

# Omics and AI driven radiotherapy approaches in H&N cancers

Vincent GREGOIRE, MD, PhD, Hon. FRCR (IE, UK)  
Centre Léon Bérard, Lyon, France



The Truth is rarely pure and never  
simple ...

Oscar Wilde

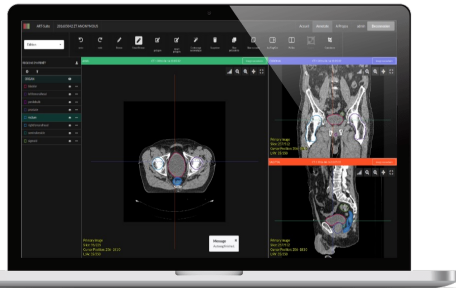


# The challenges for 2022 and beyond

- Automatic primary tumor GTV and nodal CTV delineation
- Omics profile as prognostic factor
- Omics profile to change the treatment intensity



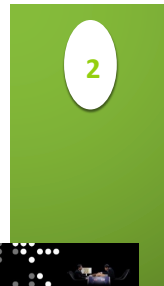
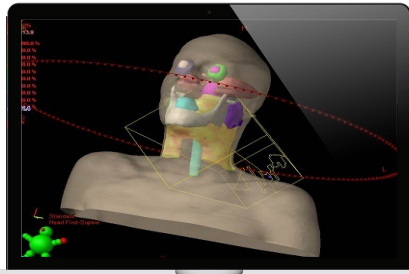
# AI-based software to improve target and OAR volume delineation?



## Plan preparation

Multi-modal, multi-organ organ segmentation through Unique combination of Deep and transfer learning

Auto-identify organs at risks and tumors in patients anatomy in a few minutes with medical accuracy



## Dose Optimization:

Unique combination of parallel multi-objective Master-Slave optimization & reinforcement learning

Produce the best possible treatment plan in minutes instead of hours /days, protecting 30% more organs at risk



“A system’s ability to correctly interpret external data, to learn from such data, and to use those learnings to achieve specific goals and tasks through flexible adaptation”

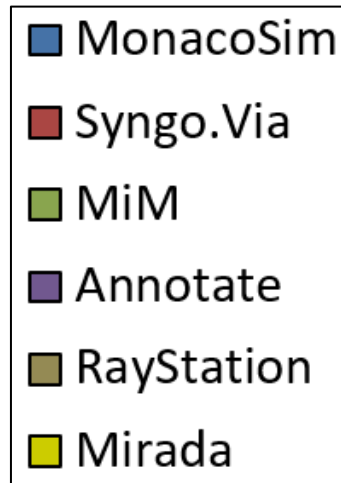
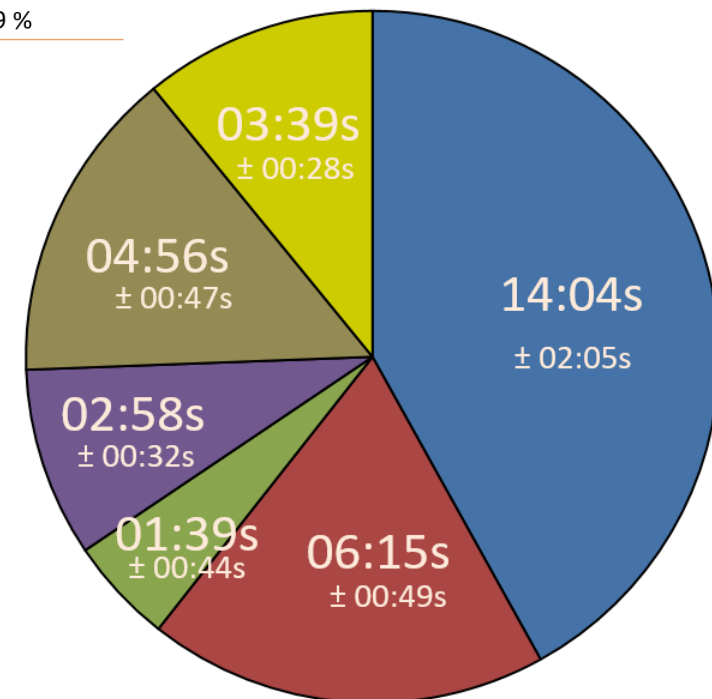
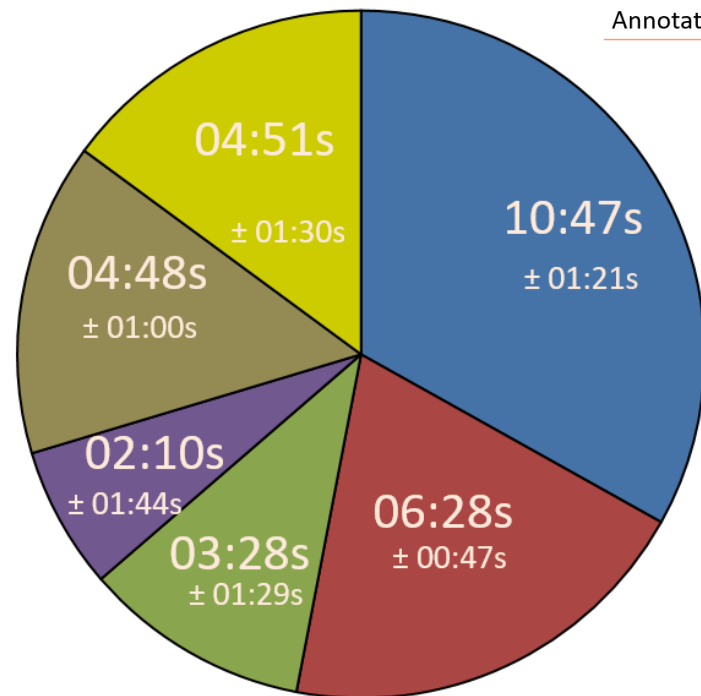
# AI for OAR delineation

Mean saved time in comparison to MonacoSim

	PELVIS	THORAX
Syngo.Via	40 %	56 %
Raystation	55 %	65 %
Mirada	55 %	74 %
MiM	68 %	88 %
Annotate	80 %	79 %

## PELVIS





## THORAX



# Automatic AI-based GTV delineation



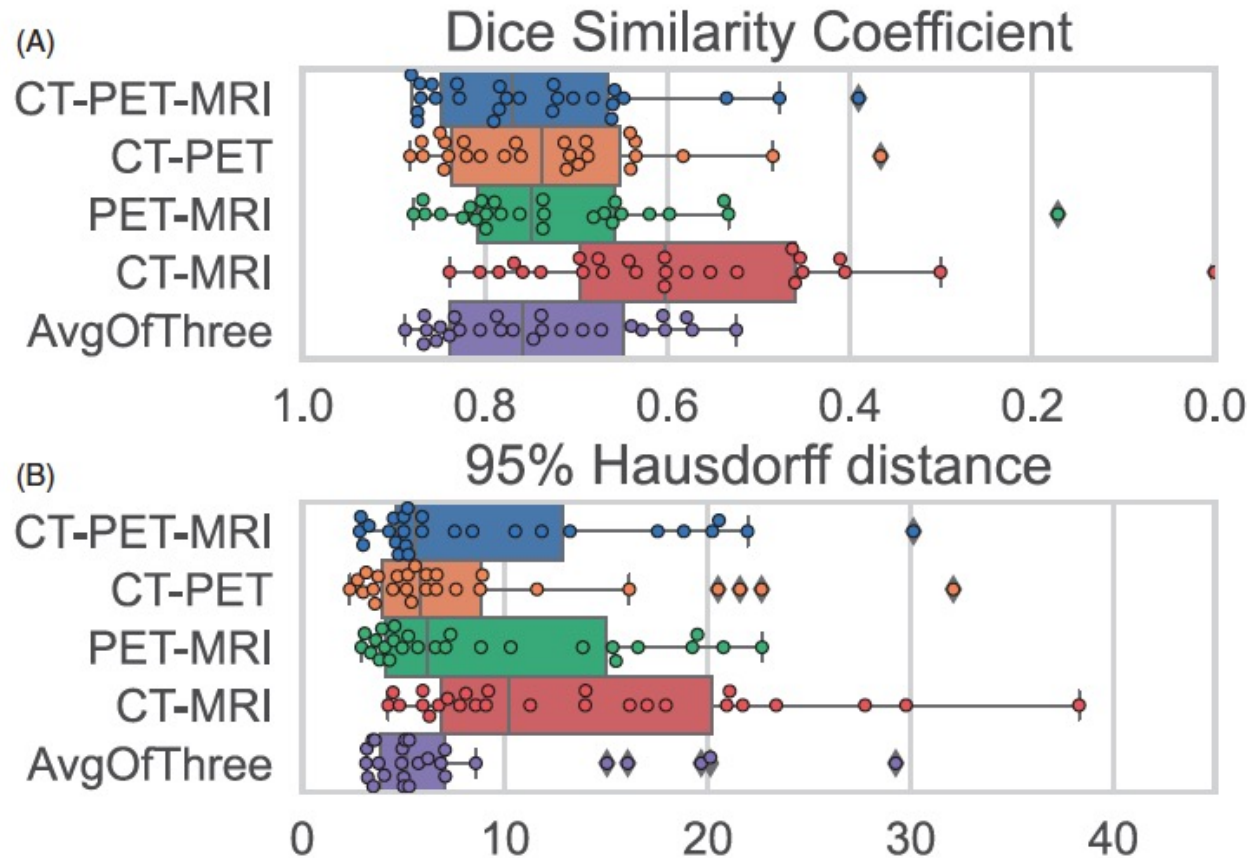
## Comparing different CT, PET and MRI multi-modality image combinations for deep learning-based head and neck tumor segmentation

