Cholangiocarcinoma is an important hepatobiliary cancerous disease which is extremely prevalent in Indochina (1). The patients with this cancer usually manifest severe hyperbilirubinemia and hyperalkalinephosphatasemia (2). The prognosis of disease in the patient presenting with late stage disease is usually grave (3). A local endemic chronic parasitic infection, opisthorchiasis is known for its etiopathological relationship with this cancer (4).

In the same tropical endemic area, Chikungunya virus (CHIKV) infection, another mosquito borne infection, is also prevalent. An interesting epidemiological observation is the null prevalence of concurrent CHIKV infection and cholangiocarcinoma.

Objectives
In this study, the authors used bioinformatics pathway analysis for clarification on this interesting phenomenon. From analysis, no co-occurrence of the two diseases is explainable from the pathway network.

Materials and Methods
Based on bioinformatics technique, the authors used standard pathway expression analysis, as used in referenced publication (7), for network appraisal. Starting from database literature searching for the reports on the pathway described in cholangiocarcinoma and CHIKV virus infection, the identified collected pathways from all reports were assessed to determine the common pathway between the two disorders (CHIKV infection and cholangiocarcinoma). The network mapping of the identified common pathway was further performed to represent the possible same pathomechanism.

Results
There are detected common pathways between CHIKV infection and cholangiocarcinoma (8, 9). The identified common node from network analysis is the vimentin expression. The competitive mechanism in case with concurrent CHIKV infection and cholangiocarcinoma is observed and hereby presented in Figure 1.
Discussion
The pathway mapping with expression analysis is an important standard informatics tool for clarification on the pathogenesis of medical disorders. In oncology, this bioinformatics technique can be applied for appraisal of the complex pathological network in malignancy. Also, the situation of co-pathology between cancer and non-cancer diseases can be analyzed by this approach. The good example is the previous publication using network analysis for clarifying the pathophysiological process in co-occurrence of hepatitis C infection and renal cell carcinoma (7).

In this report, the authors successfully identified the common pathways via vimentin between CHIKV infection and cholangiocarcinoma. While CHIKV uses vimentin for replication process, the carcinoma cholangiocarcinoma cell uses vimentin in metastasis and cellular migration. It is no doubt that this is a competitive process between the two medical problems. In fact, both disorders, CHIKV infection and cholangiocarcinoma, are common in Indochina, however, there is no report on co-occurrence of the two diseases. Of interest, the concurrence between dengue and other less common malignancy such as osteosarcoma is published in the literature (10).

Conclusion
The identified competitive mechanism via vimentin is a possible explanation for the observation of non-concurrence in the tropical endemic Indochina setting of both public health problems.

Authors’ contribution
Both authors wrote the manuscript equally.

Conflict of interests
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Ethical issues (including plagiarism, misconduct, data fabrication, falsification, double publication or submission, redundancy) have been completely observed by the authors.

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