



#### INCORPORATING DYNAMIC MOTION IN PENELOPE

C. Le Loirec, B. Poumarède, E. Barat, T. Dautremer, T. Montagu, L. Guérin, A. Batalla and D. Lazaro cindy.le-loirec@cea.fr

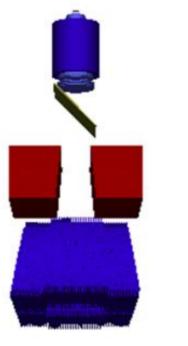
# Objectives

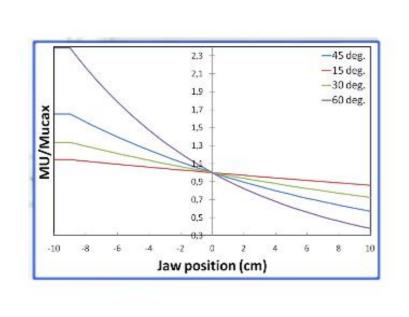
The traditional way to take time into account in Monte Carlo (MC) simulations is to simulate individual static component fields separately and integrate the results. This method can be very efficient but leads to a high level of phase space file storage. To avoid it the position probability sampling (PPS) method<sup>1</sup> in which the position of a geometrical object is treated as a random variable during the simulation has been developed. We purpose here to incorporate this method in PENELOPE in the case of a virtual wedge.

#### Monte Carlo simulation

We used the 2006 release of the Penelope code to model the Siemens Artiste linac with a full description of the Siemens 160 MLC and the OptiVue<sup>TM</sup> 1000 EPID (Siemens Medical Solutions).

Virtual wedge and motion of dynamic jaw



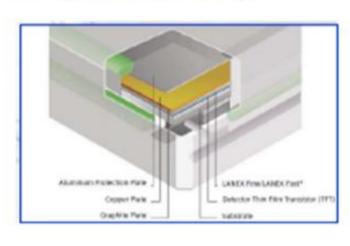


160 MLC<sup>™</sup> (Siemens)<sup>2</sup>



Optivue 1000 EPID (Siemens)<sup>3</sup>



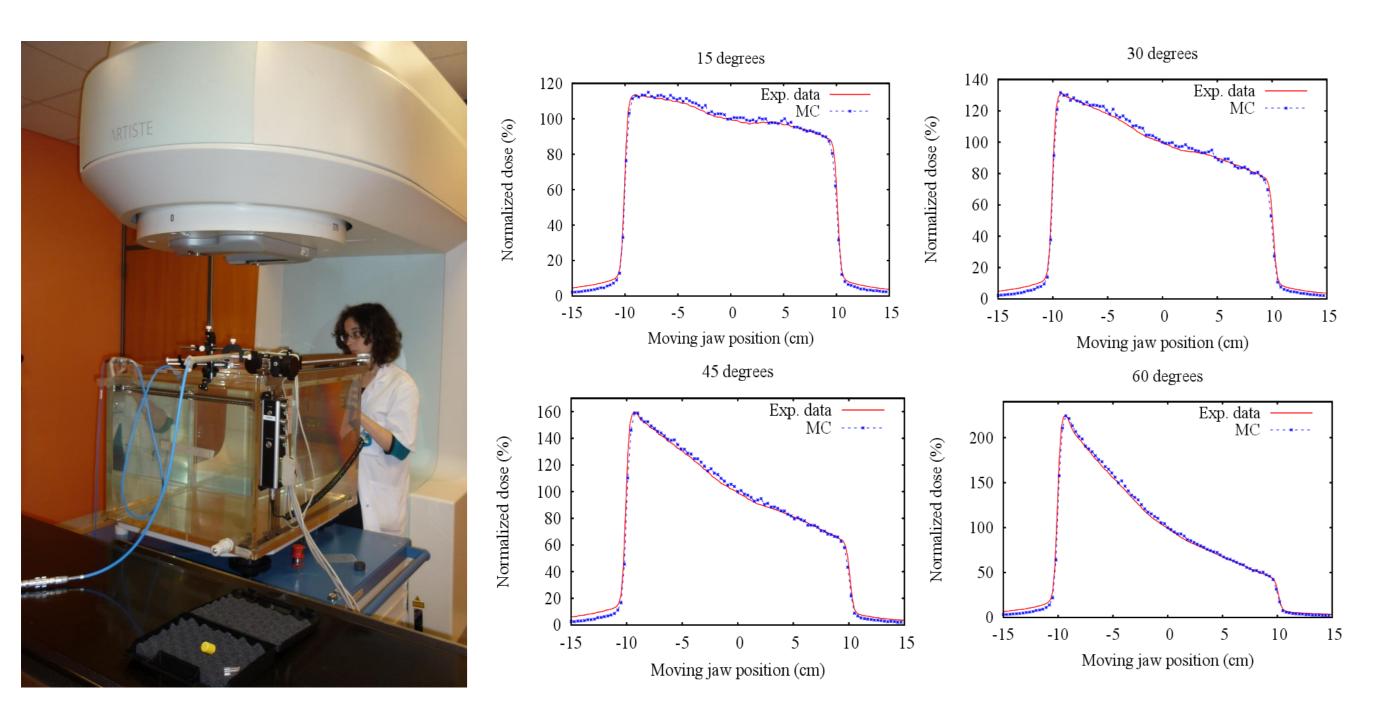


To model the dynamic jaw motion of the virtual wedge, the PPS method has been implemented in PENMAIN. This implementation required an adequate modelling of the jaws to allow their motion without a complete re-initialization of the geometry for each particle.