Jintao Ren<sup>a,b,c</sup> , Jesper Grau Eriksen<sup>a,d</sup> , Jasper Nijkamp<sup>a,b,\*</sup>  and Stine Sofia Korreman<sup>a,b,c,\*</sup> 

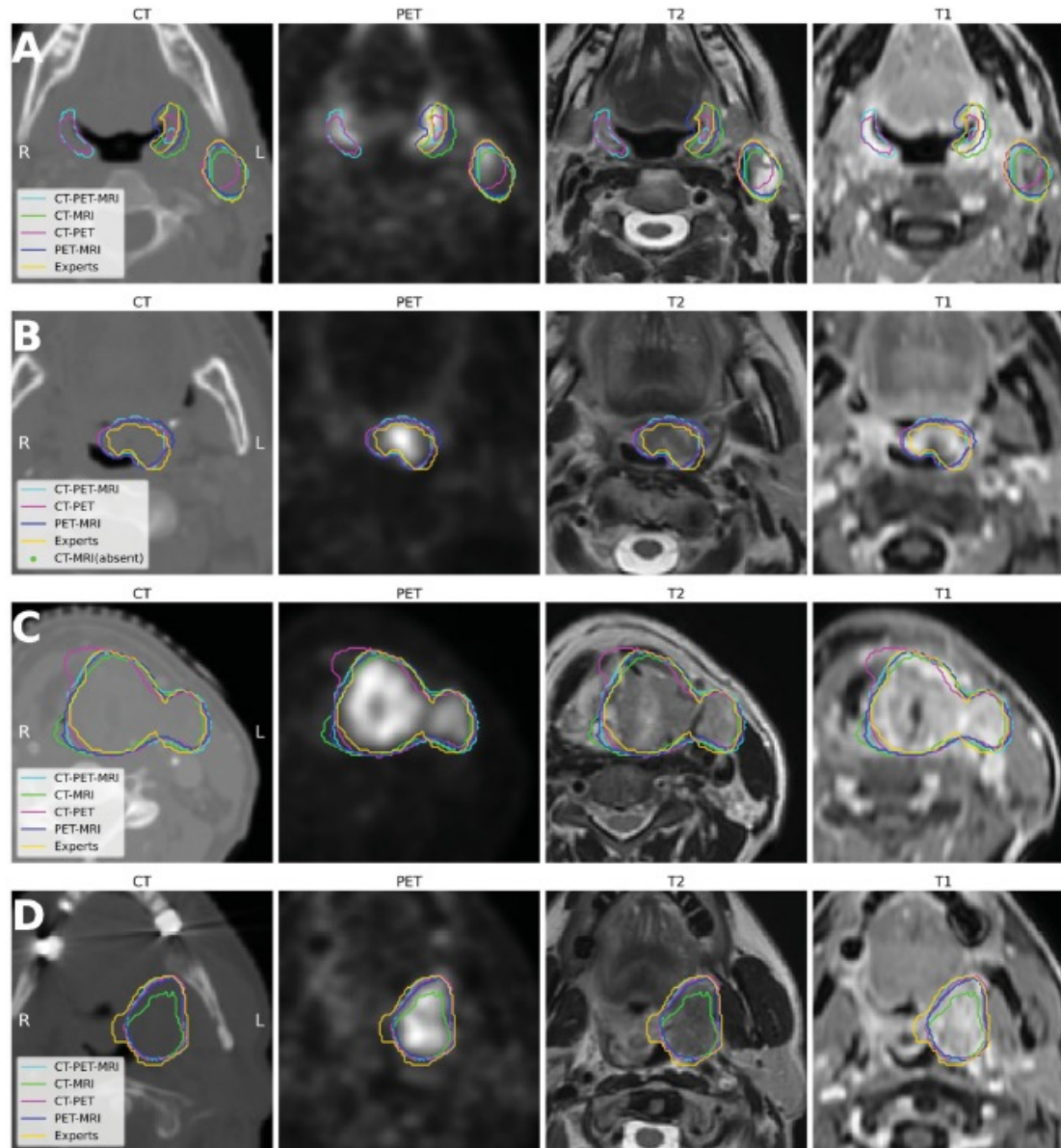
<sup>a</sup>Department of Clinical Medicine, Aarhus University, Aarhus, Denmark; <sup>b</sup>Danish Centre for Particle Therapy, Aarhus University Hospital, Aarhus, Denmark; <sup>c</sup>Department of Oncology, Aarhus University Hospital, Aarhus, Denmark; <sup>d</sup>Department of Experimental Clinical Oncology, Aarhus University Hospital, Aarhus, Denmark

- 153 patients with pharyngo-laryngeal SCC
- 60% T1-T2; 75% N<sup>+</sup>
- CT, coronal MRI-T1, axial MRI-T2, mDixon MRI, FDG-PET acquired with an immobilization mask

# Automatic AI-based GTV delineation

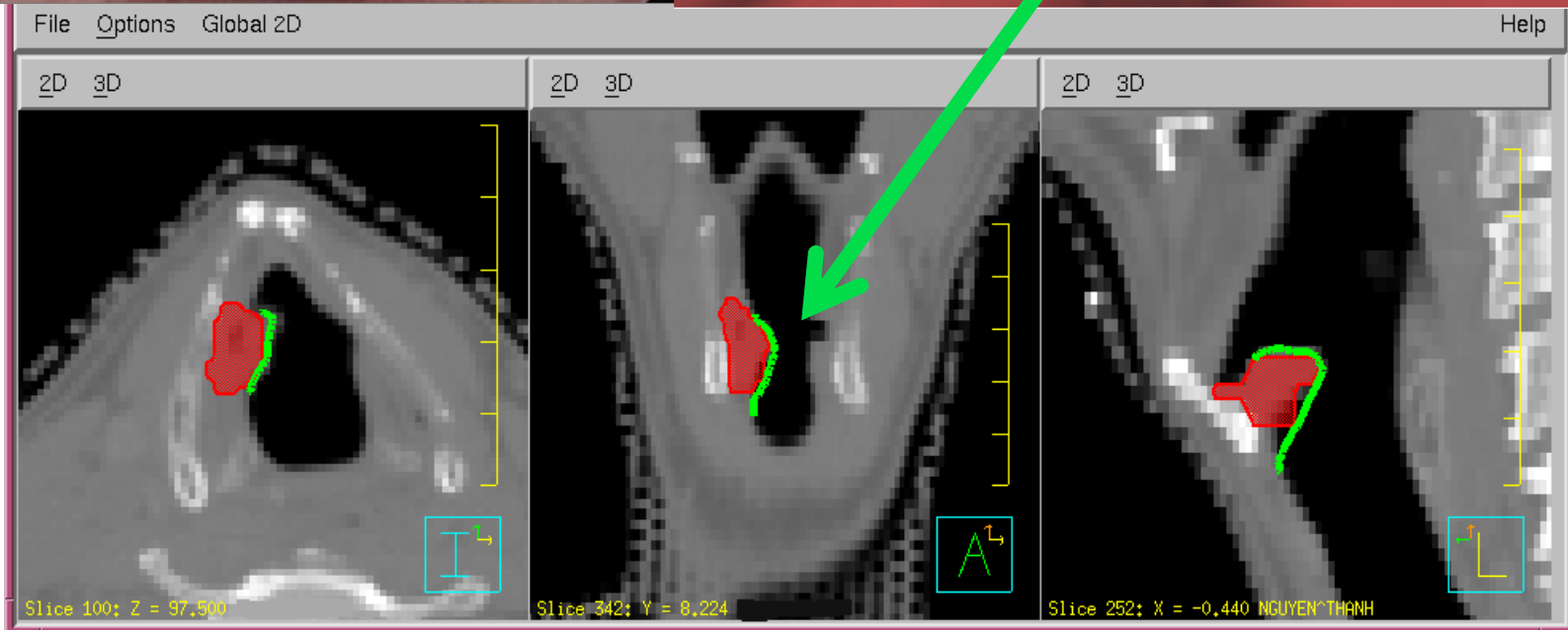
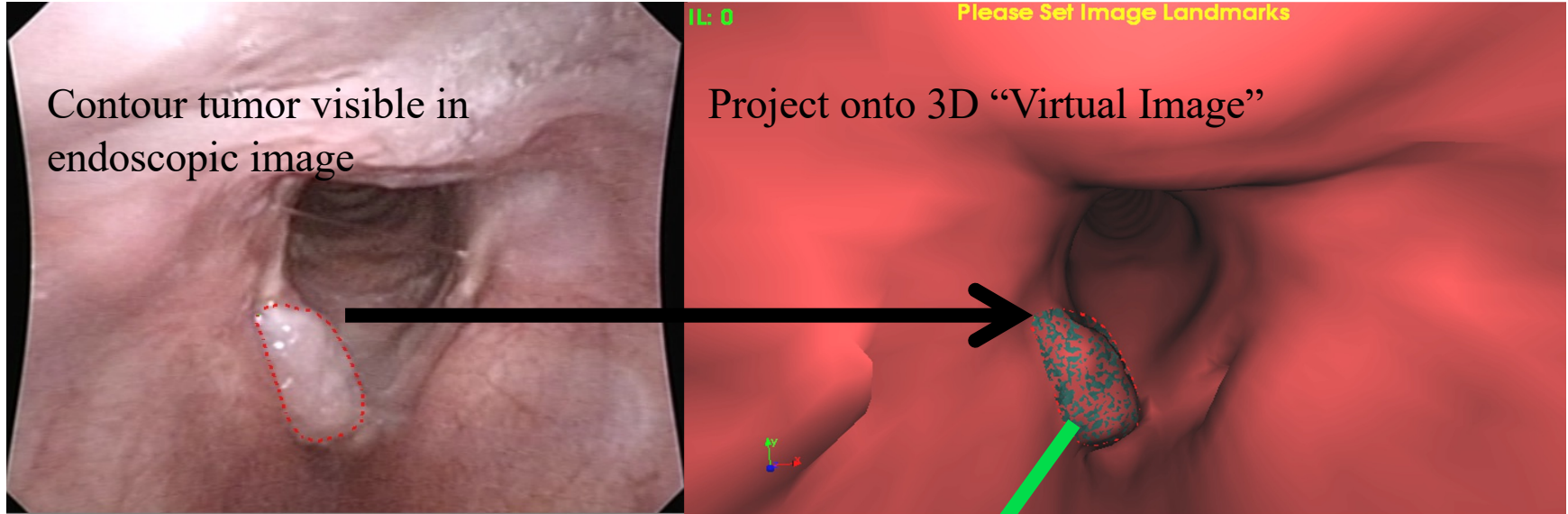


