ERRATUM

Erratum to: Systems biology for molecular life sciences and its impact in biomedicine

Miguel Ángel Medina

Published online: 6 June 2013 © Springer Basel 2013

Erratum to: Cell Mol Life Sci DOI 10.1007/s00018-012-1109-z

Unfortunately, in the original publication of the article Figs. 4, 5, 6, 7 and 8 were published in low resolution. The higher resolution figures are given below.

The online version of the original article can be found under doi:10.1007/s00018-012-1109-z.

M. Á. Medina Department of Molecular Biology and Biochemistry, University of Málaga, Málaga, Spain

M. Á. Medina CIBER de Enfermedades Raras (CIBERER), Málaga, Spain

M. Á. Medina (🖂) Departamento de Biología Molecular y Bioquímica, Facultad de Ciencias, Universidad de Málaga, 29071 Málaga, Spain e-mail: medina@uma.es Fig. 4 Regulatory network around the seven signature genes predicted for pancreatic cancer by network-based ranking of marker genes in the study described in [122]. a Representation of all the direct neighbors for the seven candidates, namely, STAT3, FOS, JUN, SP1, CDX2, CDEBPA and BRCA1. **b** A subnetwork of genes regulated by FOS. c Physical protein-protein interactions between the transcription factor SP1, STAT3, JUN and FOS, and the transcription coactivator BRCA1. This figure is taken from Ref. [122], published under the Creative-Commons license





Fig. 5 A map of the major biosignaling pathways disrupted in cancer. This figure was obtained from Wikipedia Commons, originally derived from the review on the hallmarks of cancer [141]



Fig. 6 Different schedules of pharmacological treatment in time. **a** Conventional chemotherapy delivers the maximum tolerated dose in an only session or in short cycles of 2–5 days, followed by a long resting period (around 3 weeks) to allow the patient to recover. **b** Lowdose metronomic chemotherapy delivers low doses on an oscillatory or continuous schedule. Images **a** and **b** are taken from a previously published review from our group [83]. **c** Therapies can be based on delivering drugs with a single target ("single hit" treatment) or in combinations of drugs with different targets. Combinations can be delivered simultaneously or in time-staggered schedules. In this last case, the order of administration can be crucial. In the figure, the schedule "first drug B, then drug A" is not as effective as the sched-

ule "first drug A, then drug B." This is due to the fact that drug A induces a network re-wiring pushing tumor cells toward a state of increased sensitivity to drug B. This image is taken from the Preview commentary "Network medicine strikes a blow against breast cancer" [125] published in the journal *Cell* concerning the article published in the same journal describing that a sequential application of erlotinib followed by doxorubicin enhances triple-negative breast cancer cell death by rewiring apoptotic signaling networks [124]. The image is reproduced here with permission from Elsevier. **d** Other possible schedules are waiting to be tested. For instance, in the figure two different time-staggered combinations administered at two different metronomic frequencies are depicted

Fig. 7 Human disease-omes. The human disease network (a) and the disease gene network (b), taken from the original article by Goh et al. [137] published in the *Proceedings of the National Academy of Sciences* and reproduced here with permission





Fig. 8 The network of orphan diseases based on shared genes, taken from the original article by Zhnag et al. [140] published in the American Journal of Human Genetics and reproduced here with permission

from Elsevier. **a** The loosely connected 184 subnetworks of the network of orphan diseases. **b** A zoom of the largest subnetworks showing the 76 modules within it