以及从模型中去除某病例后对其他病例残差的影响。参照瓦里安说明书及文献^[10, 16]报道方法,对每个危及器官模型中的可疑离群值进行分批处理(每次

1~2个),及时评估统计学参数并验证计划以确认模型优化效果。

1.2 MA 辅助的模型改进和统计学确认

将未经人工统计学确认的初始模型及其包含的原始计划信息以 DICOM 格式从 Eclipse 计划系统中导出(所有计划均依照 HIPPA 做匿名处理),并一键上传服务器,由 MA 自动批量统计用于建模的原始计划数据的几何学特征、剂量学特征,并对初步拟合的 DVH 预测模型进行分析,评估回归模型参数的可决系数 (R^2)、Z-scores、SR 和 CD。参考报告的建议检查各离群值并进行批量处理。由于每次处理完离群值后均需要重新拟合新的模型,从而可能产生新的离群值,因此需要将重新拟合后的模型重复上述步骤,直至不再提示新的离群值且各项统计学指标均变好。

1.3 模型验证和剂量学参数比较

另选 20 例同类型的临床测试计划,验证比较统计学确认前后 RapidPlan 模型的优化效果,并与临床计划比较。所有计划按处方剂量归一(95% 体积满足 100% 处方剂量),计算比较如下剂量学参数:① PGTV 及 PTV 的均匀性指数 (HI_{PGTV} 和 HI_{PTV}), $HI = (D_{2\%} - D_{98\%}) / D_{50\%}$; ② PGTV 与 PTV 的适形指数 (CI_{PGTV} 和 CI_{PTV}), $CI = V_{100\%} / V_{target}$; ③ 股骨头及膀胱的平均剂量。

1.4 统计学方法

用 SPSS 21.0 软件提供的 Shapiro-Wilk 方法检验数据分布正态性,符合正态分布采用配对 t 检验,不符合正态分布则采用非参数检验, $P < 0.05$ 为统计学有显著意义。

2 结果

2.1 模型构成计划整体特征描述

模型数据库中,所有股骨头平均剂量的均值 \pm 标准差为 (16.70 ± 2.19) Gy, 最大最小值分别为 20.90 和 11.20 Gy。总体积的均值 \pm 标准差为 (200.60 ± 53.92) cm³, 最大最小值分别为 334.91 和 95.82 cm³。射野内体积的均值 \pm 标准差为 (200.60 ± 53.92) cm³ (100.00% \pm 0.00%), 最大最小值分别表示为 334.91 cm³ (100.00%) 和 95.82 cm³ (99.98%)。与目标靶区重叠体积的均值 \pm 标准差分别表示为 (0.05 ± 0.01) cm³, 最大值为 0.05 cm³ (0.02%), 最小值为 0。MA 找出所有 8 个股骨头离群值一共经历了 5 轮分析,表 1 列举了每轮报告的剂量学离

表 1 5 轮分析报告的股骨头剂量学离群值(MA 未报告几何离群值)

Tab.1 Dosimetric outliers of femoral heads reported in 5 rounds of analysis (no geometric outlier was reported by Model Analytics)

Round (#of outliers)	D _{mean} /Gy		Actual	t/s
	Estimated range	Actual		
First Round (2)	14	18	20	95
	12	17	18	
Second Round (2)	13	18	19	125
	14	18	19	
Third Round (2)	16	20	21	200
	15	19	20	
Fourth Round (1)	14	18	19	180
Fifth Round (1)	13	17	18	155

All outliers were ascribed to the actual mean dose outside the estimated range.

群值及其原因(MA 未报告几何离群值)。

所有膀胱平均剂量的均值±标准差为(25.10±2.96) Gy,最大最小值分别为 34.53 和 18.57 Gy。总体积的均值±标准差为(283.90±169.77) cm³,最大最小值分别为 744.34 和 55.19 cm³。射野内体积的均值±标准差为(245.40±148.84) cm³(86.23%±7.53%),最大最小值分别为 633.14 cm³(99.79%)和 40.35 cm³(60.99%)。与目标靶区重叠体积的均值±标准差分别表示为(38.50±29.22) cm³(13.77%±7.53%),最大最小值分别为 161.44 cm³