# Automatic AI-based GTV delineation



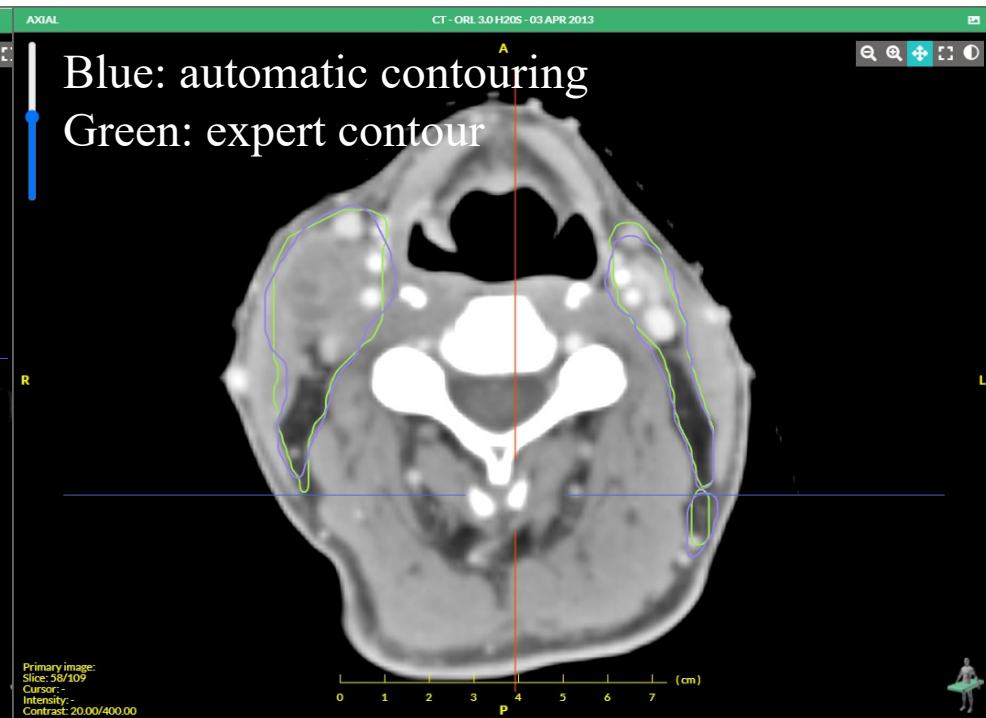
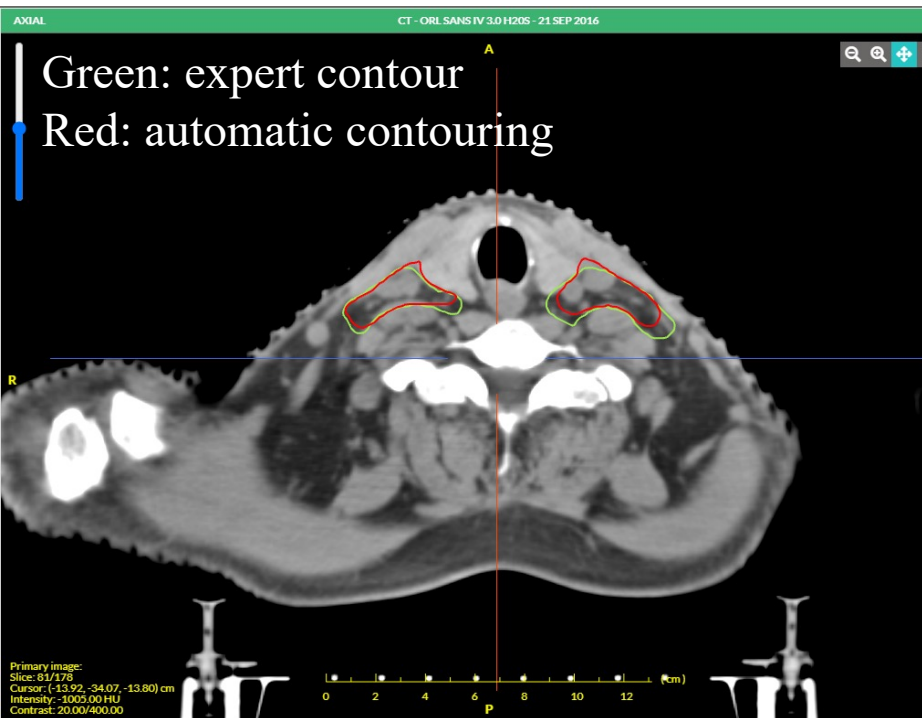


# Endoscopic Contouring



LEON  
BERARD

# Automatic nodal target volume delineation



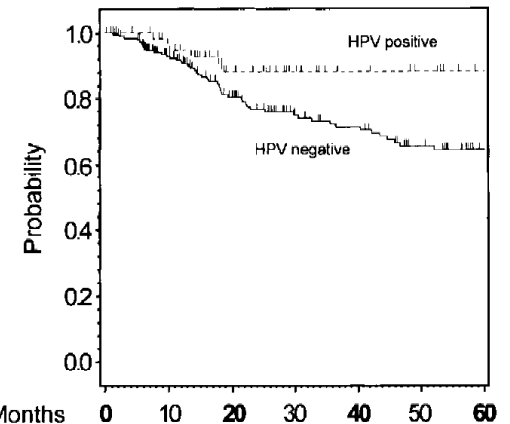
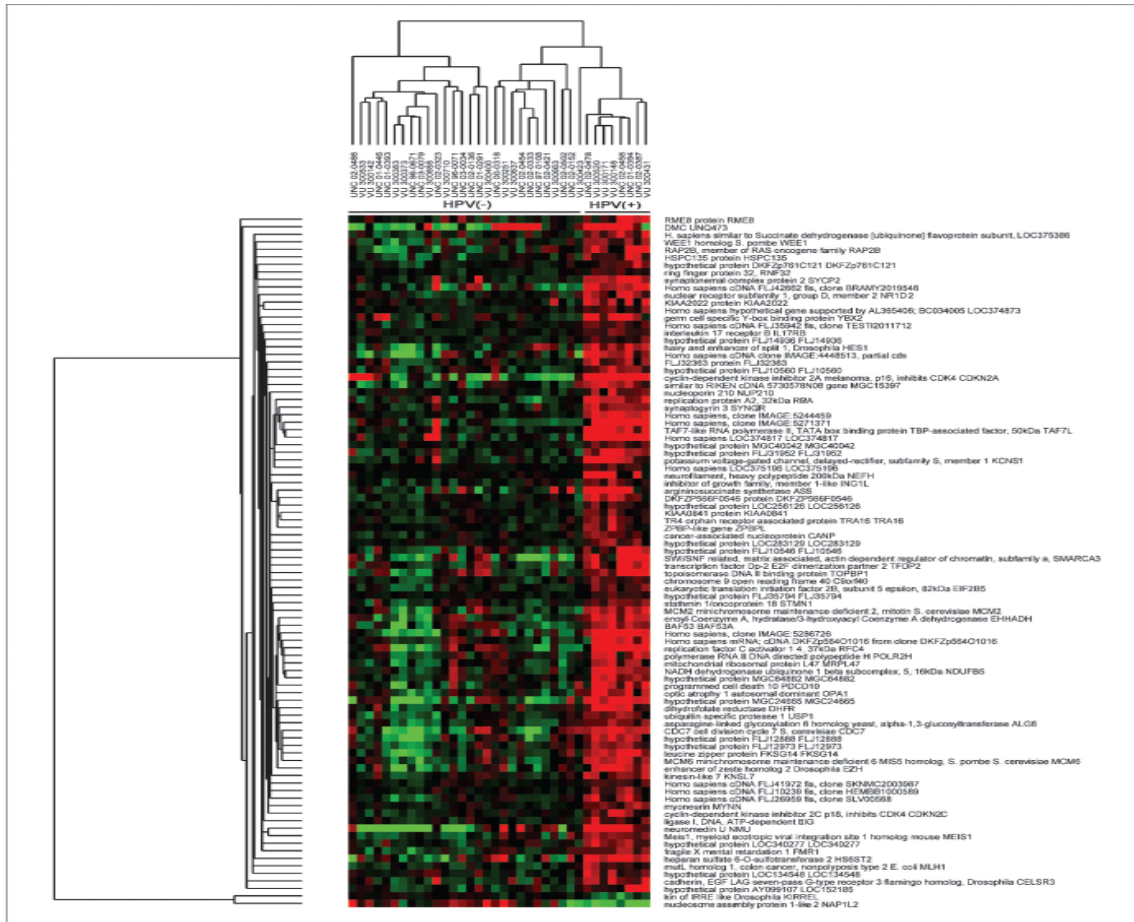


