Supplementary Materials B: molecular and numerical dissipation in root-mean-square budgets

As mentioned in Section 4.3, we have observed non-negligible levels of spurious numerical dissipation with the CFD solver that we have retained for the study, *i.e.*, the parallel code AVBP (Schonfeld & Rudgyard 1999; Moureau *et al.* 2005), which employs a time-explicit finite-element two-step Taylor-Galerkin scheme (Colin & Rudgyard 2000) which provides third-order accuracy in space and time.

AVBP is commonly used for unstructured meshes on very complex industrial applications. The numerical scheme relies on a distributed-residual scheme in a cell-vertex approach, which is less-widespread and makes delicate the computation of the different terms in the various root-mean-square budgets. Furthermore, since we have preferred to post-treat the different terms with standard spatial discretisation on the structured grid, our post-processing includes a possible discretisation error with the actual terms seen by the numerical scheme. These errors lead to an underestimated level of molecular dissipation, and yield unclosed root-mean-square balances. We have observed this issue on both budgets of enthalpy $\widetilde{h''h''}$ and turbulent kinetic energy k, and we have further investigated. As we explain hereinafter, we have identified that the molecular dissipation could be safely estimated as the complementary term to all the others, so that the sum of all terms gives exactly zero, yielding a closed balance.

We have performed the DNS of an adiabatic $2\pi\delta$ channel flow at $\mathrm{Re}_\tau = 180$ with two meshes. The former has similar resolution to the one used in our work, and in agreement with the usual resolutions of the literature, in particular Kawamura *et al.* (2000); we will call it M1. The latter, instead, has been extremely (and excessively) refined: $256 \times 192 \times 256$ points in the streamwise, wall-normal and spanwise directions, respectively, for a total of ~ 12.5M nodes; we will call it M2. More information is given in table 1.

We have extracted the budgets of k in both cases, and obtained the results shown in figure 1. As one can see, M1 does not allow us to close the balance when each term is computed according to its definition. With M2, the balance is, on the other hand, perfectly closed. Observe that the only term which strongly varies between the two is the computed dissipation; other than that, there are negligible discrepancies near the wall for the molecular diffusion and near the peak for the production. Hence, the imbalance seen with M1 is largely retrieved within the molecular dissipation computed on M2. This proves that our problem is due to the computed molecular dissipation which (i) can be degraded in our post-processing of the cell-vertex scheme and (ii) should be augmented with the residual numerical dissipation.

Since the resolution of M2 would be infeasible in our simulation's domain (which, recall, is $22\pi\delta$-long in the streamwise direction), we have retained a pragmatic determination of dissipation in the present study: we have added the imbalance to the computed physical dissipation to yield a total dissipation. Concerning the wall-normal turbulent heat flux $\widetilde{v''h''}$, we have encountered much fewer issues, since molecular dissipation plays a less significant role and the dominating loss term is $\overline{h'\partial p'/\partial y}$, which is well predicted.

	Size	Number of nodes	ΔX^+	ΔZ^+	ΔY^+
M1	100, 179, 100	1.79M	11.3	5.65	0.34-3.1
M2	256, 192, 256	12.5M	4.42	2.2	0.34-2.23

Table 1: Size, number of nodes and resolutions of M1 and M2.

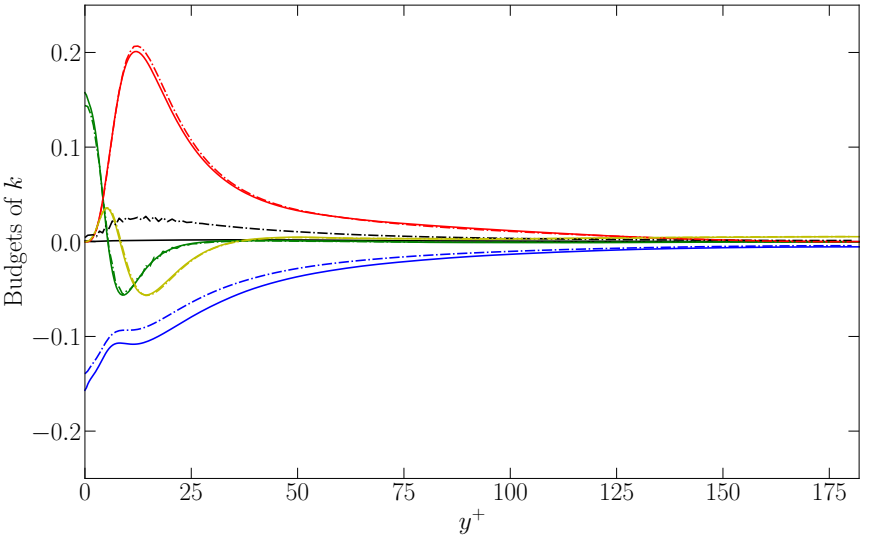

Figure 1: Budgets of k. Production (red), dissipation (blue), molecular diffusion (green), turbulent diffusion (yellow), sum of terms (black). M1 (dashed-dotted lines), M2 (solid lines).

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