Dear Anonymous Referee #1
Tanks for your opinion here follow the answers of your questions:
About your general comments:

1 – As you see the ultimate goal of our work is the assessment in real time, it means on line. In this way much have to be done in order to develop cytometers and methods able to cover all biological components (Viruses, Bacteria/Archea, Cyanobacteria, Fluorescent Eukaryotes and Zooplankton at the same time).
Although I already have submitted another paper to other journal (technical) describing the methods used, I will focus this paper on the technical issue as you suggested, but I thought to have submitted this article to a microbial or ecosystem functioning committee. In fact, the idea of this work was to show the behavior of the system.

2 – With the exception of the mouth of the bay and the channel which vessels can access the port, this bay is very shallow due to a large submerged sand bank. Our fixed monitoring station, for instance, is only 5 meters depth. Faced with this situation, a vertical profile did not bring much information once the water column is nearly homogeneous. On the other hand, growth activity needs incubations with tritiated leucine or thymidine which avoid the goal of real time monitoring as some other biochemical determinations. The use of two cytometers is know and show the role of viruses and bacteria in the system however, we are working to redesign the CytoBuoy system in order to became this instrument able to detect both groups.

3 – The descriptions of Brussard (2000) procedures will be included as suggested.

4 – The background noise is of Figure 2b will be included in the new figure, but it is worth to say that the presentation of gated cytograms filtering noise is a common procedure in cytometry.

5 – The term G3 was used to show that we have also detected 3 groups. To my knowledge, it is not easy to be found in natural waters (at least for us, this group sometimes is present; sometimes not). Zubkov (2001) states they are groups of proteobacteria however, I can not say this once the sample was fixed and dead, impossible to make biochemical classifications if this group was isolated by a sorter. Another way could be identification from 16S RNA what is far from our work. It is worth to say that abundance "patterns" of sub-populations of microorganism in natural samples are extremely variable due to huge variability. That is why I have used the sum of groups to find a correlation in "long-term" time series. Anyway, I will try to follow your suggestion to provide a careful and temporary description. The reference to Marie et al. 1999 will be included, sorry it was a terrible mistake.

6 – We are trying to develop a local (small scale/inside-bay) model which compartments are related to each component. Sub-populations needs more knowledge about specific interactions, it is a step forward. Separately these groups (sub-populations) did not presented any direct temporal pattern however when analyzed together we find that one shown in Figure 3. The spatial distributions of the 3 cases of SACW are the average value of them. It is a special case of this location that should be taken into account in our model. The common situation, patterns without SACW on the surface, will be presented in the new version of the article.