# The challenges for 2022 and beyond

- Automatic primary tumor GTV and nodal CTV delineation
- Omics profile as prognostic factor
- Omics profile to change the treatment intensity



# Genomics profile as prognostic factor: the HPV status

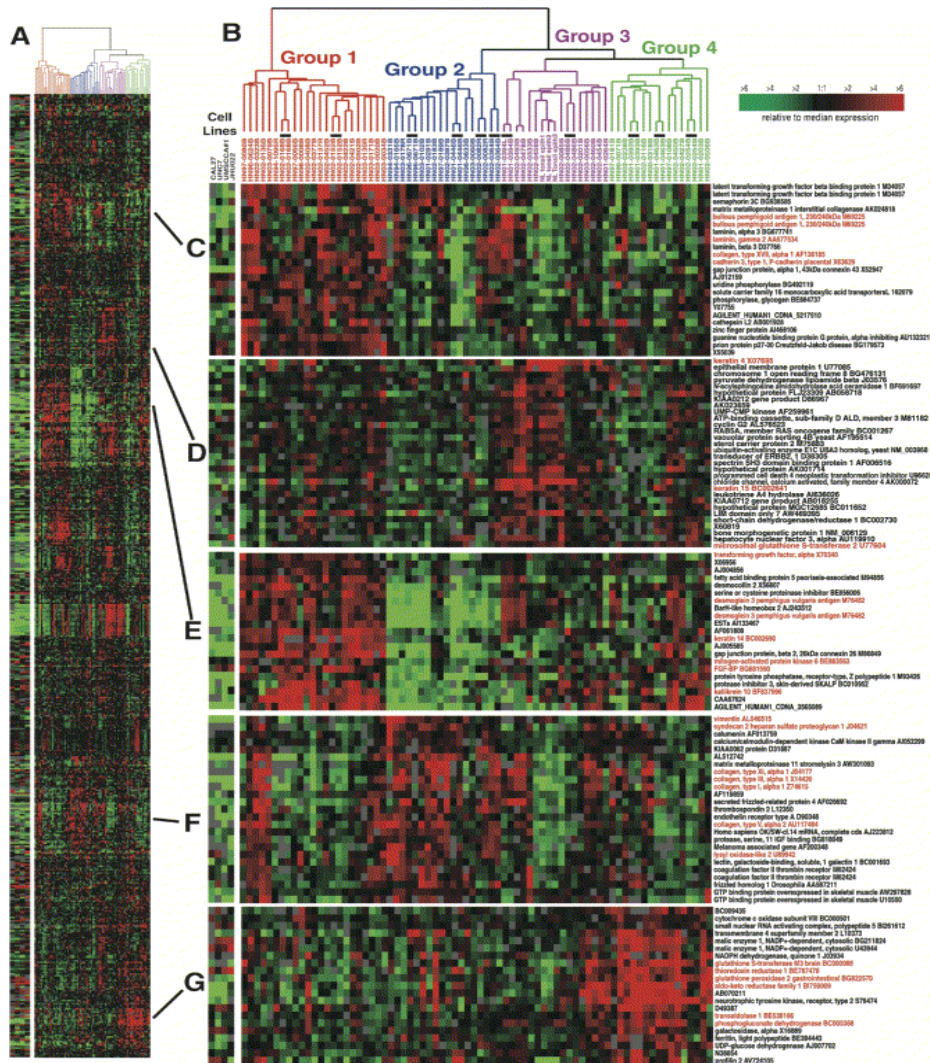


Time in Months	0	10	20	30	40	50	60
Number at risk:							
HPV positive	61	37	18	10			
HPV negative	191	116	75	48			

Fig. 2. Cluster diagram of 91 genes that are differentially expressed between HPV<sup>+</sup> and HPV<sup>-</sup> HNSCC tumors. HPV<sup>+</sup> tumors form a separate cluster (right).

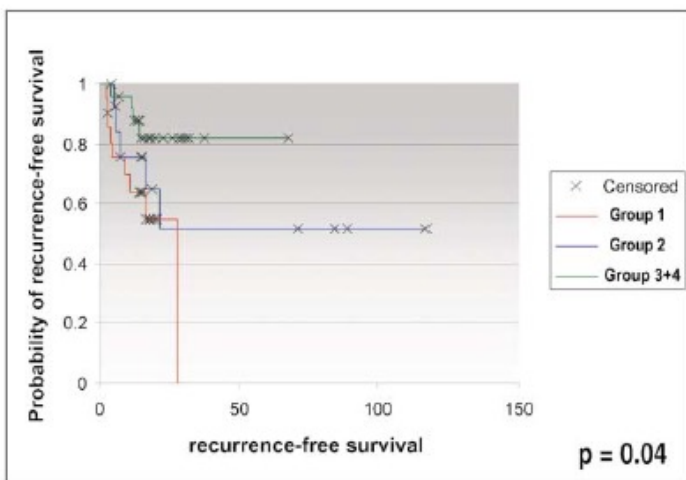
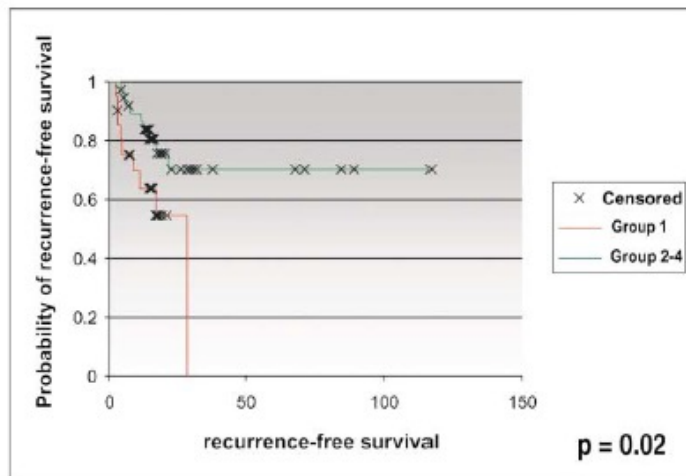


# Genomics profile as prognostic factor: HNSCC gene expression



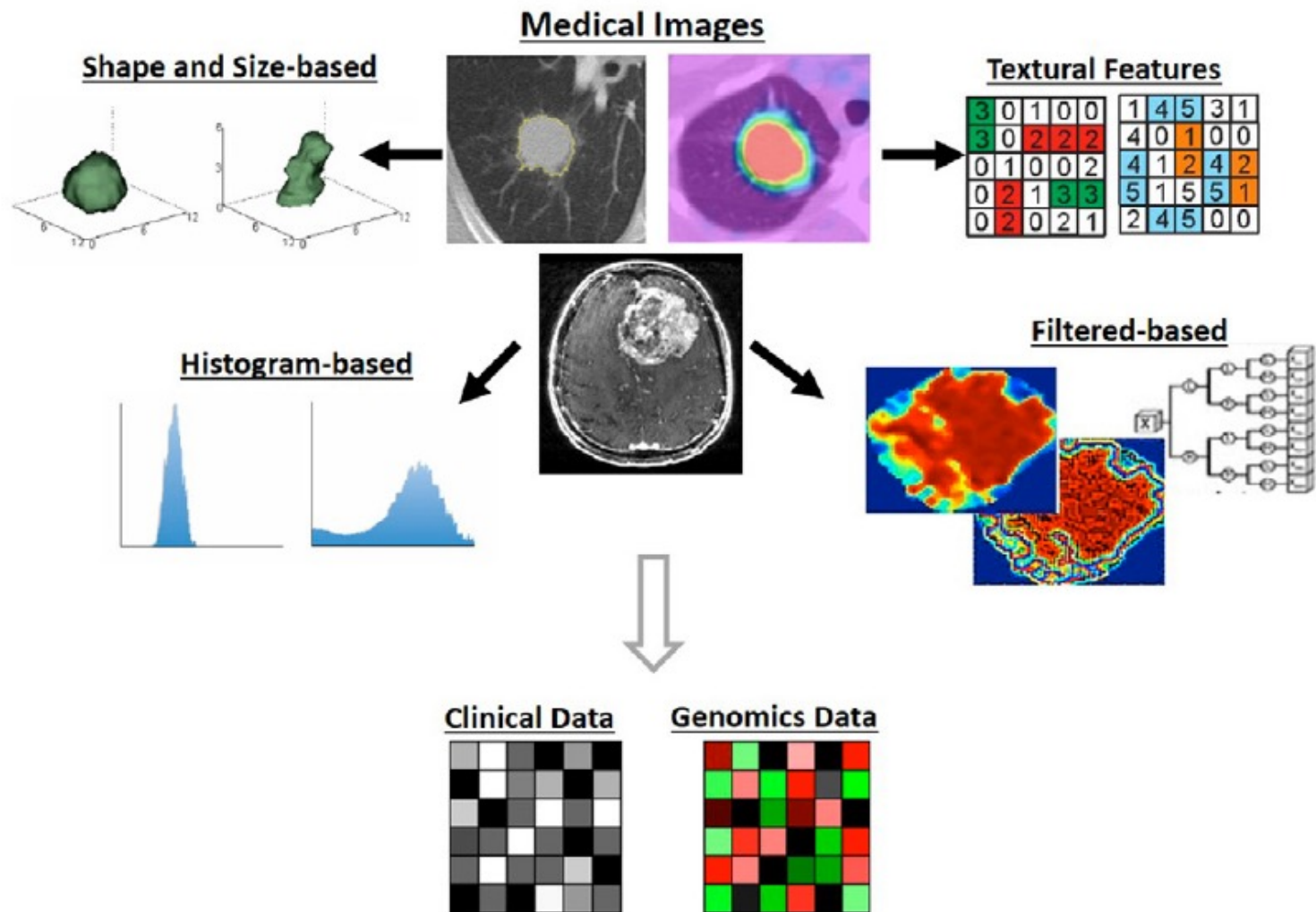
- Group 1: EGFR-pathway signature
- Group 2: mesenchymal-enriched signature
- Group 3: normal epithelium-like subtype
- Group 4: high level of antioxidant subtype