(39.01%)和 0.29 cm³(0.21%)。只用一轮 MA 分析就找出了所有 3 个不同原因的膀胱离群值(耗时 95 s),分别为:几何离群值 1 的射野内体积 38.50%显著低于均值 86.23%;几何离群值 2 与靶区的重合体积 161.44 cm³显著高于均值 60.99 cm³;剂量学离群值 1 的平均剂量 30 Gy 显著高于预测范围 24~29 Gy。

2.2 剂量学比较和统计学确认

表 2 展示 20 例测试计划分别使用验证前后 RapidPlan 模型的优化结果与原临床计划之间的比较。

表 2 验证前后 RapidPlan 模型优化结果与原临床计划之间的比较(20 例测试计划结果)

Tab.2 Dosimetric comparison of 20 clinical plans and their re-optimized results using RapidPlan models before and after verification

		HI		CI		D _{mean} /Gy	
		PGTV	PTV	PGTV	PTV	Femoral head	Urinary bladder
Clinical	Mean	0.06	0.27	1.03	1.02	14.95	24.74
	SD	0.01	0.08	0.03	0.03	1.59	4.54
Before	Mean	0.05	0.26	1.07	1.05	11.13	22.72
	SD	0.00	0.01	0.06	0.02	1.47	3.49
After	Mean	0.05	0.26	1.07	1.06	10.83	23.06
	SD	0.00	0.01	0.06	0.02	1.69	3.45
	P1 value	0.00 [*]	0.03 [*]	0.02	0.00	0.00 [*]	0.06 [*]
	P2 value	0.00 [*]	0.03 [*]	0.00	0.00	0.00 [*]	0.06 [*]
	P3 value	0.68 [*]	0.69 [*]	0.43	0.37	0.03 [*]	0.06 [*]

^{*} Paired t test; [^] Friedman test, otherwise Wilcoxon test. P1: Clinical vs. Before; P2: Clinical vs. After; P3: Before vs. After; HI: Homogeneity index; CI: Conformity index; PGTV: Planning gross tumor volume; PTV: Planning target volume

3 讨论

MA 工具可多次上传模型文件,发现各危及器官中的离群值并提出处理建议。运行效率方面,MA 工

具仅需一键上传服务器,几分钟即可统计出建模原始计划的几何学特征、剂量学特征等,可自动提取出危及器官的最大、最小、平均剂量和标准差。MA 工

具可一次挑选出多个危及器官的离群值,即可发现结构误配等明显错误,也可报告明显偏离主要数据的点。上传所需时间与网速快慢有关。相比之下,人工方法挑选离群值时,主观性强,缺少标准,费时费力,一次只能处理极少数量的离群值^[17]。

由表1可知,第一轮两个剂量学离群值的实际平均剂量分别高于预测范围上限的11.11%和5.88%,第二轮高出5.56%和5.56%,第三轮高出5.00%和5.26%,第四轮和第五轮分别高出5.56%和5.88%。离群值数目逐轮减少,且股骨头回归模型的 R^2 变好,由0.32变成0.45。

膀胱剂量学离群值的实际平均剂量高于预测范围上限3.33%,几何学离群值的射野内体积低于均值55.35%,另一几何学离群值与目标靶区重叠体积高于均值62.22%。统计学确认后膀胱的 R^2 变好,由0.35变成0.37。

表2展示的模型优化效果中,RapidPlan计划显著优于人工优化的临床计划($P<0.05$),与早先报道一致^[17-18],具体表现在:靶区剂量更均匀、更适形(主要与模型中的靶区优化参数设置有关),危及器官受量降低(与RapidPlan生成的个体化优化参数和新的PO算法有关^[20])。其中,模型验证前后股骨头平均剂量与临床计划平均剂量相比,分别降低23.15%和27.55%,膀胱平均剂量与临床计划平均剂量相比,分别降低8.14%和6.79%。RapidPlan模型验证前后,除股骨头剂量变化有统计学意义外,其他差别不大,且无统计学意义。这些结果也与早前基于人工的模型确认结果一致^[16]。

4 结论

使用MA工具可快速获取模型构成计划的整体特征描述,并准确查找出模型中的离群值,从而提高智能放疗计划建模的效率,但统计学确认对模型的剂量学表现影响不大。

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