We have thus written a new subroutine called LOCATEVW which needs as inputs:

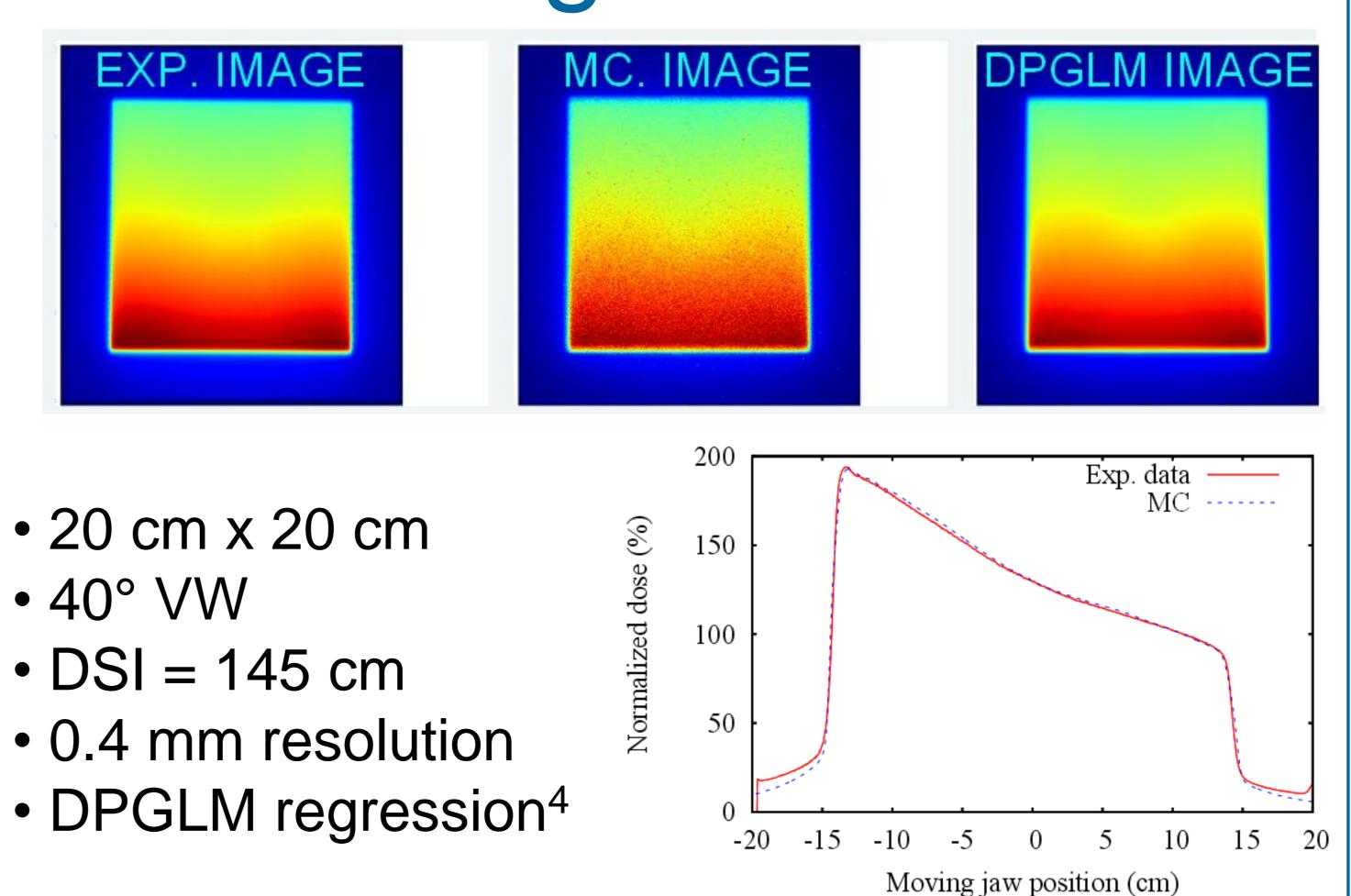
- the index of the moving jaw surface,
- the beginning and end positions of the moving jaw,
- the wedge angle  $\alpha$  and the value of  $C \times \mu$  with  $\mu$  the effective linear attenuation coefficient in water for the particular photon spectrum and C a tuning coefficient for  $\mu$ .

#### Profiles in a water tank—



- linear detector array
- 1.5 cm depth
- 20 cm x 20 cm
- 6 MV photon beam
- 100 cm SSD

## Portal images



## Conclusions

The PPS method was used to incorporate collimator motions into PENELOPE. The simulated dose profiles reproduce the experimental data with a fairly good accuracy.

## References

- <sup>1</sup> Phys. Med. Biol. **46** (2001) 2283-2298
- <sup>2</sup> MCTP 2012 Proceedings 153-158
- <sup>3</sup> MCTP 2012 Proceedings 81-86
- <sup>4</sup> Lazaro *et al* 2013 submitted in Phys. Med. Biol.





2<sup>ND</sup> ESTRO forum