# Genomics profile as prognostic factor: HNSCC gene expression

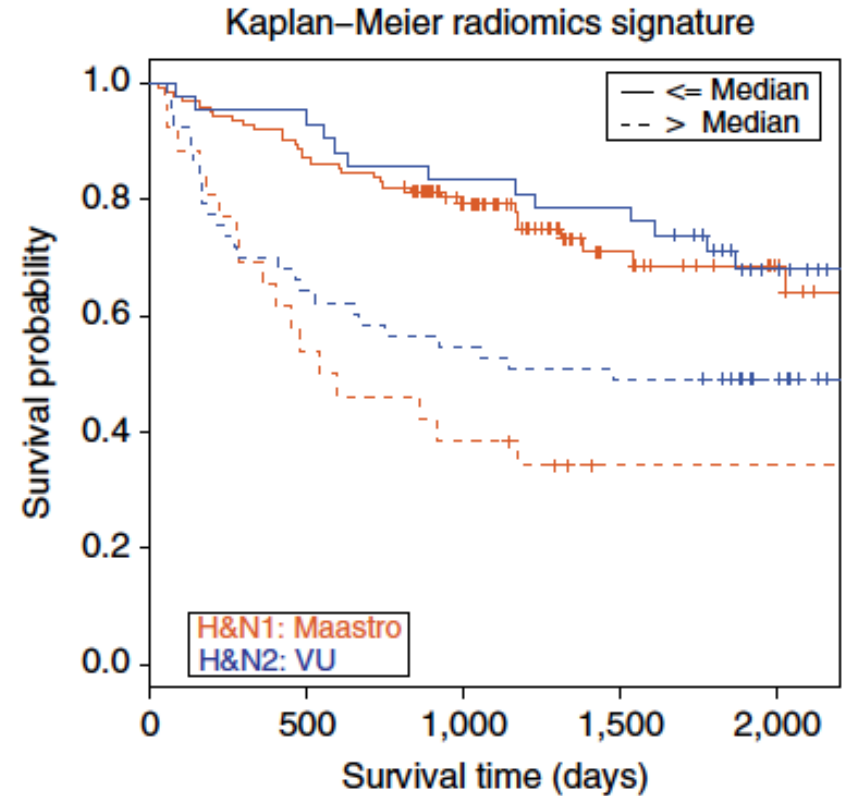
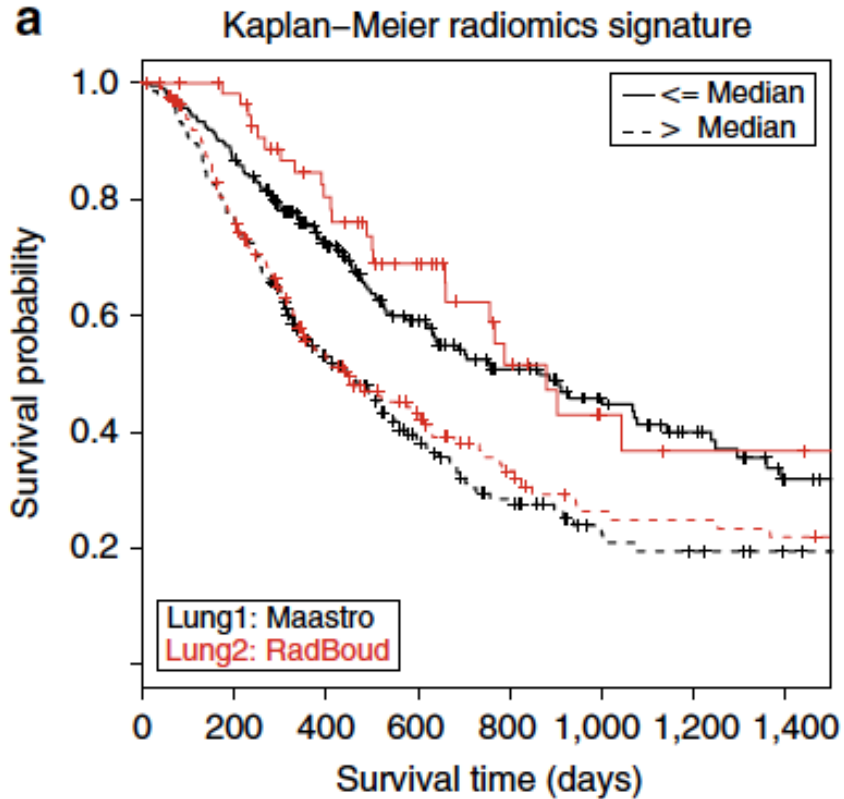


- Group 1: EGFR-pathway signature
- Group 2: mesenchymal-enriched signature
- Group 3: normal epithelium-like subtype
- Group 4: high level of antioxidant subtype

# Radiomics for treatment individualization



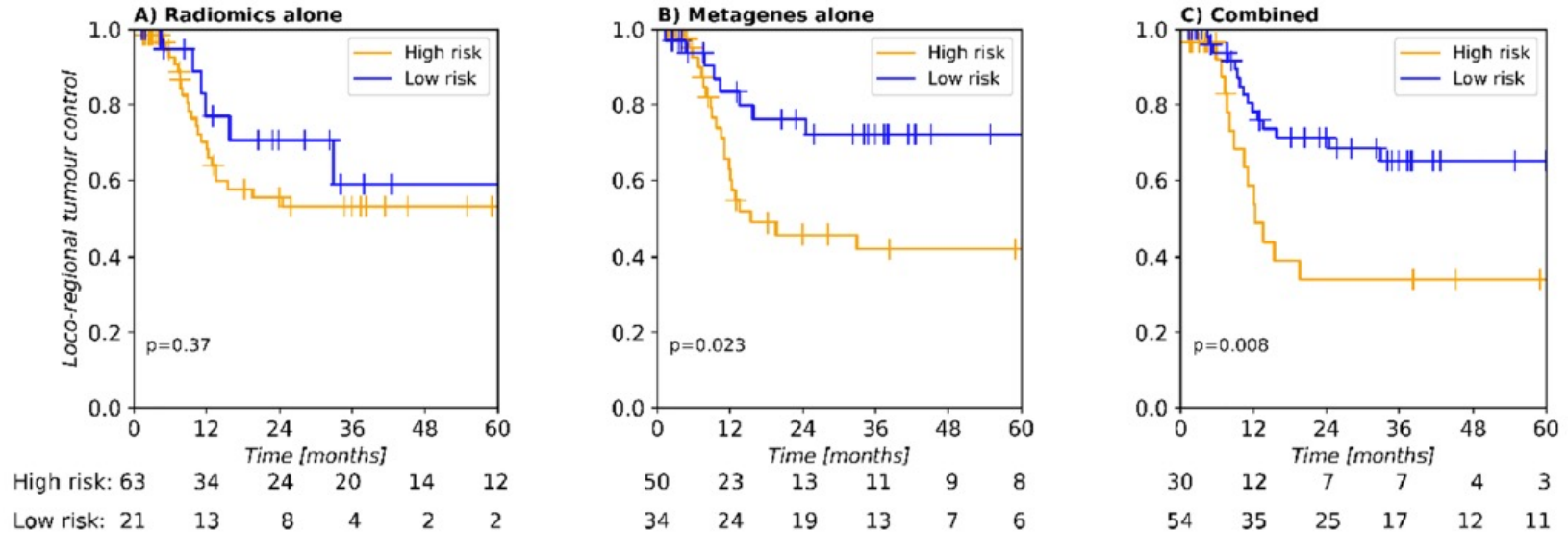
# Radiomics for treatment individualization



- 1019 patients
- $\approx$  100 stable imaging features



# RadioGenomics for treatment individualization



- 206 HNSCC patients treated by chemo-radiotherapy
- $\approx$  446 imaging features (e.g. intensity, texture, morphology)
- Four molecular subtypes



# The challenges for 2022 and beyond

- Automatic primary tumor GTV and nodal CTV delineation
- Omics profile as prognostic factor
- Omics profile to change the treatment intensity

