

Integration of omics and systems biology

Break out session

- How high throughput techniques have been used by radiobiology so far?
- Reproducibility of system responses to radiation. Is there a signature for radiation exposure of LET?
- New approaches in mathematical modelling of radiation systems biology data
- Utilisation of “omics” approaches in biodosimetry.
- Would high throughput techniques be useful for radiation protection?
- How to optimize the interaction between the experimentalist and the modelers?

Who was there.....

0 experience in omics > card
carrying experts in omics and
statistical analysis

How high throughput techniques have been used by radiobiology so far?

- Genomics - humans at risk (fairly limited identification risk factors - only after high doses) – animals models to identify genetic modulators of risk after low and high doses
- Epigenomics – starting
- Transcriptomics – ongoing - understand the pathways, systems biology
- Proteomics –ongoing – understand the pathways, systems biology

Problem to connect the dots

- Can genomics reduce the number of candidate proteins/pathways studied by other omics ?

Reproducibility of system responses to radiation. Is there a signature for radiation exposure of LET?

Clearly differences in expression profiles – proteins and RNA, after doses as low as 10cGy can be found – but cell type specific differences, tissue differences, and radiation types and dose rates: need to be better understood

Problems:

Batch effects in expression arrays

Sample preparation /storage - standard procedures

New approaches in mathematical modelling of radiation systems biology data

- Need for approaches for analysis of time series

Utilisation of “omics” approaches in biodosimetry (exposure).

- Classical way measurement of dicentric
- Omics in the pipeline but nothing validated for low doses

Proteomics not validated

Metabolomics not validated

Biological samples – saliva, blood (finger prick)

Complications – lifestyle factors

Would high throughput techniques be useful for radiation protection?

- yes to determine linearity of responses (eg gene expression but need to connect this to a health effect)
- Identification of susceptible populations – need to identify « markers » and validate them
- But not in isolation – molecular epidemiology
- Radiation protection in a clinical setting – omics could be useful – adverse responses – early, late and very late.

Clearly useful for mechanistic studies necessary for radioprotection

How to optimize the interaction between the experimentalist and the modelers?

- Multidisciplinary teams: Have everyone on-board when designing the study
- Training
- Workshops and language lessons
- Collaborations not competition

Challenges

Analysis of time series – need improved mathematical tools, signal vs noise

Data integration – different omics – each separately possible to come up with networks but putting it together is more technically challenging ...(time points)

Data mining : The same important gene from same data

- Central databases and availability to other investigators to mine for other data
- Vocabulary

Wish list

- Open access to tissue banks/
biorepositories
- Better intergreted appoaches: easy to
generate data harder to analyse it and
validate a model