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Aims and Scope
Basic & Clinical Pharmacology & Toxicology is an independent journal, publishing original scientific research in all fields of toxicology, basic and clinical pharmacology. This includes experimental animal pharmacology and toxicology and molecular (-genetic), biochemical and cellular pharmacology and toxicology. It also includes all aspects of clinical pharmacology: pharmacokinetics, pharmacodynamics, therapeutic drug monitoring, drug/drug interactions, pharmacogenetics/-genomics, pharmacoepidemiology, pharmacovigilance, pharmacoeconomics, randomized controlled clinical trials and rational pharmacotherapy. For all compounds used in the studies, the chemical constitution and composition should be known, also for natural compounds.

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heated at 160 °C for 24 h, removed the upper layer of solution, collected the precipitate, washed by deionized water and ethanol to neutral, and dried at 160 °C for 6 h.

Results: The XRD results show that the resulting products are mainly depend on the pH value of solution. Pure phase of Bi_5O_7Br can be obtained when the pH value is 11.0, and only BiOBr formed when the pH value is 1.0. The SEM and TEM images show that the synthesized Bi_5O_7Br is a layered structural particles with four angles star-shape, and the average particle size is about 27 μm. According to the Uv-vis spectra test curves, the theoretical calculation results indicate that the band-gap width of Bi_5O_7Br is 2.52 eV, which is much lower than that of TiO_2 (3.0 eV for rutile and 3.2 eV for anatase). After 5 and 20 minutes irradiation by visible light, the decolorization rate of Rhodamine solution by TiO_2 was 10 % and 22 % respectively, while that by Bi_5O_7Br was 93 % and 99 % respectively.

Conclusions: Well dispersed Bi_5O_7Br crystals with layered structure and tetragonal star shape have been obtained by simple hydrothermal synthesis. The Bi_5O_7Br has good visible-light photocatalytic performance and is expected to be widely used in the fields of catalytic degradation, disinfection and sterilization.

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095 | Digital microfluidic biochip routing method considering contamination and washing capacity

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Objectives: As an emerging device in biochemistry, digital microfluidic biochips (DMFBs) can integrate a series of basic operations into a few square centimeter chips. By embedding a programmable electrode array on the chip, DMFBs can independently control the movement of each discrete sample droplet. For a complete bioassay on the DMFBs, it will be divided into a series of successive sub-problems to be performed separately. In the process of execution, most of electrodes would be shared by different sample droplets for the limited of the number of electrodes. Thus, contaminations caused by liquid residues among droplets are inevitable and lead to lethal errors in bioassays. To remove the contaminations, washing operation is essential to ensure the correctness of bioassay. However, existing works either ignored the continuity of sub-problems and clean the contaminations only within a single sub-problem, or ignored the realistic capacity constraint of washing droplets and clean all contaminations only used a few of washing droplets. Moreover, simply deploying washing operations with droplet routing may increase the execution time of a bioassay, which is not feasible for timing-critical bioassay. To effectively remove contaminations and minimize the execution time, it is desirable to consider routing and washing all sub-problems simultaneously.

Methods: To effectively remove contaminations and minimize the execution time of a bioassay, we propose a contamination-aware routing method with realistic washing capacity constraint. Firstly, we present a top-down scheme to generate candidates of routing paths for each sub-problem, and then we construct a shortest-path model to select desirable routing solution for all sub-problems. With a decision diagram of droplets, we further propose an integer linear programming (ILP) formulation to compact the execution time of bioassay. Finally, a washing method considering realistic washing capacity is proposed to remove contaminations for all sub-problems.

Results: To evaluate the performance of simultaneous consideration of sub-problems, we compared the results obtained by simultaneous consideration with the results achieved by separately processing the sub-problems on the real-life benchmarks (e.g., In vitro diagnosis, Protein detection). Experimental results show that our proposed method significantly reduces 72% contaminations and saves 11% execution time of bioassays. Consequently, our proposed method improves both the sensitivity and efficiency of bioassays.

Conclusions: We presented a novel flow to solve the routing and washing problem with capacity constraint by simultaneous considering all sub-problems in DMFBs. Firstly, we presented an incremental iteration procedure to generate route candidates. Secondly, we proposed an optimal ILP to compact execution time. Finally, cleaning contamination by washing droplets with limited washing capacity is simultaneously considered for all sub-problems. Experimental results shown that our method can greatly reduce the number of contaminations and execution time of bioassays.

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