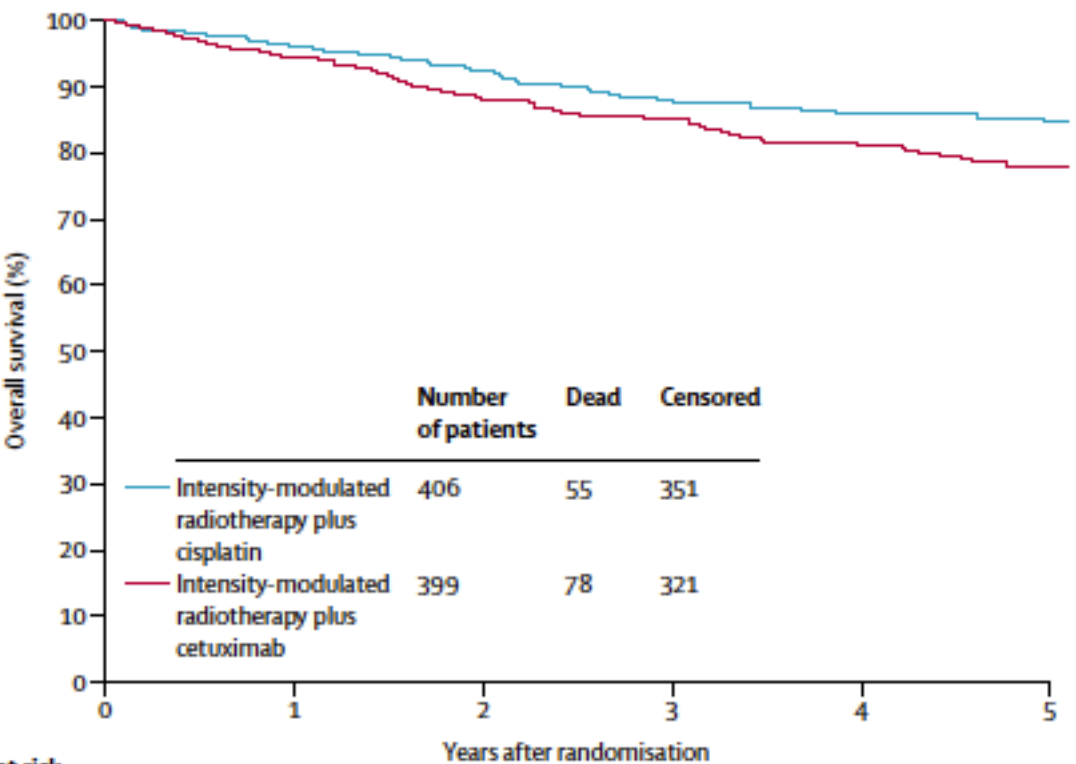




# Treatment de-intensification in HPV<sup>+</sup> H&N SCC

RTOG 1016: p16<sup>+</sup> stage III-IV oropharyngeal SCC

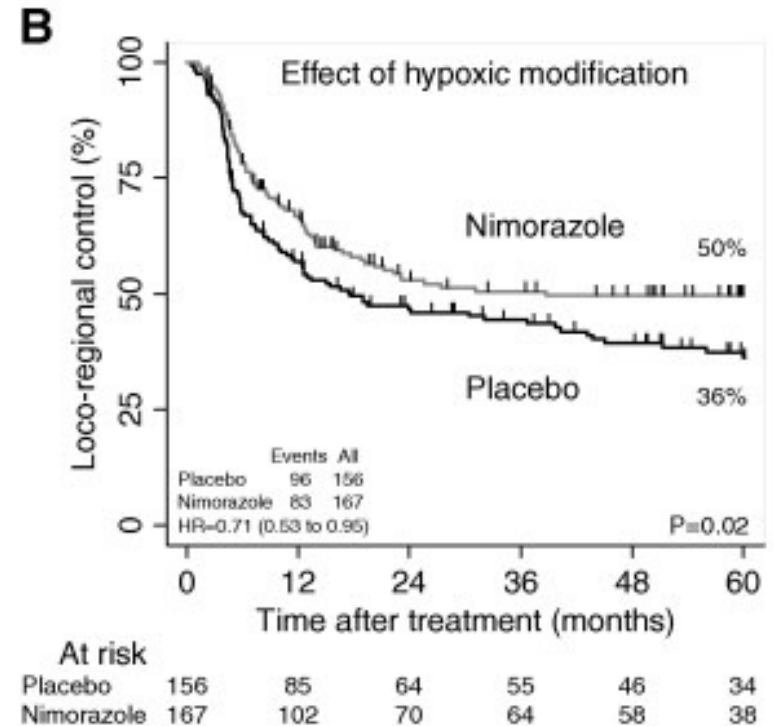
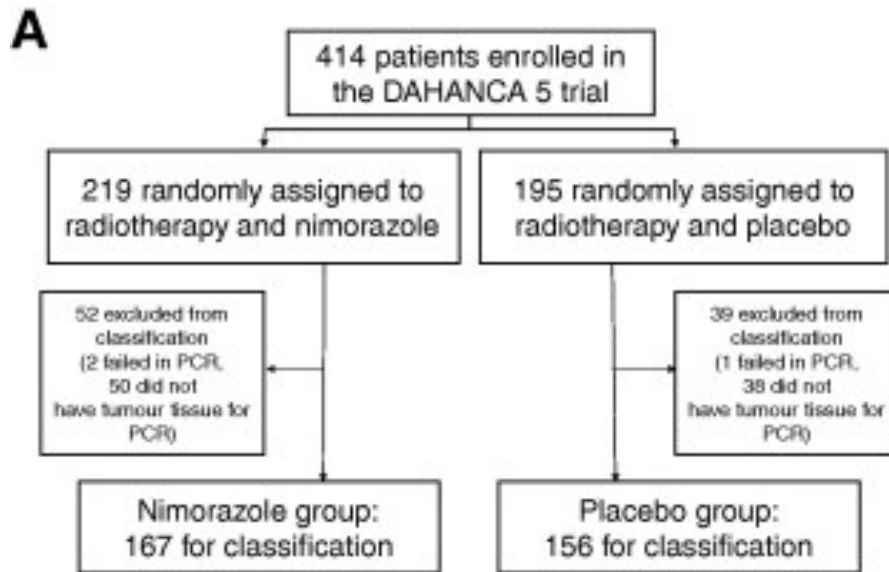
RT-cddp >< RT-cetuximab



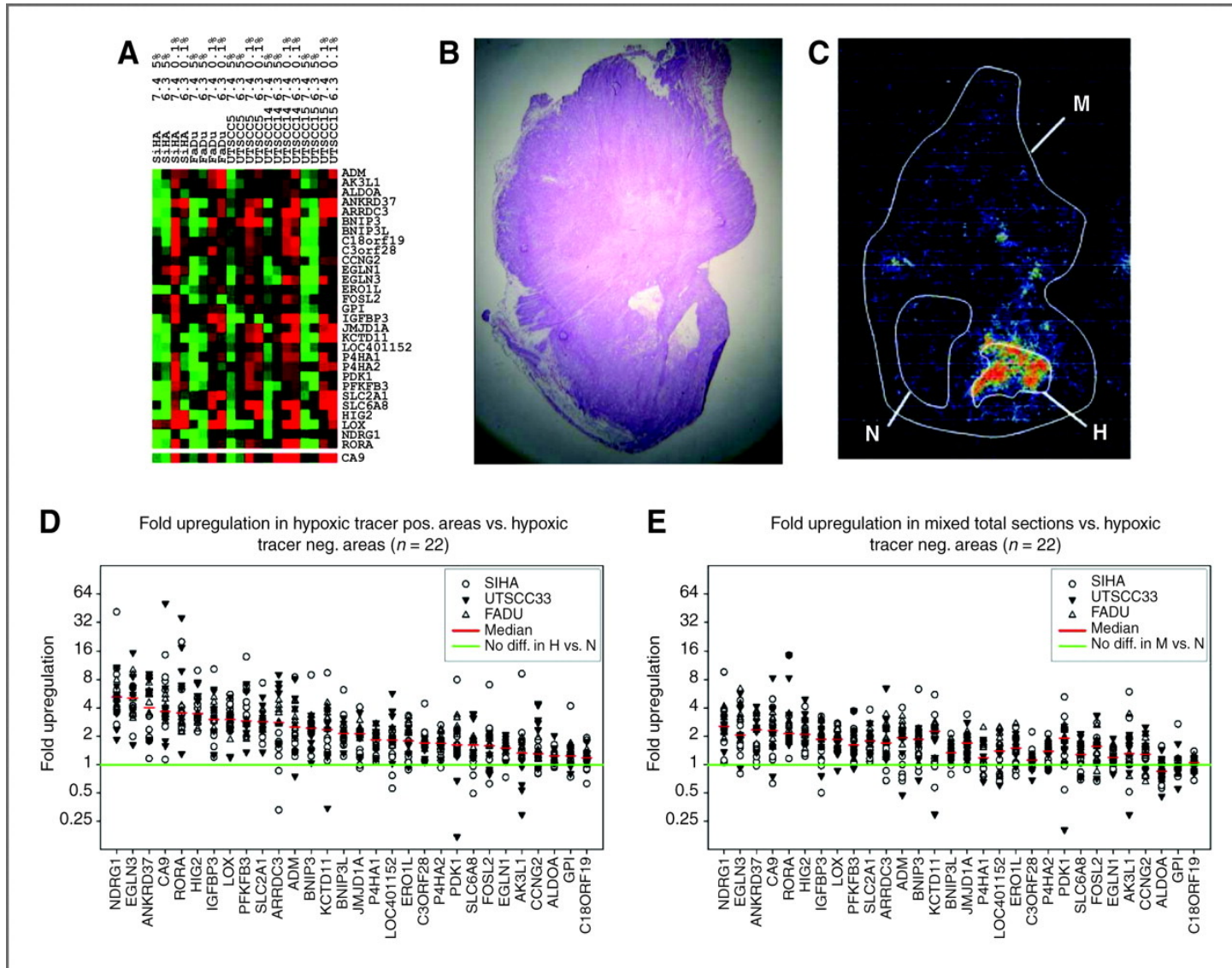
	Number at risk	0	1	2	3	4	5
Intensity-modulated radiotherapy plus cisplatin	406	372	349	314	222	100	
Intensity-modulated radiotherapy plus cetuximab	399	367	334	305	207	106	



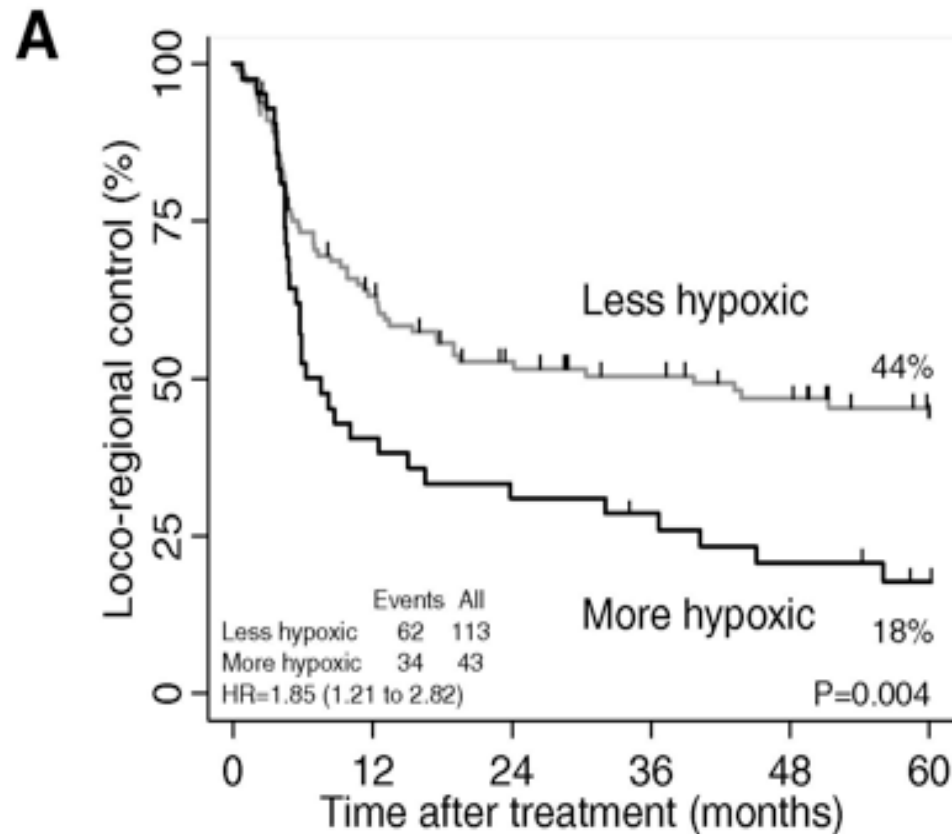
# Nimorazole as hypoxic sensitizer



# Hypoxic gene signature

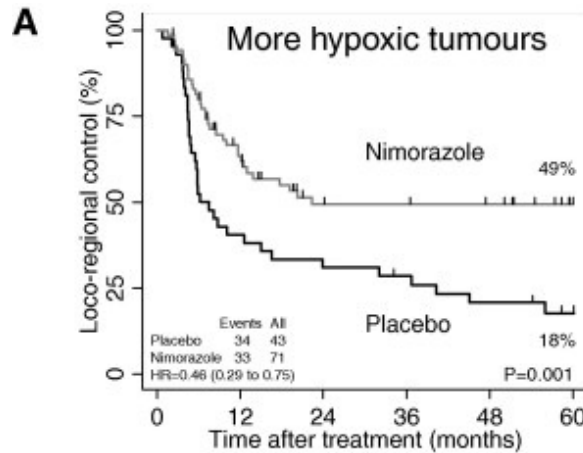


# Fifteen hypoxic gene signature in HNSCC



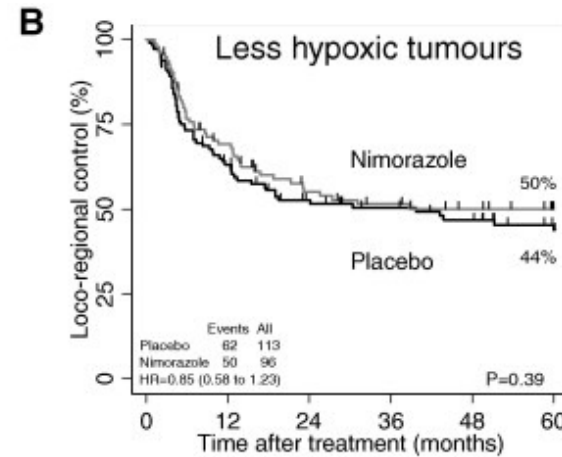
At risk							
Less hypoxic	113	68	51	44	38	29	
More hypoxic	43	17	13	11	8	5	

# Hypoxic gene signature and nimorazole in HNSCC



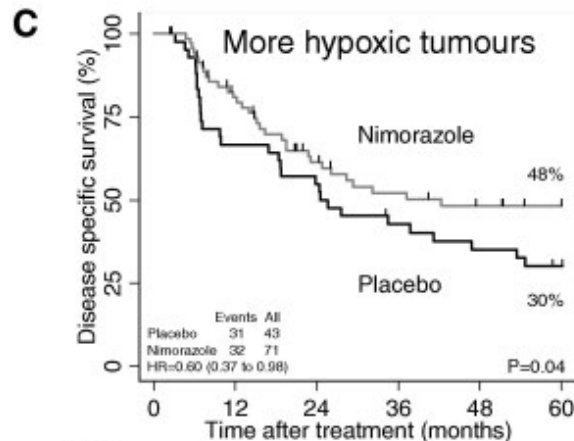
At risk

Placebo	43	17	13	11	8	5
Nimorazole	71	40	25	24	22	11



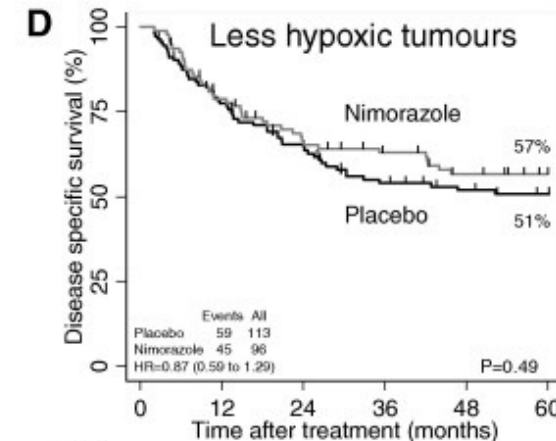
At risk

Placebo	113	68	51	44	38	29
Nimorazole	96	62	45	40	36	27




At risk

Placebo	43	28	23	17	14	11
Nimorazole	71	52	35	28	24	21



At risk

Placebo	113	85	70	55	48	44
Nimorazole	96	72	58	51	43	38



Accelerated chemo-radiotherapy with or without  
nimorazole for p16-negative HNSCC: the  
randomized DAHANCA 29 - EORTC 1219 study.

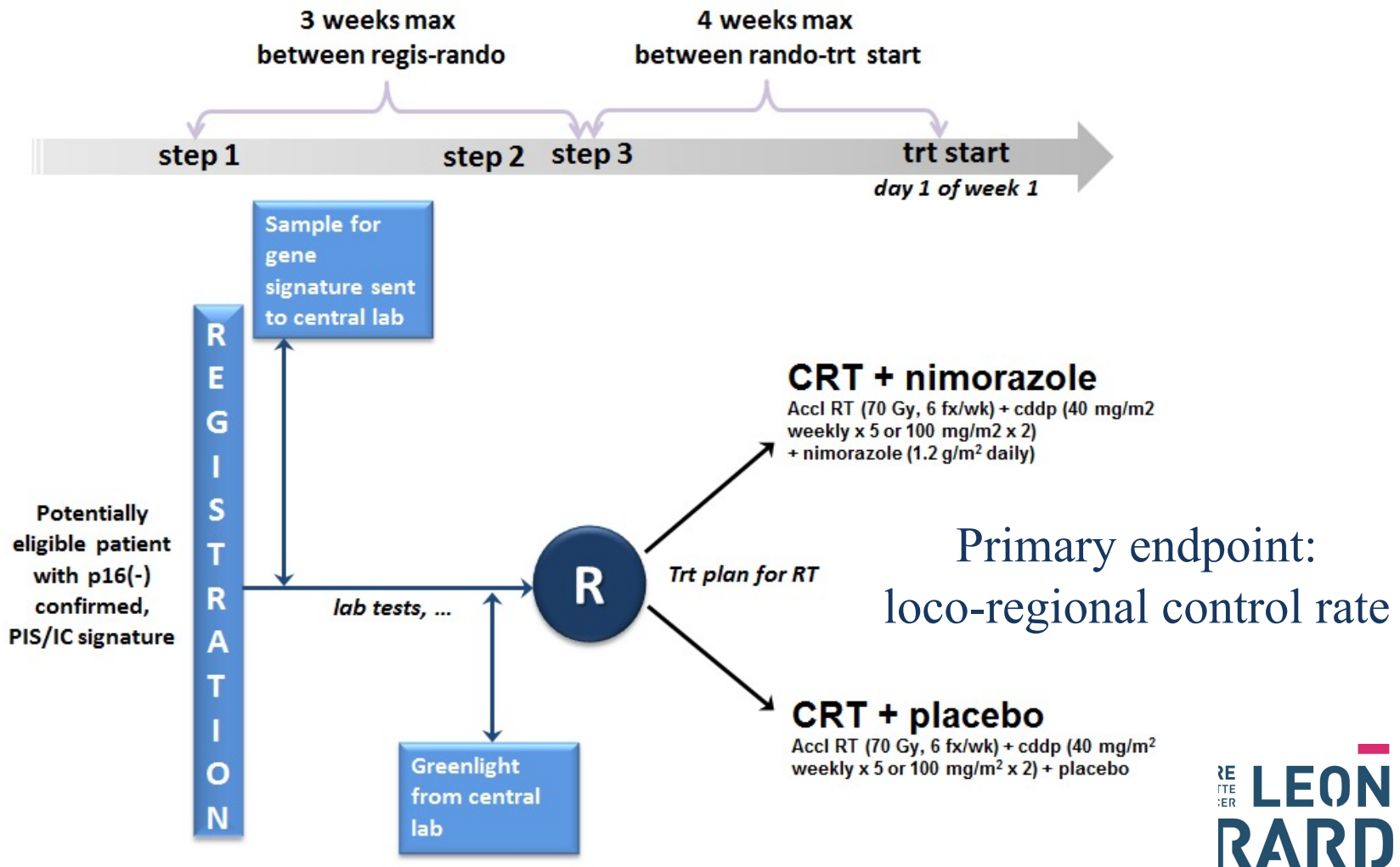
V. Grégoire, Y. Tao, J. Kaanders, J.P. Machiels, N. Vulquin, S. Nuyts,  
C. Fortpied, H. Lmalem S. Marréaud, J. Overgaard

Radiation Oncology Dept., Centre Léon Bérard, Lyon, France

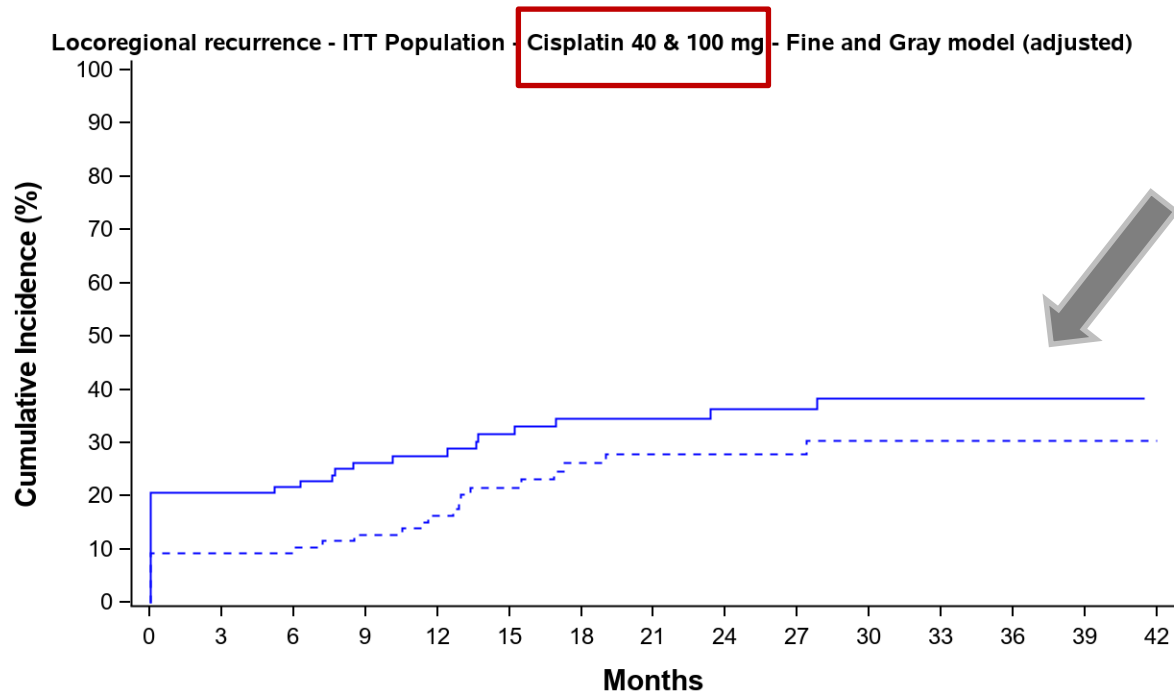


# EORTC-1219 Dahanca: study design

Blinded & randomized trial; 640 patients (200 patients in the positive hypoxic gene profile)



# Primary endpoint: loco-regional control



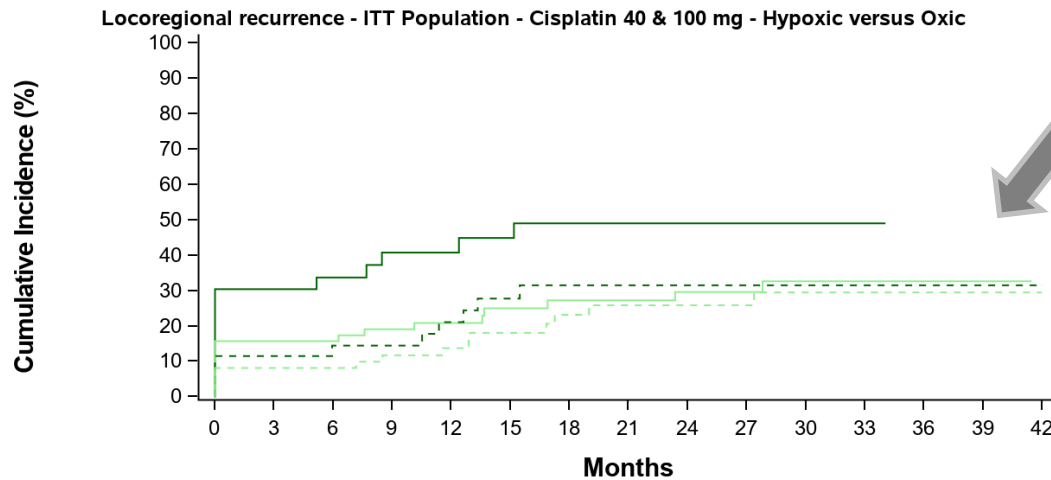
*Tail of curves driven by cisplatin 100 mg/m<sup>2</sup> only*

Randomized arm	Events/Total	Time-Point	CIF Est (95% CI)	Median (95% CI)	Adj HR (95% CI)
Nimorazole	33/97	12 months	27.5 (18.9-36.7%)	NE (NE-NE)	1.43 (0.87-2.36)
		24 months	36.2 (26.1-46.5%)		
Placebo	24/97	12 months	16.3 (9.6-24.6%)	NE (NE-NE)	Reference
		24 months	27.9 (18.5-38.1%)		

		Patients-at-Risk														
		97	71	64	52	40	34	27	26	23	18	13	9	7	4	0
Nimorazole-	97															
Placebo-	97		84	75	66	55	43	31	25	23	18	13	11	7	6	3

# Loco-regional control & hypoxic gene signature effect



*Tail of curves driven by cisplatin 100 mg/m<sup>2</sup> only*

Randomized arm * gene signature	Events/Total	Time-Point	CIF Est (95% CI)
Nimorazole / hypoxic	15/33	12 months	40.7 (23.7-57.0%)
Nimorazole / oxic	18/64	12 months	20.8 (11.8-31.5%)
Placebo / hypoxic	10/35	12 months	21.0 (9.2-36.1%)
Placebo / oxic	14/62	12 months	13.7 (6.3-23.7%)
		24 months	48.9 (30.0-65.3%)
		24 months	29.5 (18.2-41.8%)
		24 months	31.4 (16.3-47.8%)
		24 months	25.8 (14.4-38.7%)

	Patients-at-Risk														
	0	3	6	9	12	15	18	21	24	27	30	33	36	39	42
Nimorazole / hypoxic-	33	19	18	13	10	7	5	4	3	3	2	1	0		
Nimorazole / oxic-	64	52	46	39	30	27	22	22	20	15	11	8	7	4	0
Placebo / hypoxic-	35	31	27	24	21	16	10	8	6	5	4	3	1	1	1
Placebo / oxic-	62	53	48	42	34	27	21	17	17	13	9	8	6	5	2

# Summary

- AI-based automation and homogenization of OAR and TV selection and delineation
- Need of redefining the role of the Radiation Oncologist...
- Various prognostic omics signature
- No demonstration yet of omics-based treatment intensity modification



Experience is simply the name we  
give to our mistakes.

Oscar Wilde